

Result No.	Score	Query	Length	DB	ID	Description
1	2077.2	70.0	2913	6	AX814112	AX814112 Sequence
2	2077.2	70.0	2913	6	AX816331	AX816331 Sequence
3	1973.8	66.5	79178	8	AX303170	Solanum b
4	1880.8	63.4	3971	6	AX814116	AX814116 Sequence
5	1880.8	63.4	3971	6	AX816335	AX816335 Sequence
6	1880.8	63.4	3971	8	AY426261	Solanum b
7	1876.2	63.2	163635	8	AY303171	Solanum b
8	1832.2	61.8	3689	8	AY426264	Solanum t
9	1805.8	60.9	3592	6	AX814113	Sequence
10	1805.8	60.9	3592	6	AX816332	AX816332 Sequence
11	1805.8	60.9	5191	6	AX816333	AX816333 Sequence
12	1805.8	60.9	6824	8	AY336128	Solanum b
13	1805.8	60.9	7349	6	AX814114	Sequence
14	1805.8	60.9	7349	8	AY426259	Solanum b
15	1797.2	60.6	3641	8	AY426266	Solanum t
16	1786.2	60.2	3344	8	AY426265	Solanum t
17	1771.6	59.7	3260	6	AX814115	Sequence
18	1771.6	59.7	3260	6	AX816334	Sequence
19	1771.6	59.7	3260	8	AY426260	Solanum b

C	20	1736.2	58.5	3899	6	AX814117	Sequence
C	21	1736.2	58.5	3899	6	AX816336	Sequence
C	22	1736.2	58.5	3899	8	AY426262	Solanum b
C	23	1736.2	58.5	79178	8	AY303170	Solanum b
C	24	1734.6	58.5	163635	8	AY303171	Solanum b
C	25	1719.2	57.9	3196	8	AY426263	Solanum b
C	26	624.6	21.1	693	8	AP040480	Lycopersi
C	27	600.6	20.2	53203	8	AP006683	Lotus cot
C	28	592.6	20.0	120197	2	AC124216	Medicago
C	29	575	19.4	119925	8	AC123572	Medicago
C	30	554.2	18.7	118130	2	AC148359	Medicago
C	31	552.4	18.6	120576	8	AC136141	Medicago
C	32	547	18.4	696	8	AP040483	Lycopersi
C	33	544.4	18.3	708	8	AP040455	Lycopersi
C	34	542.2	18.3	124857	8	AC134049	Medicago
C	35	541.6	18.3	137702	8	AC126785	Medicago
C	36	540.4	18.2	122167	8	AC146806	Medicago
C	37	539.4	18.2	133198	2	AC137553	Medicago
C	38	538	18.1	146813	2	AC135162	Medicago
C	39	533.2	18.0	122089	8	AC137552	Medicago
C	40	530.4	17.9	65807	2	AC146556	Medicago
C	41	517.2	17.4	128758	2	AC133864	Medicago
C	42	497.8	16.8	65807	2	AC146556	Medicago
C	43	494.2	16.7	705	8	AF040482	Lycopersi
C	44	494	16.6	114098	8	AC144459	Medicago
C	45	479.2	16.2	122058	2	AC135312	Medicago

ALIGNMENTS

RESULT 1
AX814112

DEFINITION 35 Sequence from Patent EP1334979.

VERSION AX814112.1 GI:39103414

SOURCE	Solanum bulbocastanum
ADAMSON, A. J. 1971	1971

Eukaryota; Viridiplanta

asterids; lamids; sola

AUTHORS van der Vossen, E.A. and

in solanaceae

Kweek- en Researchbedrijf

Source	1. .2913
--------	----------

```
/mol_type="una
```

```
misc_feature    1.2913
```

ORIGIN

Query Match	70.0%; S
-------------	----------

Matches 2495; Conservative 0;

QY 1 ATGGCTGAGCTTTCCTTCA

Db 1 ATGGCTGAAGCTTTCATTCAA

61 CTGGATTGATTC TTGCTTT

Db 61 CTTGTAATGCTTTTCGGTTT

QY 121 ATCCAAGCTGTGCTAGAGATT

Db 121 ATTCAGCCGTCCTTGAAGATT

```
OY 181 TGGTGCAGAACTCAATGCTGTCATATGAGGCTGATGACATCTGGAGCATGTAA 240
DB 181 TGGTGCAGAACTCAATGCTGTCATATGAGGCTGATGACATCTGGAGCATGTAA 240
OY 241 ACTGAGGACCAATAGACAGAGAGAAACAATATGGGTGTATCATCCAAACGTTATC 300
DB 241 ACTGAGGACCAATAGACAGAGAGAAACAATATGGGTGTATCATCCAAACGTTATC 300
OY 241 ACCAAGGCCACA--AGATTCTCCAGTCTGAATATGGCGTTATCATCCAAAGGTTATC 297
DB 241 ACCAAGGCCACA--AGATTCTCCAGTCTGAATATGGCGTTATCATCCAAAGGTTATC 297
OY 301 ACTTTGCTCAACAATTTGGGAAAAAGATGAAAAAGATTATGAGAAACTAGATGTAT 360
DB 301 ACTTTGCTCAACAATTTGGGAAAAAGATGAAAAAGATTATGAGAAACTAGATGTAT 360
OY 298 CTTTTCCTGCAAGAGTGGGAAAAAGATGACCAAGTATGAAAAAATAAGCAAT 357
DB 298 CTTTTCCTGCAAGAGTGGGAAAAAGATGACCAAGTATGAAAAAATAAGCAAT 357
OY 361 GCAAGGGAACGAATTAAGTTTCATTTGATGAAAGACTATAGAGACAAGTGTCTCA 420
DB 361 GCAAGGGAACGAATTAAGTTTCATTTGATGAAAGACTATAGAGACAAGTGTCTCA 420
OY 358 GCTGAGGAAAAAGAAATTTTTCATTTGACGAAAAATTTGAGAGACACGCTTTTGA 417
DB 358 GCTGAGGAAAAAGAAATTTTTCATTTGACGAAAAATTTGAGAGACACGCTTTTGA 417
OY 421 CGCCAAACAGGTTTGTATTGATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAC 480
DB 421 CGCCAAACAGGTTTGTATTGATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAC 480
OY 418 CGGGAACAGGTTTGTATTGATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAT 477
DB 418 CGGGAACAGGTTTGTATTGATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAT 477
OY 481 GAGATAGGAAAAATCTGATTAACAATGTAGCATGCCCCAAACCTTCCAGTCTCCCA 540
DB 481 GAGATAGGAAAAATCTGATTAACAATGTAGCATGCCCCAAACCTTCCAGTCTCCCA 540
OY 478 GAGATAGGAAAAATCTGATTAACAATGTAGCATGCCCCAAACCTTCCAGTCTCCCA 537
DB 478 GAGATAGGAAAAATCTGATTAACAATGTAGCATGCCCCAAACCTTCCAGTCTCCCA 537
OY 541 ATACTTGGTATGGGGGAGCTAGGAAGAAGCACTTGGCCAAATGCTTCAATGATCAG 600
DB 541 ATACTTGGTATGGGGGAGCTAGGAAGAAGCACTTGGCCAAATGCTTCAATGATCAG 600
OY 538 ATACTTGGTATGGGGGAGCTAGGAAGAAGCACTTGGCCAAATGCTTCAATGATCAG 597
DB 538 ATACTTGGTATGGGGGAGCTAGGAAGAAGCACTTGGCCAAATGCTTCAATGATCAG 597
OY 601 AGAGTAATTTGAGCATTTCCATCCCAAAATTTGATTTGTCTGGAGATTTTATGAG 660
DB 601 AGAGTAATTTGAGCATTTCCATCCCAAAATTTGATTTGTCTGGAGATTTTATGAG 660
OY 598 AGAGTATCTGAGCATTTCCATCCCAAAATTTGATTTGTCTGGAGATTTTATGAG 657
DB 598 AGAGTATCTGAGCATTTCCATCCCAAAATTTGATTTGTCTGGAGATTTTATGAG 657
OY 661 AAGAGTGTATTAAGGAATTTGATCTATTTGAAGAAAGTGC--ACTTGGTGGCAGT 717
DB 661 AAGAGTGTATTAAGGAATTTGATCTATTTGAAGAAAGTGC--ACTTGGTGGCAGT 717
OY 658 AAGAGTGTATTAAGGAATTTGATCTATTTGAAGAAAGTGC--ACTTGGTGGCAGT 717
DB 658 AAGAGTGTATTAAGGAATTTGATCTATTTGAAGAAAGTGC--ACTTGGTGGCAGT 717
OY 718 GACTTGGCTCACTTCAAAAGAGCTTGGGACTTGTGAATGAAAAAATATTTGCTC 777
DB 718 GACTTGGCTCACTTCAAAAGAGCTTGGGACTTGTGAATGAAAAAATATTTGCTC 777
OY 718 GACTTGGCTCACTTCAAAAGAGCTTGGGACTTGTGAATGAAAAAATATTTGCTC 777
DB 718 GACTTGGCTCACTTCAAAAGAGCTTGGGACTTGTGAATGAAAAAATATTTGCTC 777
OY 778 GTCTTAGATGATTTTGGATGATGAGATCAAGTAATGGGCTAAGTTAAGCAAGTCTTG 837
DB 778 GTCTTAGATGATTTTGGATGATGAGATCAAGTAATGGGCTAAGTTAAGCAAGTCTTG 837
OY 778 GTCTTAGATGATTTTGGATGATGAGATCAAGTAATGGGCTAAGTTAAGCAAGTCTTG 837
DB 778 GTCTTAGATGATTTTGGATGATGAGATCAAGTAATGGGCTAAGTTAAGCAAGTCTTG 837
OY 838 AAGGTGAGCAAGTGGGCTTGTCTTAACAACACTACTCGTCTTAAGAAAGATTTGATG 897
DB 838 AAGGTGAGCAAGTGGGCTTGTCTTAACAACACTACTCGTCTTAAGAAAGATTTGATG 897
OY 838 AAGGTGAGCAAGTGGGCTTGTCTTAACAACACTACTCGTCTTAAGAAAGATTTGATG 897
DB 838 AAGGTGAGCAAGTGGGCTTGTCTTAACAACACTACTCGTCTTAAGAAAGATTTGATG 897
OY 898 ATTAATGGGACATTTGCAACCATATGAATTTGCAATTTGTCTCAAGAGATTTGTTG 957
DB 898 ATTAATGGGACATTTGCAACCATATGAATTTGCAATTTGTCTCAAGAGATTTGTTG 957
OY 898 ATTAATGGGACATTTGCAACCATATGAATTTGCAATTTGTCTCAAGAGATTTGTTG 957
DB 898 ATTAATGGGACATTTGCAACCATATGAATTTGCAATTTGTCTCAAGAGATTTGTTG 957
OY 958 TTGTTCAATGCAACGTGCTTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGCTATC 1017
DB 958 TTGTTCAATGCAACGTGCTTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGCTATC 1017
OY 958 TTGTTCAATGCAACGTGCTTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGCTATC 1017
DB 958 TTGTTCAATGCAACGTGCTTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGCTATC 1017
OY 1018 GGAAGAGGATTTGAAAAAATGTGTGTGCTCTAGCAGGCTTAAACCTTTGAGAGT 1077
DB 1018 GGAAGAGGATTTGAAAAAATGTGTGTGCTCTAGCAGGCTTAAACCTTTGAGAGT 1077
OY 1018 GGAAGAGGATTTGAAAAAATGTGTGTGCTCTAGCAGGCTTAAACCTTTGAGAGT 1077
DB 1018 GGAAGAGGATTTGAAAAAATGTGTGTGCTCTAGCAGGCTTAAACCTTTGAGAGT 1077
OY 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAAACATGTAGAGATAGTGAATTTGG 1137
DB 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAAACATGTAGAGATAGTGAATTTGG 1137
OY 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAAACATGTAGAGATAGTGAATTTGG 1137
DB 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAAACATGTAGAGATAGTGAATTTGG 1137
OY 1138 AAATTTGCTCAAGAAAGATTTTCTATCTGCTGCTCCCTGAGACTTAAGTACATCACTT 1197
DB 1138 AAATTTGCTCAAGAAAGATTTTCTATCTGCTGCTCCCTGAGACTTAAGTACATCACTT 1197
OY 1138 AAATTTGCTCAAGAAAGATTTTCTATCTGCTGCTCCCTGAGACTTAAGTACATCACTT 1197
DB 1138 AAATTTGCTCAAGAAAGATTTTCTATCTGCTGCTCCCTGAGACTTAAGTACATCACTT 1197
OY 1198 CCACTTGAATTTGAGACATGCTTTACATATGTCAGATATCCCAAGAGATCCGAATG 1257
DB 1198 CCACTTGAATTTGAGACATGCTTTACATATGTCAGATATCCCAAGAGATCCGAATG 1257
OY 1198 CCACTTGAATTTGAGACATGCTTTACATATGTCAGATATCCCAAGAGATCCGAATG 1257
DB 1198 CCACTTGAATTTGAGACATGCTTTACATATGTCAGATATCCCAAGAGATCCGAATG 1257
```

```
OY 1258 GAAAAAGGAATCTAATCTCTCTCGATGAGCAGATGTTTATTTATTCAGAAAGAAC 1317
DB 1258 GAAAAAGGAATCTAATCTCTCTCGATGAGCAGATGTTTATTTATTCAGAAAGAAC 1317
OY 1318 TTGAGCTAGAGAAATGATGATGAAATGAAATGAAATTAATCTTGAAGTCTTCTTC 1377
DB 1318 TTGAGCTAGAGAAATGATGATGAAATGAAATGAAATTAATCTTGAAGTCTTCTTC 1377
OY 1318 ATGAGGCTAGAGATGAGGAGATGAGATGAAAGATTAATCTTGAAGTCTTCTTC 1377
DB 1318 ATGAGGCTAGAGATGAGGAGATGAGATGAAAGATTAATCTTGAAGTCTTCTTC 1377
OY 1378 CAAGAGATGAAATGAAATCTGCTCAACCTTATTTCAAGATGATGATTCATCATGAT 1437
DB 1378 CAAGAGATGAAATGAAATCTGCTCAACCTTATTTCAAGATGATGATTCATCATGAT 1437
OY 1438 CTGGCAACATCTCAATTTTGGGCAAGACATCAAGCAGCAATATCCAGAAATATGTGA 1497
DB 1438 CTGGCAACATCTCAATTTTGGGCAAGACATCAAGCAGCAATATCCAGAAATATGTGA 1497
OY 1438 TTGGCAACATCTCTGTTTGAAGCAACATCAAGCAGCAATATCCAGAAATATGTGA 1497
DB 1438 TTGGCAACATCTCTGTTTGAAGCAACATCAAGCAGCAATATCCAGAAATATGTGA 1497
OY 1498 GAAAAATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1498 GAAAAATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
OY 1498 CACAGTTACACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1498 CACAGTTACACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
OY 1558 TTCCACTTGAAGAGTGTGCTGCTGAGAGGCTGTTAATCTAAGTGCATTAACCTTAAG 1617
DB 1558 TTCCACTTGAAGAGTGTGCTGCTGAGAGGCTGTTAATCTAAGTGCATTAACCTTAAG 1617
OY 1558 CCCCCCTTGAAGAGTGTGCTGCTGAGAGGCTGTTAATCTAAGTGCATTAACCTTAAG 1617
DB 1558 CCCCCCTTGAAGAGTGTGCTGCTGAGAGGCTGTTAATCTAAGTGCATTAACCTTAAG 1617
OY 1618 CAGTTACCGTCTTCCATTTGAGAGATCTAGTACATTTAAGATACCTTAACCTTGTGCAAT 1677
DB 1618 CAGTTACCGTCTTCCATTTGAGAGATCTAGTACATTTAAGATACCTTAACCTTGTGCAAT 1677
OY 1618 AAGTTACCATCTTCCATTTGAGAGATCTAGTACATTTAAGATACCTTAACCTTGTGCAAT 1677
DB 1618 AAGTTACCATCTTCCATTTGAGAGATCTAGTACATTTAAGATACCTTAACCTTGTGCAAT 1677
OY 1678 ACTAGTATTTGAGTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTAT 1737
DB 1678 ACTAGTATTTGAGTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTAT 1737
OY 1675 AGTGGCATGAGTGTGCTTCCAAAGCAGTATGCAAGCTTCAAAATCTGCAAGCTTGTAT 1734
DB 1675 AGTGGCATGAGTGTGCTTCCAAAGCAGTATGCAAGCTTCAAAATCTGCAAGCTTGTAT 1734
OY 1738 CTACATGAGCTGTCACTTCTGTTGTTTGGCCAAAGAAACAGCAACTTGTGAGCTT 1797
DB 1738 CTACATGAGCTGTCACTTCTGTTGTTTGGCCAAAGAAACAGCAACTTGTGAGCTT 1797
OY 1735 CTACATATTTGACCAAGCTTGTGTTTGGCCAAAGAAACAGCAACTTGTGAGCTT 1794
DB 1735 CTACATATTTGACCAAGCTTGTGTTTGGCCAAAGAAACAGCAACTTGTGAGCTT 1794
OY 1798 GGAATCTTTTACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857
DB 1798 GGAATCTTTTACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857
OY 1795 GGAATCTTTTACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
DB 1795 GGAATCTTTTACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
OY 1858 TTGACATGCTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
DB 1858 TTGACATGCTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
OY 1855 TTGACATGCTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
DB 1855 TTGACATGCTTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
OY 1918 CTTGATGATTTAAGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1977
DB 1918 CTTGATGATTTAAGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1977
OY 1912 CTTGATGATTTAAGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1971
DB 1912 CTTGATGATTTAAGAACTGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1971
OY 1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2037
DB 1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2037
OY 1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
DB 1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
OY 2038 TTAAGCATGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
DB 2038 TTAAGCATGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
OY 2032 TTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
DB 2032 TTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
OY 2098 GTGCTTGAAGCTTCAAAACCACTCAACTCAACTTGTGTTAACAATCAAGGGCTTCAGA 2157
DB 2098 GTGCTTGAAGCTTCAAAACCACTCAACTCAACTTGTGTTAACAATCAAGGGCTTCAGA 2157
OY 2089 GTGCTTGAAGCTTCAAAACCACTCAACTCAACTTGTGTTAACAATCAAGGGCTTCAGA 2148
DB 2089 GTGCTTGAAGCTTCAAAACCACTCAACTCAACTTGTGTTAACAATCAAGGGCTTCAGA 2148
OY 2158 GGAATCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
DB 2158 GGAATCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
OY 2218 ATGATCAGTTGCAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2277
DB 2218 ATGATCAGTTGCAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2277
OY 2209 ATTAAGCACTTCAAGAACTGCTCATGCTTACACCTTGTGTATCTGCTTGTCTAAGA 2268
DB 2209 ATTAAGCACTTCAAGAACTGCTCATGCTTACACCTTGTGTATCTGCTTGTCTAAGA 2268
OY 2278 AGTCTAGAGTTTGAAGGGGGTCTGCGGAAGTGAATGATGTTG----- 2320
DB 2278 AGTCTAGAGTTTGAAGGGGGTCTGCGGAAGTGAATGATGATGTTG----- 2320
OY 2269 AGTCTAGAGTTTGAAGGGGGTCTGCGGAAGTGAATGATGATGTTG----- 2328
DB 2269 AGTCTAGAGTTTGAAGGGGGTCTGCGGAAGTGAATGATGATGTTG----- 2328
OY 2321 ---ATTCTGAGATTCCTTACAGAGAGGTTTCACTCTCTGAGAAACCTTAATATACG 2376
DB 2321 ---ATTCTGAGATTCCTTACAGAGAGGTTTCACTCTCTGAGAAACCTTAATATACG 2376
```

[illegible]

TITLE Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)

PUBMED 12872003

REFERENCE 2 (bases 1 to 79178)

AUTHORS Song J., Braeden, J.M., Naeem, K.S., Raasch, J.A., Wielgus, S.M., Haberlach, G.T., Kuang, H., Austin-Phillips, S., Helgeson, J.P., Liu, J., Tallon, L.J., Zaborsek, J., Buell, C.R. and Jiang, J.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

COMMENT Address all correspondence to: rbue11@tigr.org. Clone CB3A14 is from Solanum bulbocastanum chromosome 8. The orientation of the sequence is from SP6 to T7 end of the clone. Genes were identified by a combination of several methods: Gene prediction programs including GenScan+ (Chris Burge, <http://CCK-081.mtc.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and GeneSplicer (Michael Perera and Steven Salzberg, contact mpere@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/cdb/cgi.shtm>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Location/Qualifiers

FEATURES

SOURCE 1. 79178

organism="Solanum bulbocastanum"

mol_type="genomic DNA"

db_xref="taxon:147425"

chromosome="8"

clone="CB3A14"

gene complement(1..>3631)

locus_tag="CB3A14.1"

note="similar to growth regulating factor 1 GB:AAE17567 GI:6573149 (Oryza sativa); EST BE922572 from this gene"

mRNA complement(join(1..375,2184..2562,3394..>3631))

CDS /locus_tag="CB3A14.1"

repeat_region /product="putative growth-regulating factor"

repeat_region complement(join(1..375,2184..2562,3394..3631))

repeat_region /locus_tag="CB3A14.1"

repeat_region /codon_start=1

repeat_region /product="putative growth-regulating factor"

repeat_region /protein_id="AAP45157.1"

repeat_region /db_xref="GI:32470630"

repeat_region /translacion="MSGNSTSVAGAGGGGEGGNGYGYRPPPTAVQWQELHQAM IYKTLVAGLPVLPDLVPIRSPFAISLRFPHHSLGCSYGGKFDPERCRRTDG KKWCSKDAVPSDCSRHMRGRNRSKPVSOSLSTOSLSTMSKQITGSSNTER ONSSSGFQNMPLIVSVNSGTLNYSATKIQMPASVGIYNNKYRIAGITRADER NLSSSEKATVRSLSGKGTDTSTWLPSPVSSSPVRSKNDQLGSSSTWMLPULER MIDATISRRRHQCFPSGDIIDSPGVTEKHQSMRPFNEWPTAKESWNSLDDGS"

repeat_region /rpt_family="C-rich"

repeat_region 5239..5298

repeat_region /rpt_family="AT-rich"

repeat_region 5478..5502

repeat_region /rpt_family="AT-rich"

repeat_region 6851..6916

repeat_region /rpt_family="TATGG)n"

repeat_region 7172..7193

repeat_region /rpt_family="AT-rich"

gene 7660..16706

locus_tag="CB3A14.12"

note="highly similar to Mob1 like protein GB:CAC4010 GI:19309913 (Medicago sativa subsp. falcata); contains Pfam profile PF03637 (Mob1 phocein family); EST B6589654,

mRNA join(7660..7817,8857..8905,9929..10037,11268..11361,13685..13818,14444..14607,16411..16706)

CDS /locus_tag="CB3A14.12"

repeat_region /product="putative Mob1/phocein family protein"

repeat_region join(7795..7817,8857..8905,9929..10037,11268..11361,13685..13818,14444..14607,16411..16485)

repeat_region /locus_tag="CB3A14.12"

repeat_region /codon_start=1

repeat_region /product="putative Mob1/phocein family protein"

repeat_region /protein_id="AAP45162.1"

repeat_region /db_xref="GI:32470635"

repeat_region /translacion="MSLFGLRNQRTPRPPKASGSAQGLRRHIDATLGSGNLREA VRLPEGRDIEMLVNTVDNFQYNLLYGLTECTEPCETMTAGPYEYRMDGVQ IKKIEVSAPKVEVYVNDVETQDDSLFPGRGAPPSNPKDVVKTIFRLRPVYA HIYSHRQKIVSLKEAHNLNCFHFLFTHEPGLIDKKELAPQEIIESIIIVY"

repeat_region 16833..16854

repeat_region /rpt_family="AT-rich"

repeat_region complement(18598..>21580)

repeat_region /locus_tag="CB3A14.2"

repeat_region /note="contains Pfam profile PF04819 (plant viral response family)"

repeat_region complement(join(18598..19075,21234..>21580))

repeat_region /locus_tag="CB3A14.2"

repeat_region /product="putative plant viral-response family protein"

repeat_region complement(join(18598..19075,21234..21580))

repeat_region /locus_tag="CB3A14.2"

repeat_region /codon_start=1

repeat_region /product="putative plant viral-response family protein"

repeat_region /protein_id="AAP45159.1"

repeat_region /db_xref="GI:32470632"

repeat_region /translacion="MGSEFPGHVLPGTFLVIGVHWSALVYSSNPKSFRVWSPV GPDPKIVLELYVIAIGFDICIEIPYSHTLVVGVNPPVMMNFHAGMILMF VIREGLIVLSKRTSFLPLREGALCIATATASAEVPLPEFSTHKGLEGVYHLLV LIGLCITITAGALMPTSPFLDLASGVSVALQGMFTOTATLIGPMPDCCQKGNL VMCRSESEVARGELANLQLESMLEFVALATTAAYGRASETGKHIDKNSHLPDGG"

repeat_region 19594..19617

repeat_region /rpt_family="AT-rich"

repeat_region 20891..20925

repeat_region /rpt_family="AT-rich"

repeat_region 22668..22692

repeat_region /rpt_family="T)n"

repeat_region 22954..23034

repeat_region /rpt_family="AT-rich"

repeat_region 23085..23140

repeat_region /rpt_family="AT-rich"

repeat_region 23319..23371

repeat_region /rpt_family="AT-rich"

repeat_region 23685..23705

repeat_region /rpt_family="AT-rich"

repeat_region 23772..23821

repeat_region /rpt_family="A-rich"

repeat_region 24167..24292

repeat_region /rpt_family="T)n"

repeat_region 24312..24369

repeat_region /rpt_family="AT-rich"

repeat_region complement(24447..>26791)

repeat_region /locus_tag="CB3A14.3"

repeat_region /note="similar to transposase related protein GB:CA851950 GI:5690095 (Zea mays)"

repeat_region complement(join(24447..24871,24982..25195,25412..25663,25874..26005,26221..26418,26711..26791))

repeat_region /locus_tag="CB3A14.3"

repeat_region /product="putative transposase-related protein"

repeat_region complement(join(24447..24871,24982..25195,25412..25663,25874..26005,26221..26418,26711..26791))

repeat_region /locus_tag="CB3A14.3"

repeat_region /codon_start=1

repeat_region /product="putative transposase-related protein"

repeat_region /protein_id="AAP45161.1"

repeat_region /db_xref="GI:32470634"

repeat_region /translacion="MKSEQLVLAVKTDNSDKFGQNNIFKFIWTVAFVAGSDYIG VMEETPKSWMKSFSTTLPIALRCNGSYDMDIASVIKADELTCBPDLSELCGNSNE


```

Db 39932 TGAACCTAGGAAACCTTAATCTCTATGCTCAATTAATCTCGCATCTTGAGAGGTGAA 39873
Qy 1983 GAAATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGCATCTTTAG 2042
Db 39872 GAAATATAGGCGCAAAAGAGCAATTTATCTGCAAAAGAGAAATCTGCATCTTTAG 39813
Qy 2043 CATGAAATGGGATGATGATGAACTGCAAGTATATATGATGATGCAAAAGATGAGTCT 2102
Db 39812 CATGAGTTGGAATTAATCTTTG---GAACCATATATATGATGATGCAAAAGATGAGTCT 39756
Qy 2103 TGAAGCTCTCAAAACCACTCTCAATCTGATCTTTTACATTCAGGCGCTTCAGAGAT 2162
Db 39755 TGAAGCTCTCAAAACCACTCTCAATCTGATCTTTTACATTCAGGCGCTTCAGAGAT 39696
Qy 2163 CCGTCTCCAGAGCTGATGAAATCACTGATCTTTTGAAGAAATGTTGCTCATATGAAATCAT 2222
Db 39695 CCATCTCCAGAGCTGATGAAATCACTGATCTTTTGAAGAAATGTTGCTCATATGAAATG 39636
Qy 2223 CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTTGAGTGTGCTGCTTGAAGAGTCT 2282
Db 39635 CAACCTTCAGAAATCTGCTCATGCTTACCAACCTTTGAGTGTGCTGCTTGAAGAGTCT 39576
Qy 2283 AGAGTTGTGAGAGGGGCTCTGCGGAAGTGAATGTTG-----A 2321
Db 39575 AGAGTTTACACTGGGGGCTCTGCGGATGTGGAATGTTGAAGAAATGATGATGTTCA 39516
Qy 2322 TTCTGAGATTTCCCTCAACAAGAGAGTTTCCATCTCTGAGAAAATTTAATATCGGAAT 2381
Db 39515 TTCTGAGATTTCCCTCAACAAGAGAGTTTCCATCTCTGAGAAAATTTAATATGGAATCT 39456
Qy 2382 TGGTATCTGAAAAGGATGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2441
Db 39455 TGGTATCTGAAAAGGATGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39336
Qy 2442 GATAGAGATTAATATGTTGCTGATGTTGTTTATTCACACCTTTCTTCTGCAAGAAAT 2501
Db 39335 GATAGAGATTAATATGTTGCTGATGTTGTTTATTCACACCTTTCTTCTGCAAGAAAT 39336
Qy 2502 GGTATGTTAGTGGGAGCAAGTCAAGATGCAATAGTTCAGTTCATATCTCATATGAGG 2561
Db 39335 GGTATGTTAGTGGGAGCAAGTCAAGATGCAATAGTTCAGTTCATATCTCATATGAGG 39276
Qy 2562 TCTTACTTCCCTCAAAATTCGCTATACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2621
Db 39275 TCTTACTTCCCTCAAAATTCGCTATACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39216
Qy 2622 CAAAAGCTTGCAAAATCTCAATATCTGATATCTCTTTTACTTCAATCTTAAAGAGCT 2681
Db 39215 CAAAAGCTTGCAAAATCTCAATATCTGATATCTCTTTTACTTCAATCTTAAAGAGCT 39156
Qy 2682 GCTTACAGCTGCTGCTGATGCTCAATGCTTTGAAGCATGCAAAATCTCATAGTGTATGC 2741
Db 39155 GCTTACAGCTGCTGCTGATGCTCAATGCTTTGAAGCATGCAAAATCTCATAGTGTATGC 39096
Qy 2742 ACTAGAGAGTCTCCCGAGAGAGAGTGTGAAGGTTAATTTCACTCAGACAGTTATCAT 2801
Db 39095 ACTAGAGAGTCTCCCGAGAGAGAGGAGTGTGAAGGTTAATTTCACTCAGACAGTTATCAT 39036
Qy 2802 AACATATCTGTAATGCTCAATATGTTTACCGAGAGAGATTTGACAGCACTTACAGCCCTGAC 2861
Db 39035 CCAGAGCTGAGAGAGATGCTTAAATGTTTACCGAGAGAGATTTGACAGCACTTACAGCCCTGAC 38976
Qy 2862 AAATTTATCATGTTGATGTTTGTTCACACCTGCGCAAGCGGTGTGAAGAGAGATGAGAG 2921
Db 38975 AAATTTATCATGTTGATGTTTGTTCACACCTGCGCAAGCGGTGTGAAGAGAGATGAGAG 38916
Qy 2922 AGACTGTGACAAAATTTGCTCAATCTCTGAGTGTATTTATTA 2966
Db 38915 AGACTGTGACAAAATTTGCTCAATCTCTGAGTGTATTTATTA 38871

```

```

AX814116
LOCUS AX814116 3971 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 39 from Patent EP1334979.
ACCESSION AX814116
VERSION AX814116.1 GI:39103418
KEYWORDS
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1
AUTHORS van der Vossen, E.A. and Allefs, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
JOURNAL Patent: EP 1334979-A 39 13-AUG-2003;
KweeK-en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1..3971
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
1..3971
/misc_feature
/note="RGC3-b1b"
ORIGIN
Query Match 63.4%; Score 1880.8; DB 6; Length 3971;
Beet Local Similarity 85.5%; Pred. No. 0; Mismatches 342; Indels 27; Gaps 6;
Matches 2173; Conservative 0;
426 AACAGTTTGTGTTGATGAGACCAAGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
Db 1454 ACCAGTTTGTGTTGATGAGACCAAGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1513
Qy 486 AGTGAATTCGTATTAACATGTTAGCAATGCCCAACCTTCAGTCTCTCCATATCT 545
Db 1514 AGTGAATTCGTATTAACATGTTAGCAATGCCCAACCTTCAGTCTCTCCATATCT 1573
Qy 546 TGGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
Db 1574 TGGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1633
Qy 606 AATTGAGCATTTCCATCCCAAAATATGAGATTTGTTCTCGAGAGATTTTAAATGAGAGAG 665
Db 1634 AACTGAGGTTTCTATCCCAAAATATGAGATTTGTTCTCGAGATTTTAAATGAGAGAG 1693
Qy 666 GTTATTAAGAGAAATTTGATATCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
Db 1694 GTTATTAAGAGAAATTTGATATCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1753
Qy 726 TCCACTTCAAAAGAGCTTTCGGAGCTTGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 785
Db 1754 TCCACTTCAAAAGAGCTTTCAGAGGTTCTGAATGAGAGAGAGAGAGAGAGAGAGAGAG 1813
Qy 786 TGATGTTGGAATGAGATCAAGATTAAGTGGCTTAAGTTAAGACAGCTTGAAGAGTTGG 845
Db 1814 TGATGTTGGAATGAGATCAAGATTAAGTGGCTTAAGTTAAGACAGCTTGAAGAGTTGG 1873
Qy 846 AGCAAGTGGCTTCTGTTTACCACTACTGCTTTGAAAAAGTTGGATCAATATAGG 905
Db 1874 AGCAAGTGGCTTCTGTTTACCACTACTGCTTTGAAAAAGTTGGATCAATATAGG 1933
Qy 906 AACATTTGCAACATATGAAATTTGCAAAATTTGTCACAGAAATGTTGTTGTTGTTAT 965
Db 1934 AACATTTGCAACATATGAAATTTGCAAAATTTGTCACAGAAATGTTGTTGTTGTTAT 1993
Qy 966 GCAAGTGTGATTTGGGCAACAAGAGAAATTAATCTTATCTTGTGCTATCGAAAGAG 1025
Db 1994 GCAAGTGTGATTTGGGCAACAAGAGAAATTAATCTTATCTTGTGCTATCGAAAGAG 2053
Qy 1026 GATTGTGAAAAATGTTGTTGTTGCTCTTACAGCTTAAATCTTGGAGGATTTTTCG 1085
Db 2054 GATTGTGAAAAATGTTGTTGTTGCTCTTACAGCTTAAATCTTGGAGGATTTTTCG 2113

```

Oy		2166	TCTCCAGACTGGAATCACTCAGTTTGGAAAATGTTCCTCATATTGAATCATACG	2282
Db		3176	TCTCCAGATTGGATGAATCAATCAGTTTGGAAAATGTTCCTCATATTGAATTAAGAAG	3233
Oy		2226	TTGCAAAAATGCTCATAGCTTAACACCCTTTGGTAGCGTCCCTTGCTPAAAAAGCTTAGA	2288
Db		3236	TTGTAAAAATCGCTCATGCTTAACACCCTTTGGTAGCGCTTGTCTPAAAAAGCTTAGA	3299
Oy		2286	GTTGTGAGGGGGTCTGGGAAAGTGAATGATGTGATTCGGATTCCTCAACAAGAAAG	2341
Db		3286	GTTACACACCGGGTCAGCAGATGTGGAGTATGTGAATAATATGTTCAATCCG---GAAAG	3355
Oy		2406	AAAGGAAGAAAGAACGCAATGCCCTGTGCTTGAAGAGATPAGATTAATGTGTGCCAT	2465
Db		3413	AAAGGAAGAAAGAAAGCAATGCCCTGTGCTTGAAGAGATPAGATTAATGTGTGCCAT	3477
Oy		2466	GTTTGTATTTCOAACCTTTCTTCTGTCAAGAAATGGTAGTAAAGTGAGGCAAGTCA	2522
Db		3473	GTTTGTATTTCOAGCCCTTTCTTCTGTCAAGAAATGGTAGTAAAGTAAATG-----CGACAGA	3522
Oy		2526	TGCATATAGTTTCAGTTCATATCTAATCTCATGGCTCTPACTTCCGCCAAATTGCGTA	2589
Db		3527	TGCATACAGTTTGAAGTTCATATCTAATCTTAAGGGCTCTTACTTCCCTTGACATTAGCA	3588
Oy		2586	TAACAAAAGAGATGCTTCACTCCCAAGAAAGAGATGTTCAAAGCCCTGCAAAATTCGAATA	2645
Db		3587	TAAAGTAAGAGCTACTCACCTCCCAAGAAAGATGTTCAAAGCCCTGCAAAATTCGAATA	3648
Oy		2646	CTTGAATATCTCTTTTACTTCATCTTAAGACCTGCTPACCAAGCCCTGCTAGCTTCAA	2705
Db		3647	CTTGAATATCTCTTCTTTAGGAATCTCAAGAGTTCACAGCCCTGCTAGCTTCAA	3706
Oy		2706	TGCTTTGAAGCATCTGAAAATTCATAGTGTATGACTAGAGAGTCTCCCCAGAGAAG	2765
Db		3707	TGCTTTGAAGAGTCTCAAAATTTGAATTTGTAAACGCACTAGAGAGTCTCCCCAGAGAAG	3766
Oy		2766	TGTGAAGGTTTAAATTTCACTCAACACAGTTATTCATATACTGTGAATNGCTPACATG	2825
Db		3767	GGTAAAAAGTTTAACTTCACCTCACCGAGTGTCTGTAGTAACGTATGATGATPAAATG	3826
Oy		2826	TTTACCGGAGGATTTGACGACCTTAAAGCCCTCACAAATTTATCACTGAGTTTTC	2885
Db		3827	TTTTACCGGAGGATTTGACGACCTTAAAGCCCTCACAAATTTATCACTGAGTTTTC	3886
Oy		2886	AACACTGGCCAGCGGTGTGAAGAGGAAATPAGAGAAAGACTGGTACAAATTTGCTCAT	2945
Db		3887	AATATGATTTAAAGCGGTGTGAAGAGGAAATPAGAGAAAGACTGGGCAAAAATTTGCTCAT	3946
Oy		2946	TCTCTGATGTTTATTTATTAG 2967	
Db		3947	TCCATATTGACTCTATATGAG 3968	
RESULT 5				
LOCUS	AX816335	3971 bp	DNA	linear PAT 09-DEC-2003
ACCESSION	AX816335	Sequence 52 from Patent WO03066675.		
VERSION	AX816335.1	GI:39646826		
SOURCE	Solanum bulbocastanum			
ORGANISM	Solanum bulbocastanum			
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteridae; lamiales; Solanales; Solanaceae; Solanum.			
REFERENCE	Allefs,J.J. and van der Vossen,E.A. Gene conferring resistance to phytophthora infestans (late-blight)			
AUTHORS	1			
TITLE				

Db	1994	GGAGGTGCAATTTGGACACCAAGAAATTAATCCAAACTTGTGGCAATCGAAAGGA	2053
Qy	1026	GATTGTGAAAAATGTGGTGTGTGTCCTCTAGACAGCTAAACCTCTGGAGGTATTTTTCG	1085
Db	2054	GATGTGAAAAAATGTGTGTGTGTGTCCTCTAGACAGCAAGACTCTGGAGGTATTTTTCG	2113
Qy	1086	CTTTAAGAGAGAAAGAACAGTGGGAACATGTGAGAGATAGTGAATTTGGAAATTTGCC	1145
Db	2114	CTTCAGAGAGAAAGAAAGAAATGGGAACATGTGAGAGACAGTCCGATTTGGAAATTTGCC	2173
Qy	1146	TCAGAAGAAAGTTCATTTCTGCGCCCTGAGACTTAGTTACATGACCTTCCACTTGA	1205
Db	2174	TCAGAAGTAAAGTTCATTTCTGCGCCCTGAGACTTAGTTACATGACCTTCCACTTGA	2233
Qy	1206	TTTGAGACAATGCTTTTACATATTTGTCAGTATTTCCCAAGGATACCGAAATGAAAAAGG	1265
Db	2234	TTTGAGACAATGCTTTTGTGTATTTGTGCGGTATTTCCCAAGGACACCAAAATGGCAAGGA	2293
Qy	1266	AAATCTAATCTCTCTGTGATGGCACATGTGTTTTATTTTATCGAAGGAACTTGGAGCT	1325
Db	2294	AAATCTAATCTCTTTTGTGATGGCACATGTGTTTTCTTTTATCGAAGGAAATTTGGAGCT	2353
Qy	1326	AGAGAAATAGTATGATTAAGATATGGAATTTATCTTGAGGTCTTTCTTCCAAAGAT	1385
Db	2354	AGAGAAATAGTATGATTAAGATATGGAATTTATCTTGAGGTCTTTCTTCCAAAGAT	2413
Qy	1386	TGAAGTTAAATCTGGTCAAACTTTATTTCAAGATGATATCTCAATTCATGATCGGCAAC	1445
Db	2414	TGAAGTTAAATCTGGTCAAACTTTATTTCAAGATGATATCTCAATTCATGATTTGGCTAC	2473
Qy	1446	ATCTCTATTTTCGCGCAAGCACATCAAGCAGCAATATCGAGAAATTAATTTGAGAAATTA	1505
Db	2474	ATCTCTGTTTTCAAGCAACCATCAAGCAGCAATATTTGTGAATTAATGCTAATTTATGA	2533
Qy	1506	CATACATATGATGTTCATTGGTTTCACTAAAGTGTATCTTCTTATCTCTTCCCACTT	1565
Db	2534	TGGATATATATGATGTTCATTGGTTTGTGCAAGTGTATCTTCTTATCTCTTCACTCTT	2593
Qy	1566	GCAAGAGTTTGTCTCGTTGAGGGTGCCTTAATCTAAGTACACATTAATAAATTAGACAGTTAC	1625
Db	2594	GCAAGAGTTTGTCTCATTTAAGGGTGCCTTAATCTAAGAACTCGAAGCTTAATTAATTAATTC	2653
Qy	1626	GTCCTTCAATTTGAGATCTTAGTACATTTTAAGATACCTAACTGTCTGGCAATTAAGTAT	1685
Db	2654	ATCTTCAATTTGAGATCTTAGTACATTTTAAGATACCTGAATCTGTCTGGCAATTTTAAGAT	2713
Qy	1686	TCGTATGCTTCCAAACCAAGTTATGCAAGCTTCAAAATTTGCAAGCTCTTGATCTACATGG	1745
Db	2714	TCGTATGCTTCCAAAGAGATTATGCAAGCTTCAAAATTTGCAAGCTCTTGATCTACATTA	2773
Qy	1746	CTGTCAATTCATTTTGTGTGGTGGCCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCT	1805
Db	2774	TTGGGACTCTCTTCTTGTGTGGTGGCCAAAAGAAAGAAAGTGTGTGTGTGTGTGTGTGTGT	2833
Qy	1806	TTTATCTTGATGGTGTCTATGATTTGACTTGTATGCGACCAAGATAGGATCTTTGACATG	1865
Db	2834	TTTATCTTGATG---GCTGTTCATTGAGCTCAACGCAACCAAGATAGGATTTGTCATG	2890
Qy	1866	CTTTAAGACTTAAAGTATTTGTGTGTGGAAATTCAGAGAAAGAAAGTTGTCAACTTGGTGA	1925
Db	2891	CTTTAAGCTTCTAAGTTGTCTTGTATTTATTTGGCA---AGAGAAAGAAAGTTATCAACTTGGTGA	2947
Qy	1926	ATTACGAAACCTGATCTCTATGGCTCAATTTGAATCAAGATCGATGTGAGAGAGAAAGAA	1985
Db	2948	ACTAATAAACCTAATCTCTATGGCTCAATTTCAATTCACAAACTTGCACAGATGAAAGAA	3007
Qy	1986	TGATATGATCAAAAGAGCAATTTATCTGCAAAAGAAATATGCAATCTTTAAGCAT	2045
Db	3008	AGATATGATCAAAAGAGCAATTTATTTATCTGTAAAGCAATATGCAATCTTTATGCT	3067
Qy	2046	GAAATGGATGACGATGAAGCTCCACGTATATATGATCAGAAAAAGTTGAAGTCTTGA	2105

Db	3068	GAGTTGGGACCTTGTATGAAA---ACATAGATATGATTCA-----GAAGTCTTGA	3115
Oy	2106	AGCTCTCAAAACACACCTCCAACTGACTGTGTTTAACATCAGGGGCTTCAGAGAAATCCG	2165
Db	3116	AGCCCTCAAAACCACTCCAACTCGAAATATTTTGAATCAATGAGCTTCGAGGAATCCG	3175
Oy	2166	TCTCCGACCTGGAATGAATCACTCAAGTTTGA AAAATGTTGTCTCTATTTGAATATCATCG	2225
Db	3176	TCTCCGAGTTGGATGGAATCAATCAGTTTGA AAAATGTTGTCTCTATTTGAATTTAGAGC	3235
Oy	2226	TTGCAAAAACGCTCATGCTTACACCACTTGGAGCTGCTGTCTAA AAAAGTCTAGA	2285
Db	3236	TTTGAAAAACCTGCTCATGCTTACCACTTGGAGAGCTGCTGTCTAGAAAATCTAGA	3295
Oy	2286	GTTTGTGAGGGGGGTCTGCGGAAGTGAAGTATGTTGATTTGGAATCCCTACMAAGAGAG	2345
Db	3296	GTTACACACCGGGGTCAAGAGATGAGGATATGTTGAAGATATATGTCATCTG---GAG	3352
Oy	2346	GTTTCCATCTCTGAGAAAATTAAATATACCGGAATTTGGTAAATGGAAGATTGCTGA	2405
Db	3353	GTTTCCATCTCTGAGAAAATTGTTAATAGGACCTTTAGATATCTAA AAGATTTGCTGA	3412
Oy	2406	AAAGGAAGGAAGAAAGCAATGCCCTGTGCTTGAAGAGATGAGATTAATATGTTGCCAT	2465
Db	3413	AAAGGAAGGAAGAAAGCAATCCCTGTGCTTGAAGAGATGACATTTATCTGTGCTCCAT	3472
Oy	2466	GTTTGTATTTCCAAACCTTTCTTCTGTCAAGAAATTTGTAATGAGGGGCAAGTCAGA	2525
Db	3473	GTTTGTATTTCCAAACCTTTCTTCTGTCAAGACATTAAGTTATTTG-----CGACGA	3526
Oy	2526	TGCAATAGGTTTCAAGTTCCATATCTAATCTCATGCTCTTACTTCCCTCCAAATTCGCTA	2585
Db	3527	TGCAACAGTTTGGAGGTCAATATCTAATCTTAGGGCTCTTACTTCCCTTGACATTAGCAA	3586
Oy	2586	TAACAAGAAGATGCTTCATCCCGCAAGAAAGATGTTCAAAAAGCCTTGCAATCTCAATA	2645
Db	3587	TAACTGAAAGCTAATTCTTCCAGAAAGAGATTTCAAAAAGCCTTGCAATCTCAATA	3646
Oy	2646	CTTGAATATCTCTTTTACTTCTTCAATCTTAAAGAGCTCCCTACCAAGCTGGCTAGCTCAA	2705
Db	3647	CTTGAATATCTCTTTTACTTCTTGAATCTCAAGAGTTCCTTACCAAGCTGGCTAGCTCAA	3706
Oy	2706	TGCTTTGAAGCATTTGAAATTCAATAGTTGTATATGCACTAGAGAGTCTCCCGAGGAAG	2765
Db	3707	TGCTTTGAAGAGTCTCAAAATTTGAATTTGTAAAGCACTAGAGAGTCTCCCGAGGAAG	3766
Oy	2766	TGTGAAGAAGTTTATTTCACTCAACAGATTATCATTAACAATACGTGAATATGCTACATG	2825
Db	3767	GGTAAAAAGTTTAACTTCACTCAACCGAGTGTCTGTACGTAACTGTATGATGCTTAANA	3826
Oy	2826	TTTACCGAGAGGATTTGAGACACTTAACAGCCCTCACAAATTTATCAGTTGAGTTTGTCC	2885
Db	3827	TTTACCGAGAGGATTTGAGACACTTAACAGCCCTCACAACTTTAACAATTACTCAATGTCC	3886
Oy	2886	AACACTGAGCAAGCGGTGTGAAGAAAGGAATAGGAAGAAGCTGTACAAATTTGCTCAT	2945
Db	3887	AATAGTATTCAAGCGGTGTGAAGAAAGGAATAGGAAGAAGCTGTACAAATTTGCTCAT	3946
Oy	2946	TCTCTGCTGTTTATTTATTTAG	2967
Db	3947	TCTCATTTTGACTCTATATGAG	3968
RESULT 7			
AY303171			
LOCUS			
DEFINITION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Solanum bulbocastanum			
Solanum bulbocastanum			
163635 bp DNA linear PLN 15-AUG-2003			
AY303171 Solanum bulbocastanum chromosome 8 clone 17013, complete sequence.			
AY303171.1 GI:32470640			
HTG.			

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 163635)
Song,J., Bradeen,J.M., Naess,S.K., Raasch,J.A., Wielgus,S.M., Haberlach,G.T., Liu,J., Kuang,H., Austin-Phillips,S., Buell,C.R., Helgeson,J.P. and Jiang,J.
Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight
Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)
2 (bases 1 to 163635)
Song,J., Bradeen,J.M., Naess,K.S., Raasch,J.A., Wielgus,S.M., Haberlach,G.T., Kuang,H., Austin-Phillips,S., Helgeson,J.P., Liu,J., Tallon,L.J., Zaborsky,J., Buell,C.R. and Jiang,J.
Direct Submission
Submitted (22-MAY-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
Address all correspondence to: rbuell@tigr.org
Clone 177013 is from Solanum bulbocastanum chromosome 8. The orientation of the sequence is from SP6 to T7 end of the clone. Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHMM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and GenesPlacer (Mahaletia Perlea and Steven Salzberg, [contact mperlea@tigr.org](http://contact.mperlea@tigr.org)), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/cgi.shcml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).
Location/Qualifiers
1..163635
/organism="Solanum bulbocastanum"
/mol_type="genomic DNA"
/db_xref="taxon:147425"
/chromosome="8"
/clone="177013"
<1..>811
/locus_tag="177013.24"
/join(<1..345,682..>811)
/locus_tag="177013.24"
/product="hypothetical protein"
/join(<1..345,682..811)
/locus_tag="177013.24"
/note="predicted by genemarkHMM"
/codon_start=2
/product="hypothetical protein"
/protein_id="AAP45168.1"
/db_xref="GI:32470642"
/translation="DPDLIRIYEPDGDREGFVADIEGKPERLRSVYMTADTTLOR YATIRSKAVTVIEKOTALGPRDITKVSIGDITLVNDVLTAVTSGILMTVLEANA FGSLFMTESVYELVETMGPNPELIDCQULFELLPQERVAAGAQTSEGTWLSNGQI"
complement(12643..2664)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
<3067..>7634
/locus_tag="177013.29"
/join(<3067..3304,3388..3488,4038..4246,7049..>7634)
/locus_tag="177013.29"
/product="putative xyloglucan endotransglycosylase-related protein"
/join(3067..3304,3388..3488,4038..4246,7049..7634)
/locus_tag="177013.29"
/note="similar to xyloglucan endotransglycosylase-related protein GB:AA18365 GI:1244754 (Arabidopsis thaliana)"
/codon_start=1

/product="putative xyloglucan endotransglycosylase-related protein"
/protein_id="AAP45169.1"
/db_xref="GI:32470643"
/translation="WDYRVLVSYSKSTIPSSILLIYIPATETTAAANTYKAFNL STIRREGSPILFSDFNIRSGSPDRSRILLINKSGSGVISTEYVNGFSAISKLA IYTAGIVAPYTSNADPPEKKNHDLIEFLGNVNGQWRROTMYNGVSKRGEERY RMWFPSDFHQSILMTPKNLTIFYIDETPLREVRNRPANGDEPSKPMELVATITWA SSWATNGKAKADVYKDFEATLMDLIEGCIYDPTQIIPSTCTDSAKLLADVSY ITPERRKSKMEFRERYMYSYCYDNLTPVPVPPPCVIVQSRDLFRSGLRQMKRG GSHSHSQTIRKRPGRSRRRKKVVGASKSGRGSAAAM"
complement(13312..3349)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
complement(5122..5143)
/rpt_family="(TA)n"
complement(6049..6077)
/rpt_family="AT_rich"
complement(<8645..>11610)
/locus_tag="177013.33"
complement(join(<8645..8953,9033..9183,9272..9509,9590..9800,9895..10091,10581..>11610))
/locus_tag="177013.33"
/product="putative receptor protein kinase"
complement(join(8645..8953,9033..9183,9272..9509,9590..9800,9895..10091,10581..11610))
/locus_tag="177013.33"
/note="similar to receptor protein kinase GB:AA23542 GI:836954 (Ipomoea triloba)"
/codon_start=1
/product="putative receptor protein kinase"
/protein_id="AAP45176.1"
/db_xref="GI:32470650"
/translation="MKRGDVLNLSQVLDSEGRFKLGFPSIPQNTNTYLGIVAGDPV EKLMLANPTPLTNSGLTLIDSTGLTSGKTVINATPLTGLSALVLAQDSGN FVQDTERKNTLWQSDPHFTSCILPKMKGYNTLTQOMNTLSMLVSSAPAPAGATL SLBAIDAPQLVLSRRGEVWTSGANMNGQFPLPESRISATTYQYNLMVSGTDMF FQEAETGSGFSPSLELFDGAIAGAGDSIYRKYKPCFAGDSQSQQLPECRKQGD KPEQKQGDFTLDGTTSTVYDNASIQLGDQCMHSGCVGFTTNSNGTGLISNG KRPRVDESEGRKKREHTRKEMNAADSPNNTKEDPVAVDQIKTIRGGLTAAANR FSSDNLCGEGRPVYKQFPDREVALIRLSTSSQGLAEFKNELILAKOVHRULY RVLCCHIGHDEKRLIYEMPNKSLDFLPDEPKKLLDMQKREILIEGLAQGLYLHK YSRMARVIRHDLKASNLVLDENMNPKLADGLAIRPQNTETAVTRVGVGTGMARF AMEGAPSIKSDVPSFGLVLMLEILISGRNMSLQGFNRLNLIGVAMELMKGCLEIKD PDLDELIDYEOFLRVIVHGLICVQEGATRPTMSDVISMLCNGSMELPAXQAPAFPTG RDLIESYSSNKTCCSINDCSITVTEAR"
complement(<12526..>15441)
/locus_tag="177013.32"
complement(join(<12526..12834,12979..13066,13157..13394,13479..13689,13770..13966,14062..14130,14268..>15441))
/locus_tag="177013.32"
/product="putative receptor protein kinase"
complement(join(12526..12834,12979..13066,13157..13394,13479..13689,13770..13966,14062..14130,14268..15441))
/locus_tag="177013.32"
/note="similar to receptor protein kinase GB:AA23542 GI:836954 (Ipomoea triloba)"
/codon_start=1
/product="putative receptor protein kinase"
/protein_id="AAP45167.1"
/db_xref="GI:32470641"
/translation="MKSLANSIFILITLFFSHTCIINLSVAATISLKPQDELNHSQ VLDSEGRKFLGFFSISQTNNTYLGIVAGDQDDKLWLANPTPLKNSGLTIDTTL GTLKITSQGVTVNITPPLTSSIRALOGSGNLVLDQETLWQSDPHFTNTLPF GKIKGYNLTITKQNTLTSWLSSTYIPASGAFTLSTSIDAPOLVIRRREGVVISGAW RNQSPFLTALDSSNRYVINLTVSEKDGVPQPDAPDGSFPSIELNPNNAIYVGGG DSRVATLNERCYGTSQDCVSNQPEPRKQGDPEKQSGVPIIDRSKNSNSYDNAST SLGDCKMRQWCHSCVGFSTTSNGTCIILWNNGEKFQVDSGNTVAKVLAVSSKSA IYVPMKISGFCISYVRRLKQAEKRRESEYIRLETASGFPDNTMKKEGDEREVQDL IPSFGVLAATNPFSSENMLGEGGFGPYKGFPGREVAVYGLRSTSGOGLVEPKEE LILIAKQHTNLRVIVGCCIHEDGKLLIYEMPNKSLDFLPDEPKKLLDMQKREIL IEGLAQGLYLHKYSRMARVIRHDLKASNLVLDENMNPKLADGLAIRPQNTETAVT RIVGVTGYAPFAEGAPSTISDVPSRGIIMLEIAMELMKGCLEIKDPLAGDLC TLLLRVIVHGLICVQEGATRPTMSDVISMLCNGSMELPAXQAPAFPTGRNETSHS

	repeat_region	AGIKAKQYSVNDSCITVIEAR"	complement(17040..17075)	/rpt_family="AT_rich"
	gene	<17424..>.19717	/locus_tag="177013.25"	join(<17424..17782,18415..>.19717)
	mRNA	/locus_tag="177013.25"	/product="hypothetical protein"	join(17424..17782,18415..19717)
CDS		/locus_tag="177013.25"	/note="predicted by fgenesh"	/codon_start=1
		/product="hypothetical protein"	/protein_id="AAP45173.1"	/db_xref="GI:32470647"
		/translaction="MEENTYEMESSTSTRPRVSDEBEDISKOYHVKMGEPFHDDHEE	DYRSGYGGDDEMKPTKTEIVPGWLYGMSGFHTVLPIPLPILISQTLPMQQOL	GIVNAKIGCGCRORLELEYEMLTDKRMNAPGREYSLAEMTSTISMIIGLIIAAVPVGLF
		SIHLDYGYQOILIAASTRAIGELFCIPAPFPKTRMIFPPYIAYVAANTTVSSCHARR	LGMRLGVGSPIRKQSFDRAVASWSLSHSTAACLGALAAASATYMLRXSDSFT	SLMWVISFSGLIMFLGMWHIATSNRGQADLHTNSAPRTHWVISIPKYPAAGSLAGV
		FLESFTWCITFAGVLYSIGDCIDIPVNLIYMLTFIFPLVSLPLTHFOQLIRADA	VMMOLGFIILSAIVSGFGFYRYHDNMNKHIFFETRIOTANGIILHAFGRWLMDSP	SKEGAFSWPFWSWIRALGACGAPALASTSPNIENMSGVAVCAIIGKIILLIGNISN
		PFGAKAACHVDKSERGSPPTGLDIVEIKEPEPTVEQREVKQT"	complement(20398..20420)	/rpt_family="AT_rich"
repeat_region		/rpt_family="AT_rich"	complement(21006..21044)	/rpt_family="AT_rich"
repeat_region		complement(21081..21103)	/rpt_family="AT_rich"	complement(21321..21365)
repeat_region		complement(21865..21893)	/rpt_family="AT_rich"	complement(223096..23166,22544..23662,23792..23959,
repeat_region		complement(223096..225535)	/locus_tag="177013.26"	24672..24782,24905..24979,25082..25535))
gene		complement(24672..24905..24979,25082..25535))	/locus_tag="177013.26"	/product="hypothetical protein"
mRNA		complement(24672..24905..24979,25082..25535))	/locus_tag="177013.26"	/note="predicted by genemarkerHM"
CDS		/codon_start=1		
	Query Match	63.2%; Score 1876.2; DB 8; Length 163635;		
	Beet Local Similarity	85.4%; Pred. No. 0;		
	Matches 2170; Conservative	0; Mismatches 343; Indels 28; Gaps 6;		
Oy	426 AACAGCTTTTGTTGAATGAACCAACTTTATGGAAGAACAAGAAAGCAGAT	485		
Db	101446 ACCAGGTTCTGTGTTTAACCTGAATCACAACTTTATGGAAGGACAAAAGAAAGATAGAT	101505		
Oy	486 AGTGAATACTCTATTAACATATTAGCAATGCCCAAACAATCTCCAGTCCTCCCAATACT	545		
Db	101506 AGTGAATACTCTATTAACATATTAGCAATGCCCAAACAATCTCCAGTCCTCCCAATACT	101565		
Oy	546 TGGTATGGGGGAGCTAAGAAAGACGACTCTTGCGCCAATAGTCTTCAATGATCAGAGAGT	605		
Db	101566 TGGTATGGGGGAGCTAAGAAAGACGACTCTTGCGCCAATAGTCTTCAATGATCAGAGAGT	101625		
Oy	606 AATTGAGCATTTCCATCCCAAAATATGATTTGTGCTCGGAAGATTTTAAATAGAAGAG	665		
Db	101626 AACTGAGGCTTTCATCCCAAAATATGATTTGTGCTCGGAAGATTTTAAATAGAAGAG	101685		
Oy	666 GTTAGTAAGAATAATTGTGAATCTTATTAAGAAAAAGTCACTTGTGGATGAGACTTGGC	725		
Db	101686 GTTAGTAAGAATAATTGTGAATCTTATTAAGAAAAAGTCACTTGTGGATGAGACTTGGC	101745		
Oy	726 TCACACTTAAGAAAGCTTCGGAGCTGCTGAATGGAATAAATATTTGCTGCTTAAAG	785		

Db	101746	TCACCTTGAAAGAGCTTCAAGATTGCTGAATGGAAAAAATATCTTCTGTCTTAA	101809
Qy	786	TGATGTTGGAAATGAAGATCAAGATAGTGGCTTAAGTAAAGACAATCTTGAAGTTGG	845
Db	101806	TGATGTTGGAAATGAAGATCAAGATAGTGGCTTAATTAAGACAGTCTTGAAGTTGG	101865
Qy	846	AGCAAGTGGCGCTTCTGTTCTTACCACTACTGCTCTTGAAAAGTTGGATTCAAATTATGGG	905
Db	101866	AGCAAGTGGTGCATTTGTTCTTAACAACACTCTGCTTGAAAAGTTGGATTCAAATTATGGG	101925
Qy	906	AACATTGCACCATATGAATTGTCAAAATTTGTCCTAAGAAAGATGTGTGTGTGTTCAAT	965
Db	101926	AACATTGCACCATATGAATTGTCAAAATCTGCTCTCAGAGGATTTGTGTTTGTTCAT	101985
Qy	966	GCAACGTGCATTTTGGGCAACAAGAAATTAATCTTAATCTTGTGCTATCGGAAAGGA	1025
Db	101986	GCAGGTGCATTTTGGCAACAAGAAATTAATCTTAATCTTGTGCTATCGGAAAGGA	102045
Qy	1026	GATTGTGAAAAAATGTGGTGTGTGCTCTTAGCACTTAAACTCTTGGAGGTATTTTGGG	1085
Db	102046	GATTGTGAAAAAATGTGGTGTGTGCTCTTAGCACTTAAACTCTTGGAGGTATTTTGGG	102105
Qy	1086	CTTTAAGAGAGAAGAAAGACAGTGGGAAACATGTGAGATAGTGAATTTGGAAATTTGCC	1145
Db	102106	CTTTAAGAGAGAAGAAAGAGATGGGAAACATGTGAGAGACGTCCGATTTGGAAATTTGCC	102165
Qy	1146	TCAAGAGAAAGTTCTATTTCTGCCCTGAGACTTGAATTCATCACTTCACCTTGA	1205
Db	102166	TCAAGATGAAGTTCTATTTCTGCCCTGAGACTTGAATTCATCACTTCACCTTGA	102225
Qy	1206	TTTGAACAATGCTTTACATTTGTGCAGTATTTCCAAAGATACCGAAATGGAAAGGG	1265
Db	102226	TTTGAACAATGCTTTGTATTTGTGCGGTATTTCCAAAGGACACCAAAATGGCAAGGA	102285
Qy	1266	AAATCTATCTCTCTGCGATGGGACATGATTTTATTTATGAAAGGAACTTGGAGCT	1325
Db	102286	AAATCTATCTCTTTTGGATGGGACATGATTTTCTTTATGAAAGGAAATTTGGAGCT	102345
Qy	1326	AGAGATGTAAGTATGAAGTATGAATGAATTAATATCTTGAGGTCTTCTTCCAAAGAT	1385
Db	102346	AGAGATGTAAGTATGAAGTATGAATGAATTAATATCTTGAGGTCTTCTTCCAAAGAT	102405
Qy	1386	TGAAGTTAAATCTGTGCAAACTTATTTCAAGATGATGATCTCATTCATGCTGGCAAC	1445
Db	102406	TGAAGTTAAATCTGTGTAACCTTATTTCAAGATGATGATCCTCATTCATGATTTGGCTAC	102465
Qy	1446	ATCTCTATTTTCCGCAACACATCAAGAGCAATTCGGAAGAAATATGTGMAAAATTA	1505
Db	102466	ATCTCTGTTTTCAGCAAAACATCAAGAGCAAAATTCGTAAGAAATTAATGCTAATTAATA	102525
Qy	1506	CATACATATGATGTCATTTGGTTTCACTAAAGTGTATCTTTTACTCTTCCCACTT	1565
Db	102526	TGATATATGATGTCATTTGGTTTCCGTAAGTGTATCTTTTACTCTTCCCACTT	102585
Qy	1566	GCAGAGTTTGTCTGTGAGGGTGCTTAATCTTAAAGTACATAAACTTAAGCAGTTACC	1625
Db	102586	GCAAAAGTTTGTCTCATTTAAGGGTGCTTAATCTTAAAGAACTTGAACCTTAATCAATTACC	102645
Qy	1626	GTCCTTCCATTTGGAATCTAGTACATTTAAGATCCTTAACCTTGTGCGAATACTAGTAT	1685
Db	102646	ATCTTCCATTTGGAATCTAGTACATTTAAGATCCTTGAACCTTGTGCGAATACTAGTAT	102705
Qy	1686	TGCTAGTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTCTGATCTTACATGG	1745
Db	102706	TGCTAGTCTTCCAAAGAGATTAATGCAAGCTTCAAAATCTGCAAGCTCTTGAATTAATTA	102765
Qy	1746	CTGTCAATTCATTTGTGTGTTTCCAAAGAAAGCAAGCAACTTGTAGTCTTGGAAATCT	1805
Db	102766	TTGCGACCTCTTCTTGTGTTTCCAAACAAACAAAGTAAACTTGTAGTCTTCCGAATCT	102825
Qy	1806	TTTACTTGAATGTTGCTATGATATGATCTTGTATGCAACAAGATAGATCTTTGAACATG	1865
Db	102826	TTTACTTGAATGTTGCTATGATATGATCTTGTATGCAACAAGATAGATATGTTGAACATG	102882

QY 1866 CCTTAAGACTTAAAGTATTTGTGGGGAATTGAGAAAAGTGTCACTTGGCA 1925
 DB 102883 CCTTAAGCTCTTAAGTCTTGTGTATTTG6---CAAGGAAAAGTTATCAACTTGGTGA 102938
 QY 1926 ATTAAGAAAAGTGAATCTTAATGCTCAATTTGAATCAAGCATCTTGAGAGATGAGAA 1985
 DB 102939 ACTAATAAACTTAATCTTAATGCTCAATTTGAATCAAAAAGTTGACAGATGAGAA 102998
 QY 1986 TGAATATGATGAGAAAAGGCAATTTATCTGAAAAGAAAATCTGCATCTTTAAAGCAT 2045
 DB 102999 AATATGAGATGAGAAAAGGCAATTTATCTGAAAAGCAACTGCATCTTTTATGCTT 103058
 QY 2046 GAAATGGGATGAGCATGAGTCAAGTCAATATATGATGAGAAAAGTTGAAGTCTTGA 2105
 DB 103059 GAGTTGGGATCTTGAATGAGAAA---ACATGATATGATTTCA-----GAAATCTTGA 103106
 QY 2106 AGCTCTCAAAACCACTCCATCTGATCTTGTATTAATCAAGGAGCTTCAAGAAATCG 2165
 DB 103107 AGCCCTCAAAACCACTCCATCTGATTAATTAAGAAATCAATGAGCTTCAAGAAATCGT 103166
 QY 2166 TCTCCAGACTGAGATGATCACTCAAGTTTGAATAAGTGTCTATTTGAATATCATG 2225
 DB 103167 TCTCCAGACTGAGATGATCACTCAAGTTTGAATAAGTGTCTATTTGAATATTAAGAG 103226
 QY 2226 TTGCAAAAAGTCTGATGCTTACCAACCTTGTGAGAGCTGCTTGTAAAAGTCTGAG 2285
 DB 103227 TTGTGAAAAGTCTGCTGCTTACCAACCTTGTGAGAGCTGCTTGTAAAAGTCTGAG 103286
 QY 2286 GTTGTGAGAGGGGTGTGCGGAAAGTGAATATGTTGATTTCTGAGATCCCTCAAGAAAG 2345
 DB 103287 GTTACACACAGGGGTGAGCGAGAGTGAATATGTTGATTAATATGTTCTGCTG--GAAG 103343
 QY 2346 GTTTCATCTCTGAGAAAAGTAAATATATACGGCAATTTGTGATCTGAAGAGTGTCTGA 2405
 DB 103344 GTTTCATCTCTGAGGGAATCTGTTATATGGAATTTGATATCTTAAGAAAGTGTCTGA 103403
 QY 2406 AAAGGAGAGAGAGAGCAATGCTGTGCTTGAAGAGATGAGATTAATGTTGCCCTAT 2465
 DB 103404 AAAGGAGAGAGAGAGCAATGCTGTGCTTGAAGAGATGAGATTTACTGTGCCCTAT 103463
 QY 2466 GTTGTATTTCCAAACCTTGTCTGTCGAGAAATGCTATGATGAGGAGCAAGTCTGAG 2525
 DB 103464 GTTGTATTTCCAAACCTTGTCTGTCGAGAAATGAGATGATG--GAGAGAG 103517
 QY 2526 TGCATATGTTTCAAGTTCATATCTAATCTCATGAGCTCTTACTTCCCTCAAAATTCCTA 2585
 DB 103518 TGCATATGTTTCAAGTTCATATCTAATCTCATGAGCTCTTACTTCCCTCAAGATTTAGCA 103577
 QY 2586 TTAACAAAGAAATGCTTCACTCCAGAGAGATGTTCAAAAAGCTTGAATCTCAATA 2645
 DB 103578 TTAACGTAAGAACTTCACTCCAGAGAGATGTTCAAAAAGCTTGAATCTCAATA 103637
 QY 2646 CTGAATATCTCTTTTAACTTCACTTAAAGAGCTGCTTCAAGCTGCTAGTCTCA 2705
 DB 103638 CTGAATATCTCTTTTAAAGATCTCAAGAGATGCTTCAAGCTGCTAGTCTCA 103697
 QY 2706 TGTCTTGAAGCATGTGAATATCAATGTTTATGACTAGAGATCTCCCGAGAGAG 2765
 DB 103698 TGTCTTGAAGCATGTGAATATCAATGTTTATGACTAGAGATCTCCCGAGAGAGAG 103757
 QY 2766 TGTGAAGAGTTTATTTCACTCAACAGTTTATCAATCAATCTGTGAATGCTTACATG 2825
 DB 103758 GGTGAAGAGTTTATTTCACTCAACAGTTTATCAATCAATCTGTGAATGCTTAAATG 103817
 QY 2826 TTTACCGAGAGATTTGAGCACTTAAGAGCTTCAAAATTTATCAATGATTTTGTCC 2885
 DB 103818 TTTACCGAGAGATTTGAGCACTTAAGAGCTTCAAAATTTATCAATGATTTTGTCC 103877
 QY 2886 AACACTGGCCAGAGGTTGTGAAGAGGAAATGAGAAAGACTGTGACAAATTTGCTCAT 2945
 DB 103878 AATATGATTTCAAGCGGTGTGTGAGAGGAGAAATGAGAGACTGTGACAAATTTGCTCAT 103937

QY 2946 TCTCGTGTGTTTATTTATTA 2966
 DB 103938 TCCATATTTGACTATATGTA 103958
 RESULT 8
 LOCUS AY426264
 DEFINITION Solanum tuberosum blight resistance protein SH10 gene, partial cds.
 ACCESSION AY426264
 VERSION AY426264.1
 KEYWORDS GI:39636784
 SOURCE
 ORGANISM Solanum tuberosum (potato)
 Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE
 AUTHORS Van Der Vossen, E., Sikkema, A., Hekkert Bt, B.L., Gros, J., Stevens, P., Mueken, M., Mouters, D., Pereira, A., Sikkema, W. and Aliefs, S.
 TITLE An ancient R gene from the wild potato species Solanum bulbocastanum confers broad-spectrum resistance to Phytophthora infestans in cultivated potato and tomato
 JOURNAL Plant J. 36 (6), 867-882 (2003)
 PUBMED 14675451
 REFERENCE 2 (bases 1 to 3689)
 AUTHORS van der Vossen, E. and Sikkema, S.
 TITLE Direct Submission
 JOURNAL Submitted (03-OCT-2003) Bioscience, Plant Research International, Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
 FEATURES
 source
 1..3689
 /organism="Solanum tuberosum"
 /mol_type="genomic DNA"
 /db_xref="taxon:4113"
 /chromosome="VIII"
 /map="CT88-CT64"
 /note="SH83-92-489"
 join<1..427,1271..>(3689)
 /product="blight resistance protein SH10"
 join(1..427,1271..>(3689)
 /note="confers broad-spectrum resistance to Phytophthora infestans in potato and tomato"
 /codon_start=1
 /product="blight resistance protein SH10"
 /protein_id="AB029074.1"
 /db_xref="GI:39636785"
 /translation="MAEAFIVLIDNLTSLFKELVLLFGFQNEFRQLSSIFSTIOAV
 LBDADKOLNDKRLBNWLOKNAAYEVDIDDEKTKATRSQSAAGRYHPKVPFR
 HVGKMDQVKKLNAIAEERKNFHLHEKIIERQVREBTSVLTPEVYGKDEDE
 IVKILNNVSDQHLSTVPIIGMGIGKTTLQVFNQDRITVEHPSKIMIVSDPD
 EKRILKAIESTIEGRPIGEMDLPIOKKLOELNGKRYFVLDVNMEDQKMANLR
 AVLKAGSAPATLATRLREKVSIMGTLOPYLSLMSQEDCLLTICAFRQGEINP
 NVALGKEIVKSGGVPPLAKTLTGILFKREBEREHRDEIWNLPQERSIIPAL
 RLSYHLPLDLKQCFAYCAVFPKDTMEKEKILISMAHGFLLGKLOEDVNGEVS
 KEI,CLRSFQETEARCGKTYFMDIJDHLATLSASSTSSNIEIKVGPYRMS
 IGFTFVSSVPSLSQKFEVSLVNLISNHFELSSIGDLYHMKCLDSNGSIRSL
 PROLKQLOTLIDHNCYSLSCLPRBSKGLSNLFPHGDELSNMPRTGSLTFL
 KTLKMICGLOKRGVOLDKLRDYNVYSGEITELHFRVYNMADKAKANLSAQNLSLI
 NMSKRGHRTYSBEVRVTEALKPKNLTCLTISCFRGRPRPBMNHSVLKAVSIEI
 SCNRKSCILPPRGLPCLKRLLELQKSAEVEVDGFPTRRFPSLRLTIGEPLNK
 GLKKKEGKPEVLEKMTIFYCHMFVYVLTLSNFPALSLSHSHNNEVTSLEELFKS
 FANLYKLISLFYNLKEIPSSIACLNALKTIEIHSLSALESIPEBGVGLTSLTELTV
 YDCEMLKFLPELQHLTALVLSLKLRCQLKRC"
 ORIGIN
 Query Match 61.8%; Score 1832.2; DB 8; Length 3689;
 Best Local Similarity 85.2%; Pred. No. 0;
 Matches 2120; Conservative 0; Mismatches 298; Indels 69; Gaps 4;
 QY 426 AACAGTTTGTGTTGAATGAAACCAAGTTTATGGAAGAGCAAAAGAAAGACGAGAT 485
 ||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1266 ACCAGTCTGTATTAAGTAAACCCCAAGTTATGAAAGACAAAGAGGAATGAGAT 1325
QY 486 AGTGAATAATCCGATATAAATATGTAAGCAATGCCCAACATCTCCAGTCTCCCAATACT 545
Db 1326 AGTGAATAATCCGATATAAATATGTAAGCAATGCCCAACATCTCCAGTCTCCCAATACT 1385
QY 546 TGTGATGAGGAGGAGCTAGAGAAAGACATCTTGGCCCAATGCTTCAATGATCAGAGAT 605
Db 1386 TGTGATGAGGAGGAGCTAGAGAAAGACATCTTGGCCCAATGCTTCAATGATCAGAGAT 1445
QY 606 AATTGAGCAATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTAATGAAAGAG 665
Db 1446 TACGAGCAATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTAATGAAAGAG 1505
QY 666 GTTGATAAGGAAATTTGTAATCTATTGAAAGAAAGTC---ACTGTGGCAGTGAAT 722
Db 1506 GTTACTAAAGGCAATCATGAAATCTATTGAAAGAAAGGCACTACTTGGTGAATGAGACT 1565
QY 723 GGTCTCACTTCAAAAGAGCTTCGGGACTTGTGTAATGAAAGAAATATTTGCTGCTT 782
Db 1566 GGTCTCACTTCAAAAGAGCTTCAGAGATGTGTAATGAAAGAAATATTTGCTGCTT 1625
QY 783 AGATGATGTTTGAATGAAAGATCAAGATTAAGTGGCTTAAGTTAACAAGCTTTGAAGT 842
Db 1626 AGATGATGTTTGAATGAAAGATCAAGAGTGGCTTAATTTAAGAGCAATCTTGAAAGT 1685
QY 843 TGGAGCAAGTGGGCTGCTGTTCTTAACCACTACTGCTTGAAGAAAGTTGATCAATAT 902
Db 1686 TGGAGCAAGTGGGCTGCTTGTCTTACCACTACTGCTTGAAGAAAGTTGATCAATAT 1745
QY 903 GGGAAATTTGCAACCATATGAAATGATGTCAAATTTGTCTCAAGAGATTTGGTGTGTT 962
Db 1746 GGGAAATTTGCAACCATATGAAATGATGTCAAATGCTCTCAAGAGATTTGGTGTGTT 1805
QY 963 CATGCAAGCTGATTTGGGCAACCAAGAAATTAATTTTAATCTTTGGGCTATGAGAA 1022
Db 1806 CATGCAAGCTGATTTGGGCAACCAAGAAATTAATTTTAATCTTTGGGCTATGAGAA 1865
QY 1023 GGAATTTGTGAAAGAAATGTTGGTGTGCTCTAGACAGCTTAAATCTTTGAGGATTTT 1082
Db 1866 AGAGATTTGTGAAAGAAATGTTGGTGTGCTCTAGACAGCTTAAATCTTTGAGGATTTT 1925
QY 1083 GCGCTTTAAGAGAGAAAGACAGTGGAAATGTCAGAGATGAGATTTGGAAAT 1142
Db 1926 GCGCTTTAAGAGAGAAAGACAGTGGAAATGTCAGAGATGAGATTTGGAAAT 1985
QY 1143 GCTCTAAGAGAAAGTTCTATTCTGCTGCTGCTGAGACTTAAGTATCACTTCCACT 1202
Db 1986 ACCTCAAGAGAAAGTTCTATTCTGCTGCTGCTGAGACTTAAGTATCACTTCCACT 2045
QY 1203 TGAATTTGAGCAATGCTTATCAATTTGTCAGTATTTCCCAAGATTAACCAAGAAAGGAAA 1262
Db 2046 TGAATTTGAGCAATGCTTATCAATTTGTCAGTATTTCCCAAGATTAACCAAGAAAGGAAA 2105
QY 1263 GGGAAATCTAATCTCTCTCGAATGGCACATGTTTTTATTTATGAAAGAACTTTGGA 1322
Db 2106 AGAAAGCTAATCTCTCTCTCGAATGGCCACGGTTTTCTTTATTTGAAAGAAATTTACA 2165
QY 1323 GCTAAGAGATGAGTAATGAAAGTATGAAATTAATTAATCTTGAAGTCTTTCTTCCAGA 1382
Db 2166 GCCAGAGAGATGAGTAATGAAAGTATGAAAGAAATTAATCTTGAAGTCTTTCTTCCAGA 2225
QY 1383 GATTGAAGTTAAATCTGCTCAAACTTATTCAGAGTATGATCTCATTCATGATCTGGC 1442
Db 2226 GATTGAAGTTAAATGCTGTAATACTTATTTCAAGTATGATCTCATTCATGATTTGGC 2285
QY 1443 AACATCTTATTTTGGCAAGACATCAAGACCAATATCCGAGAAATATTTGAGAAA 1502
Db 2286 TACATCTCTGTTTTCAGACAGACATCAAGTACCAATATCCGCGAAATATTTGAGAAA 2345
QY 1503 TTACATACAT---ATGATGTCATTTGTTTCACTAAGTGTATCTTCACTCTTTC 1559
Db 2346 TTACCATTAAGATGATGTCATTTGTTTCACTGAAAGTGTATCTTCACTCTCTCCTC 2405

QY 1560 CCACCTTGCAAGATTGTGCTGCTGAGGCTCTAATCTAAGTGAATATAAATCTTAACA 1619
Db 2406 TGTGTGCAAAAGTTGTGCTGTTAAGAGTGTATTAATCTAAGTAACTTAACCTTTGAGGA 2465
QY 1620 GTTACCGTCTTCCATTTGAGATCTAGTACATTTAAGATTAACCTTAACCTTGTGCAATTC 1679
Db 2466 GTTATCTCTTCCATTTGAGATCTAGTACATTAAGATTAAGTCTGAGCTTGTCTGAAATTC 2525
QY 1680 TAGATTTGTGCTGCTTCCAAACAGTTATGCAAGTCTTAAATCTGACAGCTCTGATCT 1739
Db 2526 TGAATTTGTGCTGCTTCCAAACAGTTATGCAAGTCTTAAATCTGACAGCTCTGATCT 2585
QY 1740 ACATGCTGTGATTCATCTTGTGTTTGGCCAAAGAAACAGCAAACTTGTGATCTTCG 1799
Db 2586 ACATTAATTTGATCTCTCTTCTTGTGTTCCAAAGAAACAGTAATCTTGTGATCTCG 2645
QY 1800 AATCTTTTACTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1859
Db 2646 AATCTTTTCTTGAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2705
QY 1860 GACATGCTTAAAGCTCTAAGTATGATTTGTGAGATTTGAGAAAGAAAGTGTCACT 1919
Db 2706 GACATGCTTAAAGCTCTTAAAGTATGATTTGTGAGATTTGAGAAAGAAAGTGTCACT 2765
QY 1920 TGTGAAATTAAGAAACCTGAATCTCTAATGCTCAATTTGAATTAACGCACTTTGAGAGAT 1979
Db 2766 TGTGAAATTAAGAAACCTGAATCTCTAATGCTCAATTTGAATTAACGCACTTTGAGAGAT 2825
QY 1980 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2039
Db 2826 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2885
QY 2040 AAGATGAAATGGAATGACATGAAACCTGCAATTAATTAATTAATTAATTAATTAAT 2099
Db 2886 AATCAATGATTTGAGT---AGAAAGAGCCGCAATTAATTAATTAATTAATTAAT 2942
QY 2100 GCTTGAAGCTCTCAAAACCACTCAATCTGATCTTGTAAATTAATTAATTAATTAAT 2159
Db 2943 GATTGAAGCTCTCAAAACCACTCAATCTGATCTTGTAAATTAATTAATTAATTAAT 3002
QY 2160 AATCGTCTCCAGACTGATGATTAATCACTCAATTTGAAATTTGCTCTTAATTAAT 2219
Db 3003 AATCGTCTCCAGACTGATGATTAATCACTCAATTTGAAATTTGCTCTTAATTAAT 3062
QY 2220 CATCAATTTGCAAAATCTGATGATTAATCAATCTTGTGATGATGATGATGATGATGAT 2279
Db 3063 CAGTGTGCAAAATCTGATGATTAATCAATCTTGTGATGATGATGATGATGATGAT 3122
QY 2280 TCTAAGTGTGAGAGGAGGCTGCGGAGAGTGAATGATTTCTGATTTCCCTACAG 2339
Db 3123 TCTAAGTGTGAGAGAGGAGGCTGCGGAGAGTGAATGATTTCTGATTTCCCTACAG 3182
QY 2340 AAGAGGTTTCCATCTCTGAGAAATCTTAATTAATGCGCAATTTGATTAATGAAAGAT 2399
Db 3183 AAGAGGTTTCCATCTCTGAGAAATCTTAATTAATGCGCAATTTGATTAATGAAAGAT 3242
QY 2400 GCTGAAAG 2459
Db 3243 GCTGAAAG 3302
QY 2460 CCCTATGTTGTTAATCCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2519
Db 3303 CCATATGTTGTTAATTAATCACTCTTCT--- 3330
QY 2520 GTGATGCAATGATTTCAAGTTCAATTAATCTAATGCTTCACTTCCCTCAAT 2579
Db 3331 -----TCTAATTTAGGCTCTTCACTTCCCTCAAT 3362
QY 2580 TCGTATTAACAAAGAGATGCTTCACTCCAGAGAGAGATTTCAAAAGCTTTGCAATCT 2639
Db 3363 TAGCATTAACAAAGAGATGCTTCACTCCAGAGAGAGATTTCAAAAGCTTTGCAATCT 3422

QY	2640	CAAAATCTGGAATATCTCTTTTACTTCAATTTAAAGAGCTGCTACGAGCTGGCTAG	26599
Db	3423	CAAAATCTGGAATATCTCTCTCTTTTACATCTCAAAGAGCTCTTACAGCTTGGCTTG	3482
QY	2700	TCTCAATGCTTTGAAGCATCTGAAATTCATAGTGGTTATGACATGAGAGTCTCCCGA	2759
Db	3483	TCTCAATGCTTTGAAGACACTGGAATTCATAGCTGTAGCGCATGAGAGTCTCCCGA	3542
QY	2760	GGAAGGTGTGAAGGTTTAATTTCCTACACAGTTATCCATTAACATCTGTGAATGCT	2819
Db	3543	GGAAGGGGTGAAGGTTTAATCTTCACTACAGAGTTATTTGTATGTAGCTGTGAGATCT	3602
QY	2820	ACAATGTTACCGGAGGGATTGACACACTAAGGCTTCAAAATTAATAGTTGAGTT	2879
Db	3603	AAAATTTTACCGGAGGGATTGACACACTTAACAGCTCTCAAGTTTAAACTTAGGAG	3662
QY	2880	TTGTCCAACTGTCGCGCAAGCGGTGTGA	2906
Db	3663	ATGTCCAACTGATCAAGCGGTGTGA	3689
RESULT 9			
AS814113			
LOCUS	AX814113	3592 bp	DNA linear PAT 05-DEC-2003
DEFINITION	Sequence 36 from Patent EP1334979.		
ACCESSION	AX814113		
VERSION	AX814113.1	GI:39103415	
KEYWORDS			
SOURCE			
ORGANISM	Solanum bulbocastanum		
	Solanum bulbocastanum		
	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,		
	Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,		
	asterids, lamids, Solanales; Solanaceae; Solanum.		
REFERENCE	1		
AUTHORS	van der Vossen, E.A. and Alfelfe, J.J.		
TITLE	Gene conferring resistance to phytophthora infestans (late-blight)		
	in Solanaceae		
JOURNAL	Patent: EP 1334979-A 36 13-AUG-2003;		
	Kweek-en Researchbedrijf Agrico B.V. (NL)		
FEATURES			
source	1..3592		
	Location/Qualifiers		
	/organism="Solanum bulbocastanum"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:147425"		
	1..3591		
	/note="Rpi-blb including intron sequence (position		
	428-1106)"		
ORIGIN			
Query Match	60.9%; Score 1805.8; DB 6; Length 3592;		
Best local Similarity	84.2%; Pred. No. 0;		
Matches 2159; Conservative	0; Mismatches 302; Indels 102; Gaps 7;		
QY	426	AACAGTTTTGTTTGAATGACCAACAGTTTATGGAAGACAAAAGAACGAGAT	485
Db	1102	ACCAAGTTCTGTATTAACCAACGAGTTTATGGAAGACAAAAGAACGATAGAT	1161
QY	486	AGTCAAAATCCTGTATAACATGTTAGCAATGGCCAAACCTTCAAGTCTCCCAATACT	545
Db	1162	AGTCAAAATCCTATAAACAATGTTAGTATGACCAACACTTTCAGTCTCTCCCAATACT	1221
QY	546	TGTGATGGGGGACATGAGAAAGACACTCTTGCCCAATGTGTTCAATGATCAGAGGT	605
Db	1222	TGTGATGGGGGAGATGAGAAACGACTCTTGCCCAATGTGTTCAATGACCAAGAGGT	1281
QY	606	AATTGACATTTCCATCCCAAAATATGAGATTTGTGCTCGGAAGATTTTAAATGAGAG	665
Db	1282	TATCGAGCAATTTCCAAATATGAGATTTGTGCTCGGAAGATTTTGAATGAGAG	1341
QY	666	GTTGATTAAGAAATGTGATCTATTTGAAGAAAGTC--ACTTGGTGACATGAGCTT	722
Db	1342	GTTAAATTAAGCAATGTGAAATCTATTTGAAGAAAGCACTACTTGATGATGAGCTT	1401

QY	723	GGCTCCACTTCAAAAGAGCTTCGGGACTTGTGTAATGGAAAAAATAATTGCTGCTT	782
Db	1402	GGCTCCACTTCAAAAGAGCTTCAGGAGTGTGTGAATGGAAAAAGATACCTTGCTT	146
QY	783	AGATGATGTTTGGAAATGAAGATCAAGATTAAGTGGCTTAAGTAAACAAGCTTTGAAGT	842
Db	1462	AGATGATGTTTGGAAATGAAGATCAACAAGTGGCTTAATTTAAGACACAGCTTTGAAGT	1522
QY	843	TGGAGCAAGTGGCGCTTCTGTCTTAACCACTACTGCTTGAAAGGTGGATCAATTAT	902
Db	1522	TGGAGCAAGTGGCGCTTCTGTCTTAACCACTACTGCTTGAAAGGTGGATCAATTAT	158
QY	903	GGGAACATTTGCACCACTATGAATTTGTCAAATTTGTCTAGAGATTTGTTGTTT	962
Db	1582	GGGAACATTTGCACCACTATGAATTTGTCAAATTTGTCTAGAGATTTGTTGTTT	164
QY	963	CATGCAAGCTGCAATTTGGGACCAAGAAGAAATTAATCTTAATCTTGTGGCTATCGAAA	102
Db	1642	CATGCAAGCTGCAATTTGGGACCAAGAAGAAATTAATCTTAATCTTGTGGCAATCGAAA	170
QY	1023	GGAGATTTGAAAAAAATGTGTGTGTGCTCTTACAGCTTAAACTCTTGTGAGTATTTT	108
Db	1702	GGAGATTTGAAAAAAATGTGTGTGTGCTCTTACAGCTTAAACTCTTGTGAGTATTTT	176
QY	1083	GGCCTTTAAGAGAGAAAGACAGTGGGACATGTAGAGATATGAGATTTGGAATTT	114
Db	1762	GTGCTTCAGAGAGAGAAAGACATGTAGAGACATGTAGAGACAGTCCGATTTGGAATTT	182
QY	1143	GCCTCAAGAGAAAGTTCTAATTTCTGCTGCTCCCTGAGACTTAATTCATCACTTCCTCACT	120
Db	1822	GCCTCAAGAGAAAGTTCTAATTTCTGCTGCTGCTCCCTGAGACTTAATTCATCACTTCCTCACT	188
QY	1203	TGATTTGAGACAGTCTTACATTAATGTGACATATCCCAAGATATCCGAAATGGAAAA	126
Db	1882	TGATTTGAGACAGTCTTGTGCTATGTGGGAGTGTCCCAAGAGATGCCAAATGGAAAA	194
QY	1263	GGGAATCTAATCTCTCTGTGATGACCAATGTTTTAATTTATGCAAGAAACTTGA	132
Db	1942	AGAAAAAGCTAATCTCTCTGTGATGCGCAGATGGTTTTCTTTATCAAAAGAAACATGGA	200
QY	1323	GCTAAGAGATGAGTATGAAATGATGAAATTAATCTTGAAGTCTTTCTTCCAAA	138
Db	2002	GCTAAGAGATGAGTATGAAATGATGAAATTAATCTTGAAGTCTTTTCCAAA	206
QY	1383	GATTGAAGTTAAATCTGTCAAACTTAATTTCAAGATGATCTCAATCATGATCTGC	144
Db	2062	GATTGAAGTTAAAGTGTAAATCTTAATTTCAAGATGATCTCAATCATGATTTGC	212
QY	1443	AACATCTTAATTTTGGCAGACACATAGACAGCAATATCCGAAATTAATGTGAAAA	150
Db	2122	AACATCTGTGTTTTCAGCAACATCAACACAGCAATATCCGAAATTAATTAACACAG	218
QY	1503	TTACATTAATTAATGATGATGATGATTTCACTAAAGGATATCTTCTAATCTTTTCCCA	156
Db	2182	TTACACACATTAATGATGATGATGATTTTGGCAGAGTGTGTTTTTTTACATCTTCCCC	224
QY	1563	CTTGCAAGATTTGTTCTGCTGTGAGAGTCTTAATCTTAAGTGCATTAATTAAGCAGTT	1622
Db	2242	CTTGCAAGATTTTATCTGTTAAGAGTGTCTTAATCTTAAGTGCATTAATTAAGTT	230
QY	1623	ACCGTCTTCATTTGAGAGATCTAAGTCACTTAATTAATTAATTAATTAATTAAGTT	168
Db	2302	ACCATCTTTCATTTGAGAGATCTAAGTCACTTAATTAATTAATTAATTAATTAAGTT	238
QY	1683	TATTTGATGTTTCCAAACAGTTATGCAAGCTTCAAAATCTGCAAGCTTCAATCTCA	174
Db	2359	CATGATGATGTTTCCAAAGCAATTAATGCAAGCTTCAAAATCTGCAAGCTTCAATCTCA	241
QY	1743	TGGCTGTCATTCATCTTTGTTGTTTGGCAAAAGAAACAGCAACTTTGTGATCTTCCAAA	1802
Db	2419	ATATTTGACCAAGCTTGTGTTGTTTGGCAAAAGAAACAGTAAACTTTGTGATCTTCCAAA	2478
QY	1803	TCTTTTACTGATGTTGCTATGAGATTTGAATCTTGTATGACACCAAGATAGATCTTTTAC	1862

```

|||||
2479 TCTTTACTTGAATGAGTACGACATGCTGATGTCACCAAGATAGATCATTTGAC 2538
1863 ATGCTTAAGACTCTAAGATATTTGTGTGGAAATTCAGAAAGATGCACTTGG 1922
2539 ATGCCCTTAAGACTCTAAGATATTTGTGTGGAA--GGAAGAAAGTTATCAACTGG 2595
1923 TGAATTAAGAACTGAATCTCTAATGAGCTCAATGAAATCAGCATCTTGAGAGTGA 1982
2586 TGAATTAAGAACTGAATCTCTAATGAGCTCAATGAAATCAGCATCTTGAGAGTGA 2655
1983 GAATGATATGATGCAAAAAGAAAGCAATTTATCTGCAAAAAGAAATCTGATCTTTAAG 2042
2656 GAATGATATGATGCAAAAAGAAAGCAATTTATCTGCAAAAAGAAATCTGATCTTTAAG 2715
2043 CATGAAATGGATGATGATGAAAGCTCCAGATATATATGAAATGCAAAAAGTGAAGTCT 2102
2716 CATGAGTTGGATATCTTTG--GACCAATATATATGAAATGCAAAAAGTGAAGTCT 2772
2103 TGAAGCTCTCAAAACCACTCCATCTGATCTTTAATCAATCAGGGGCTTGAGAGAT 2162
2773 TGAAGCTCTCAAAACCACTCCATCTGATCTTTAATCAATCAGGGGCTTGAGAGAT 2832
2163 CCGTCTCCCAAGCTGATGATCACTCACTTTTGAATAATGTTCTCTATTTGAATCAT 2222
2833 CCATCTCCCAAGCTGATGATCACTCACTTTTGAATAATGTTCTCTATTTGAATCAT 2892
2223 CAGTTGCAAAAATCTGCTACCTTACCACTTTGATGAGCTGCTTGTCTTAAAGTCT 2282
2893 CAATCTCAAAAATCTGCTACCTTACCACTTTGATGAGCTGCTTGTCTTAAAGTCT 2952
2283 AGAGTTGGAGAGGGGCTGCGGGAAGTGAATGTTG-----A 2321
2953 AGAGTTACACTGGGGGCTGCGGGAAGTGAATGTTG-----A 3012
2322 TTCTGATTCCTCTACAGAAGAGTTTCATCTCTGAAAACTTAATATACGGAAAT 2381
3013 TTCTGATTCCTCTACAGAAGAGTTTCATCTCTGAAAACTTAATATACGGAAAT 3072
2382 TGGTATCTGAAAGATGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2441
3073 TGGTATCTGAAAGATGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3132
2442 GATAGAGATTAATGTTGCCATGTTTGTATTCACACCTTCTCTGTCGAAGAAAT 2501
3133 GATGATTAATTAATGTTGCCATGTTTGTATTCACACCTTCTCTGTCGAAGAAAT 3169
2502 GGTAGTATGAGGAGCAAGATCAGATGCAATAGTTTCAATTCATCTCATGAGC 2561
3170 -----TCTAATCTTAGGCG 3183
2562 TCTTACTTCCCTCAAAATTCGCTATTAACAAGAGATGCTTCACTCCAGAAAGATGTT 2621
3184 TCTTACTTCCCTCAAAATTCGCTATTAACAAGATGCTTCACTCCAGAAAGATGTT 3243
2622 CAAAAGCCTGAAATCTCAATTAATCTCTTTTAACTCAATCTTAAGAGAT 2681
3244 CAAAAGCCTGAAATCTCAATTAATCTCTTTTAACTCAATCTTAAGAGAT 3303
2682 GCTTACCAAGCTGCTGATGCTCAATGCTTTGAAGATCTGAAATCTAGTTGTTATG 2741
3304 GCTTACCAAGCTGCTGATGCTCAATGCTTTGAAGATCTGAAATCTAGTTGTTATG 3363
2742 ACTAGAGAGTCTCCCGAGAGAGAGTGTGAAGGTTTAATTTCACTCAAGATTCAT 2801
3364 ACTAGAGAGTCTCCCGAGAGAGAGTGTGAAGGTTTAATTTCACTCAAGATTCAT 3423
2802 AACATAGTGTGAAGGATCAATGTTTCCGAGAGAGATTTGAGAGAGAGAGAGAGAG 2861
3424 TGAACAGTGTGAAGGATCAATGTTTCCGAGAGAGATTTGAGAGAGAGAGAGAGAG 3483
2862 AAATTTATCAGTTGATTTGTCTCAACACTGGCCAAAGCGGTGTGAAGAGAGATGAGAG 2921
|||||

```

```

Db 3484 AAGTTAAAAATTCGGGAGTGTCCAACTGATCAAGCGGTGTGAAGAGAGATGAGAGA 3543
QY 2922 AGACTGTACAAAATTTGCTCAATTCCTCGTGTGTTATTTAT 2964
Db 3544 AGACTGTACAAAATTTTCTCAATTCCTTAATGTGATATATAT 3586

RESULT 10
AX816332
LOCUS AX816332 3592 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 49 from Patent WO03066675.
ACCESSION AX816332
VERSION AX816332.1 GI:39646823
KEYWORDS
SOURCE
ORGANISM
Solanium bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanium.

REFERENCE
1
AUTHORS Allefs, J. J. and van der Vossen, E. A.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
JOURNAL Patent: WO 03066675-A 49 14-AUG-2003;
Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES
location/Qualifiers
source 1..3592
/organism="Solanium bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
1..3591
/feature
1..3591
/feature
428-1106#"

ORIGIN
Query Match 60.9%; Score 1805.8; DB 6; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;

QY 426 AACAGGTTTGTGTTGAATGAACCAAGTTTATGAAAGAGAGAGAGAGAGAGAT 485
Db 1102 ACCAGGTTCTGTATTAACCGAACCGAGGTTTATGAAAGAGAGAGAGAGAGAT 1161
QY 486 AGTGAATTCCTGATTAACCAATGTTAGCAATGCCCAACACTTCAGTCTCCCAATCT 545
Db 1162 AGTGAATTCCTGATTAACCAATGTTAGTATGCCCAACACTTCAGTCTCCCAATCT 1221
QY 546 TGGTATGAGGAGACTAGGAAAGAGAGACTCTGCCCAATGCTTCTCAATGATCAGAGAGT 605
Db 1222 TGGTATGAGGAGACTAGGAAAGAGAGAGACTCTGCCCAATGCTTCTCAATGATCAGAGAGT 1281
QY 606 AATTGAGATTTCCATCCCAAAATATGAGATTTGTGTCTGGAAGATTTAATGAGAGAG 665
Db 1282 TACTGAGGATTTCCATCCCAAAATATGAGATTTGTGTCTGGAAGATTTAATGAGAGAG 1341
QY 666 GTGATTAAGGAATTTGATGATCATTTGAAGAAAGC---ACTGCTGAGATGAGACTT 722
Db 1342 GTGATTAAGGAATTTGATGATCATTTGAAGAAAGC---ACTGCTGAGATGAGACTT 1401
QY 723 GGTTCACCTTCAAAAAGAGCTTCGGGACTTGTGATGAGAAATTAATTTGCTGCTT 782
Db 1402 GGTTCACCTTCAAAAAGAGCTTCGGGACTTGTGATGAGAAATTAATTTGCTGCTT 1461
QY 783 AGATGATTTTGAATGAAGATCAAGATAGTGGCTTAAGTTAAGCAAGTCTTGAAGT 842
Db 1462 AGATGATTTTGAATGAAGATCAAGATAGTGGCTTAAGTTAAGCAAGTCTTGAAGT 1521
QY 843 TGGAGCAAGTGGGCTTCTGTTTAAACCACTACCTGCTTGAAGAGTTGATCAATAT 902
Db 1522 TGGAGCAAGTGGGCTTCTGTTTAAACCACTACCTGCTTGAAGAGTTGATCAATAT 1581
QY 903 GGAACATTTGCAACCATATGATTTGTCAAAATTTGTCTCAAGAGATTTGTTGTTT 962
|||||

```


Dh 1582 GGGACATTCGCAACCATATGACTGTCAATCTGTCTCAAGAGATTGTGTTGTT 1641
Qy 963 CATGCAACGTCATTTGGGACCAAGAAATAAATCTTAATCTTGTCATATCGGAAA 1022
Db 1642 CATGCAACGTCATTTGGGACCAAGAAATAAATCTTAATCTTGTCATATCGGAAA 1701
Qy 1023 GGAATTTGTAAGAAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1082
Db 1702 GGAATTTGTAAGAAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1761
Qy 1083 GGCCTTTAAGAT 1142
Db 1762 GGCCTTTAAGAT 1821
Qy 1143 GGCCTAAGAT 1202
Db 1822 GGCCTAAGAT 1881
Qy 1203 TGAATTTGAGACATGCTTTTACATATTTGACATATTTGACATATTTGACAT 1262
Db 1882 TGAATTTGAGACATGCTTTTACATATTTGACATATTTGACATATTTGACAT 1941
Qy 1263 GGGAAATCTAATCT 1322
Db 1942 GGGAAATCTAATCT 2001
Qy 1323 GCTAGAGATGTAGATATGAGATATGAGATATGAGATATGAGATATGAGATAT 1382
Db 2002 GCTAGAGATGTAGATATGAGATATGAGATATGAGATATGAGATATGAGATAT 2061
Qy 1383 GATTGAGATTAATCTGTCTGCAAACTTTATTCAGAGATGATCTCATATTCATG 1442
Db 2062 GATTGAGATTAATCTGTCTGCAAACTTTATTCAGAGATGATCTCATATTCATG 2121
Qy 1443 AACATCTCTAATTTGGGACAGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAT 1502
Db 2122 AACATCTCTGTTTTCAGCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAT 2181
Qy 1503 TTACATCAATATGATGTCATTTGTTTCACTAAGTGTATCTTCTCTCTCTCTCT 1562
Db 2182 TTACATCAATATGATGTCATTTGTTTCACTAAGTGTATCTTCTCTCTCTCTCT 2241
Qy 1563 CTTCGAGAGATTTGTCGTGTGAGGGTCTTAATCTTAAGTGCATTAAGCACTTA 1622
Db 2242 CTTCGAGAGATTTGTCGTGTGAGGGTCTTAATCTTAAGTGCATTAAGCACTTA 2301
Qy 1623 ACCGCTTTCATTTGAGAGATAGTACATTTAAGATCTTAAGCTTGTCTGCAATCT 1682
Db 2302 ACCGCTTTCATTTGAGAGATAGTACATTTAAGATCTTGAACCTGTATGTC 2358
Qy 1683 TATTTGTAGTCTTCCAAACCACTTAATGCAAGCTTCAAAATCTGCACTTGTAT 1742
Db 2359 CATGCGTAGTCTTCCAAACCACTTAATGCAAGCTTCAAAATCTGCACTTGTAT 2418
Qy 1743 TGGCTGTCAATCACTTTGTTTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAT 1802
Db 2419 ATATTGACCAAGCTTTGTTTGGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAT 2478
Qy 1803 TCTTTTATCTGATGTTGCTTAATGATGATCTTGTATGCAACCAAGATAGATCT 1862
Db 2479 TCTTTTATCTGATGTTGCTTAATGATGATCTTGTATGCAACCAAGATAGATCT 2538
Qy 1863 ATGCTTTAAGCTCTTAAGTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1922
Db 2539 ATGCTTTAAGCTCTTAAGTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2595
Qy 1923 TGAATTAAGAACTGATCTCTATGGCTCAATGGAATCAAGATCTGTGAGAGATGA 1982
Db 2596 TGAATTAAGAACTGATCTCTATGGCTCAATGGAATCTGTGAGAGATGA 2655
Qy 1983 GAATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAGAGATCTGTATCT 2042
Db 2656 GAATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAGAGATCTGTATCT 2715

Qy 2043 CATGAAATGGGATGACATGAACTCCAGCTATATATGATACAGAAAAAGTTGAAGTCT 2102
Db 2716 CATGAGTTGGAATTAACCTTTG---GACCAATATATATGAATCAAGAAAGTTAAAGTCT 2772
Qy 2103 TGAAGCTCTCAAAACCACTCCAAATCTGATCTGTTTAAACATTCAGGGGCTTCAGAGAT 2162
Db 2773 TGAAGCTCTCAAAACCACTCCAAATCTGATCTTCTTTAAATCTATAGCTTCAAGAGAT 2832
Qy 2163 CCGTCTCCAGACTGATGAAATCACTCAGTTTGAAGAAATGTTGTCTATTTGAATCAT 2222
Db 2833 CCATCTCCCAAGAGATGATGATCACTCAGTATGAAAAATATGTCTCTATTTCAATTAAG 2892
Qy 2223 CAGTTGCAAAAACGCTCATAGCTTACAGACCTTTGTGAGAGTGTGCTGCTGCTGCT 2282
Db 2893 CAATCTCAAAAACGCTCATAGCTTACAGACCTTTGTGAGAGTGTGCTGCTGCTGCT 2952
Qy 2283 AAGTTGTGAGAGGGGCTGTGCGAAGTGTGATGTG-----A 2321
Db 2953 AAGTTGTGAGAGGGGCTGTGCGAAGTGTGATGTG-----A 3012
Qy 2322 TTCTGATTTCCCTTCAAGAGAGAGGTTTCCATCTCTGAGAAAATTAATATAGCGAAT 2381
Db 3013 TTCTGATTTCCCTTCAAGAGAGAGGTTTCCATCTCTGAGAAAATTAATATAGCGAAT 3072
Qy 2382 TGTATATCTGAAAAGATTTGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2441
Db 3073 TGTATATCTGAAAAGATTTGCTGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3132
Qy 2442 GATAGAGATTAATATGTTGCTGTATGTTTGTATTTCCAACTTCTCTGTCTCAAGAAAT 2501
Db 3133 GATAGATTAATATGTTGCTGTATGTTTGTATTTCCAACTTCTCTGTCTCAAGAAAT 3169
Qy 2502 GGTATGTTAGTGGGAGCAAGTCAATGCAATAGGTTTCACTTCAATATCTCATGTC 2561
Db 3170 -----TCTAATCTTATGAGGC 3183
Qy 2562 TCTTACTTCCCTCCAAATTCGTATTAACAAAGAGAGATGCTTCACTCCAGAGAGATGTT 2621
Db 3184 TCTTACTTCCCTCCAAATTCGTATTAACAAAGAGAGATGCTTCACTCCAGAGAGATGTT 3243
Qy 2622 CAAAAGCTTTCGAATCTCAAAATCTGAATATCTCTTTTACTTCAATCTTAAAGACT 2681
Db 3244 CAAAAGCTTTCGAATCTCAAAATCTGAATATCTCTGCTGCAATATCTCAAGAGCT 3303
Qy 2682 GCTACACAGCTGCTGCTAGTCTCAATGCTTGAAGATCTGAAGATCATAGTTATGTC 2741
Db 3304 GCTACACAGCTGCTGCTAGTCTGAATGCTTGAAGATCTGAAGATCATAGTTATGTC 3363
Qy 2742 ACTAGAGAGTCTCCCGAGAGAGGTGTGAAGGTTTAATTTCACTGACACAGTTATCAT 2801
Db 3364 ACTAGAGAGTCTCCCGAGAGAGGTGTGAAGGTTTAATTTCACTGACACAGTTATGTC 3423
Qy 2802 AACATCTGTGAAATCTCAATGTTTACCGAGAGATTTGCAAGCACTTAACAGCTCTGC 2861
Db 3424 TGAACACTGTAAATCTTAATATGTTTACAGAGGATTTGCAAGCACTTAACAGCTCTGC 3483
Qy 2862 AAATTTATCAGTTGATTTTGTTCACACCTGCGCAAGCGTGTGAGAGAGAGATAGAGA 2921
Db 3484 AAATTTAAATTTGCGGAGATGTTCACACCTGCGCAAGCGTGTGAGAGAGAGATAGAGA 3543
Qy 2922 AGACTGTACAAATTTCTCACTTCTCGTGTGTTATTTAT 2964
Db 3544 AGACTGTACAAATTTCTCACTTCTCGTGTGTTATTTAT 3586

RESULT 11
AX816333
LOCUS AX816333 5191 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 50 from Patent WO03066675.
ACCESSION AX816333
VERSION AX816333.1 GI:39646824
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1 Allefs, J.J. and van der Voosen, E.A.
AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
TITLE in Solanaceae
JOURNAL Patent: WO 03066675-A 50 14-AUG-2003;
Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1. 5191
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: sequence of 5.2
kb Sca I genomic DNA fragment of S. bulbocastanum BAC SPB
4 present in pRGC2-b1b"

ORIGIN
Query Match 60.9%; Score 1805.8; DB 6; Length 5191;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;

Qy 426 AACAGGTTTGTGTAATGAACCAAGTTTATGAAAGACAAAGAAAGACGAGAT 485
Db 2292 ACCAGGTTCTGATTAACGAAACCGACGTTTATGAAAGACAAAGAAAGATGAGAT 2351
Qy 486 AGTGAATTCCTGATTAACATGTTAGCAATGCCCAACACTTCCAGTCTCCCACTACT 545
Db 2352 AGTGAATTCCTGATTAACATGTTAGCAATGCCCAACACTTCCAGTCTCCCACTACT 2411
Qy 546 TGGTATGGGGGGGACTAGGAAGAAGACACTTGGCCCAATGGTCTTCAATGATCAGAGAT 605
Db 2412 TGGTATGGGGGGGACTAGGAAGAAGACACTTGGCCCAATGGTCTTCAATGATCAGAGAT 2471
Qy 606 AATTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTAATGAGAAG 665
Db 2472 TACTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTAATGAGAAG 2531
Qy 666 GTTGATTAAGGAATTTGTAATCTATTTGAAAGAAAGTC--ACTGTGGCATGAGACTT 722
Db 2532 GTTATTAAGGAATTTGTAATCTATTTGAAAGAAAGTC--ACTGTGGCATGAGACTT 2591
Qy 723 GGCTCCACTTCAAAAGAGCTTCGGACCTTGCTGAATGGAAGAAATATTTGCTGCTT 782
Db 2592 GGCTCCACTTCAAAAGAGCTTCGGACCTTGCTGAATGGAAGAAATATTTGCTGCTT 2651
Qy 783 AGATGATTTTGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGACAAGCTTGAAGGT 842
Db 2652 AGATGATTTTGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGACAAGCTTGAAGGT 2711
Qy 843 TGAAGCAAGTGGCGCTTCTGTTTCAACACTACGCTTGAAGAAAGTTGATCAATAT 902
Db 2712 TGAAGCAAGTGGCGCTTCTGTTTCAACACTACGCTTGAAGAAAGTTGATCAATAT 2771
Qy 903 GGAACATTTGCAACCATATGAATTGTCAAAATTTGTCTAAGAAGATTTGGTTGTTT 962
Db 2772 GGAACATTTGCAACCATATGAATTGTCTAAGAAAGATTTGGTTGTTT 2831
Qy 963 CATCAACGTCATTTGGGACCAAGAGAATAATATCTTAATCTTGGCTATCGAAA 1022
Db 2832 CATCAACGTCATTTGGGACCAAGAGAATAATATCTTAATCTTGGGCAATCGAAA 2891
Qy 1023 GGAAGATTTGAAAAATATGTGTGTGTGCTCTAGACGCTTAAACTCTTGAAGATTTT 1082
Db 2892 GGAAGATTTGAAAAATATGTGTGTGTGCTCTAGACGCTTAAACTCTTGAAGATTTT 2951
Qy 1083 GGCCTTTAAGAGAGAAGAAAGCAAGTGGGAACATGTGAGATATGTGATTTGGAATTT 1142
Db 2952 GTGCTTCAAGAGAGAAGAAAGCAAGTGGGAACATGTGAGATATGTGATTTGGAATTT 3011
Qy 1143 GCCTCAAGAGAAGATTTCTATTTCTGCTGCGCTGAGACTTATGATTAACATCACTTCACT 1202
|||||

Db 3012 GCCTCAAGAGAAGATTTCTATTTCTGCTGCGCTGAGAGCTTATGATTAACATCACTTCACT 3071
Qy 1203 TGATTTGAGACATAGCTTTATACATATTTGACAGTATTTCCCAAGATACCGAAATGGAATA 1262
Db 3072 TGATTTGAGACATAGCTTTATACATATTTGACAGTATTTCCCAAGATACCGAAATGGAATA 3131
Qy 1263 GGAAGATTTAATCTCTCTGGAATGGACATAGTTTATTTTATTCGAAAGAAACCTTGA 1322
Db 3132 AGAAAGTAAATCTCTCTGGAATGGAGCATAGTTTCTTTATTCGAAAGAAACATGGA 3191
Qy 1323 GCTAGAGAAATAGATTAATGAATATGAATATTAATCTTGAAGTCTTTCTTCCAGA 1382
Db 3192 GCTAGAGAAATAGATTAATGAATATGAATATTAATCTTGAAGTCTTTCTTCCAGA 3251
Qy 1383 GATTGAAGTAAATCTGCTCAACCTTAATTTCAAGATGATGATCTCATTCATGATCTGGC 1442
Db 3252 GATTGAAGTAAATCTGCTCAACCTTAATTTCAAGATGATGATCTCATTCATGATCTGGC 3311
Qy 1443 AACATCTTATTTTGGGACACATCAAGCAGCAATATCCGAGAAATATTTGAGAAA 1502
Db 3312 AACATCTTATTTTGGGACACATCAAGCAGCAATATCCGAGAAATATTTGAGAAA 3371
Qy 1503 TTACATACATATGATGTCATGATTTGCTTCACTAAAGTGTATCTTACTCTTTCCCA 1562
Db 3372 TTACATACATATGATGTCATGATTTGCTTCACTAAAGTGTATCTTACTCTTTCCCA 3431
Qy 1563 CTTCGAGAAGTTTGTCTGCTGAGGGGCTTAATCTAATGACATTAATTAAGAGTT 1622
Db 3432 CTTCGAGAAGTTTGTCTGCTGAGGGGCTTAATCTAATGACATTAATTAAGAGTT 3491
Qy 1623 ACCGCTTCCATTTGAGAGATCTAGTACATTTAAGATCTTAATCTTGTGCAATACTAG 1682
Db 3492 ACCGCTTCCATTTGAGAGATCTAGTACATTTAAGATCTTAATCTTGTGCAATACTAG 3548
Qy 1683 TATTTGATGCTTCTCAAAACGATTATGCAAGCTTCAAAATCTGCAAGCTTTGATCTACA 1742
Db 3549 CATGCGTATGCTTCTCAAAACGATTATGCAAGCTTCAAAATCTGCAAGCTTTGATCTACA 3608
Qy 1743 TGGCGTATTCACCTTGTGTGTGCTGCAAAAGAAAGCAACCTGTGTAGTCTTCGAAA 1802
Db 3609 ATATTTGACCAAGCTTGTGTGTGCTGCAAAAGAAAGCAACCTGTGTAGTCTTCGAAA 3668
Qy 1803 TCTTTTACTGATGATTTGCTATGATTTGATGATCTTATGTCACCAAGATAGATCTTTGAC 1862
Db 3669 TCTTTTACTGATGATTTGCTATGATTTGATGATCTTATGTCACCAAGATAGATCTTTGAC 3728
Qy 1863 ATGCTTTAAGCTCTAAGTATGATTTGTGTGGAAATTCAGAAAGAAAGTTGTCAA 1922
Db 3729 ATGCTTTAAGCTCTAAGTATGATTTGTGTGGAAATTCAGAAAGAAAGTTGTCAA 3785
Qy 1923 TGAATTAAGAAACCTGAATCTCTATGCTCAATTTGAATCAACGATCTTGAAGATGCA 1982
Db 3786 TGAATTAAGAAACCTGAATCTCTATGCTCAATTTGAATCAACGATCTTGAAGATGCA 3845
Qy 1983 GAATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGACTTTTAAG 2042
Db 3846 GAATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGACTTTTAAG 3905
Qy 2043 CATGAAATGGAGATGAGATGAACGTCACGATATATGATCAGAAAAAGTTGAAGTCT 2102
Db 3906 CATGAAATGGAGATGAGATGAACGTCACGATATATGATCAGAAAAAGTTGAAGTCT 3962
Qy 2103 TGAAGCTCTCAACCAACATCTCAATCTGATTTTAACAATCAAGGGCTTCAAGGAAT 2162
Db 3963 TGAAGCTCTCAACCAACATCTCAATCTGATTTTAACAATCAAGGGCTTCAAGGAAT 4022
Qy 2163 CCGTCTCCGAGCTGAGATGATCACTGAGTTTGAATAATGTTCTCTATTTGAATCAT 2222
Db 4023 CCAATCTCCGAGAGTGAATGATCACTGATTTGAATAATGTTCTCTATTTCAATTAAG 4082
Qy 2223 CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTTGTGTGAGCTGCTTGTCAAAAAGCTT 2282
Db 4083 CAACTTGCAAAAACCTGCTCATGCTTACCAACCTTTGTGTGAGCTGCTTGTCAAAAAGCTT 4142
|||||

```

QY 2283 AGAGTTGTGGAGGGGGCTGCGGAGTGAATGTTG-----A 2321
Db 4143 AGAGTTACACTGGGGGCTGCGGAGTGAATGTTGAAAGATGATATGATGTCA 4202
QY 2322 TTCTGATTCCTTACAAAGAGTTTCCATCTCGAGAAATTAATATACGCGAAT 2381
Db 4203 TTCTGATTCCTTACAAAGATTAAGTTTCATCTCGAGAAATTAATATGAGACTT 4262
QY 2382 TGGTATCTGAAGAGTGTCTGAAAAAGAGAGAGCAATGCGCTGTGTTGAGA 2441
Db 4263 TGGTATCTGAAGAGTGTCTGAAAAAGAGAGAGCAATGCGCTGTGTTGAGA 4322
QY 2442 GATAGAGATTAATGTTGGCTTATGTTTATTCACCCCTTCTCTGTGAAGAAAT 2501
Db 4323 GATGATATTTCAAGAGTGGC-----TTTTCGACCCCTTCT----- 4359
QY 2502 GGTAGTAACTGGGAGCAAGTCAGATCAATAGGTTTCAGTTCCATATCTATCTCATGAGC 2561
Db 4360 -----TTTATCTTAAGGC 4373
QY 2562 TCTTACTCCCTCAATTCGCTATTAACAAGAGATGCTTCACTCCCAAGAGATGTT 2621
Db 4374 TCTTACTCCCTCAAGATTTGCTATATTAAGTAGCTACTTCACTCCCAAGAGATGTT 4433
QY 2622 CAAAAGCCTTGCAGAAATCTCAATTAATCTTCTTCTTCAATCTTAAGAGCT 2681
Db 4434 CAAAAGCCTTGCAGAAATCTCAATTAATCTTCTTCTTCAATCTTAAGAGCT 4493
QY 2682 GCTTACCAAGCTGGCTGATGCTCAATGCTTTGAAGATCTGGAATTCATAGTTTATGC 2741
Db 4494 GCTTACCAAGCTGGCTGATGCTCAATGCTTTGAAGATTCATAGTTTATGC 4553
QY 2742 ACTAGAGAGTCTCCCGAGAGAGTGTGAAGTTTAAATTCATCTCAAGAGTTTCCAT 2801
Db 4554 ACTAGAGAGTCTCCCGAGAGAGTGTGAAGTTTAAATTCATCTCAAGAGTTTCCAT 4613
QY 2802 AACATTAAGTGAATGCTCAATGTTTACCGAGAGATTTGACAGCTTAAGAGCTTAC 2861
Db 4614 TGAACTAGTGAATGCTCAATGTTTACCGAGAGATTTGACAGCTTAAGAGCTTAC 4673
QY 2862 AAATTTATCAAGTGAATGTTTGTCCCAAGCTGCGCAAGCGGTGTGAAGAGGATATGAGA 2921
Db 4674 AAATTTATCAAGTGAATGTTTGTCCCAAGCTGCGCAAGCGGTGTGAAGAGGATATGAGA 4733
QY 2922 AGACTGTATCAAAATTTGCTCAATCTCTGCTGTTTATTTAT 2964
Db 4734 AGACTGTATCAAAATTTGCTCAATCTCTGCTGTTTATTTAT 4776

```

```

RESULT 12
LOCUS AY336128 6824 bp DNA linear PLN 15-JUL-2003
DEFINITION Solanum bulbocastanum putative disease resistant protein RGA2 gene,
complete cds.
ACCESSION AY336128
VERSION AY336128.1 GI:32693280
KEYWORDS
SOURCE
ORGANISM
Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 6824)
Song J., Braden J.M., Naess K.S., Raasch J.A., Wielgus S.M.,
Haberlach G.T., Kuang H., Austen-Phillips S., Helgeson J.P.,
Liu J., Tallon L.J., Zaborosky J. and Buell C.R.
Solanum bulbocastanum disease resistance gene RGA-2
Proc. Natl. Acad. Sci. U.S.A. (2003) In press
2 (bases 1 to 6824)
Song J., Braden J.M., Naess K.S., Raasch J.A., Wielgus S.M.,
Haberlach G.T., Kuang H., Austen-Phillips S., Helgeson J.P.,
Liu J., Tallon L.J., Zaborosky J. and Buell C.R.

```

```

TITLE Direct Submission
JOURNAL Submitted (02-JUL-2003) Department of Horticulture, University of
Wisconsin-Madison, Madison, WI 53706, USA
FEATURES
source
1..6824
/organism="Solanum bulbocastanum"
/mol_type="genomic DNA"
/db_xref="taxon:147425"
/chromosome="8"
/map="RB"
<1..>3592
/locus_tag="CB3A14.5"
join(<1..427,1107..>3592)
/locus_tag="CB3A14.5"
/product="putative disease resistant protein RGA2"
join(1..427,1107..3592)
/locus_tag="CB3A14.5"
/notes="partial sequence is present in Genbank Accession
Number AY303170; similar to Phaseolus vulgaris NBS LRR
resistance-like protein B1 in Genbank Accession Number
AAK61316"
/codon_start=1
/product="putative disease resistant protein RGA2"
/protein_id="AAP6601.1"
/db_xref="GI:32693281"
/translation="MAEAPQVLLDNLTSFLKELVLLRGDFORQLSMSTQAV
LEAOKQLNNKPLENWLQKNAATYVDDILDYETKATRFQSEGRHPEVLPFR
HVGKRDQVKKLKAIAERKNPHLEKIVQAVRETGSVLTSPQVGRKDE
IVKILINVSDAOHLVPLMGAGKTTLAQVNDQVREHPSKWI CVSEDF
EKRLKAVESIIEGRPLGEMDAPLOKQELNKRKYLVDVNDQOKWALR
AVLKVGASGAVLTTRLEKVGSIQGTGLCPREBARAHVDRDPIYMLPDESEIPL
NVAIVGEIKYKSGVIVPLAKTIGTILCPREBARAHVDRDPIYMLPDESEIPL
RLSHOLPLDKKCPAVCAVFPDQMEKELISLMAGFLSKMELVEDGVW
KEIYLSFDEIEVKQKTFKXNDLHLDAISFSAATSSNIRINHSYHMSI
GFAEVFPYTLPELKEFISLRVNLIDSTFNLPSIGDYLHLYNLHSGRSLPK
QICKQNLQTLQYCTKLCPLPKETSKLSRLNLDSSQSLTQCPRIISLTCT
LQGFVGRKKGYQIGELGNLNYGSIKISHLEBRKVDQAKENASAKNLSLSW
NMFPHYSEEVKVLKALKPHSNLSLTIGRGIHLPEMNHVYLKNIIVLITNF
RNSCLPFGDPLCELESLHMGSAADVEYVEDVIDVHSGFPRIRFPRKLDITDF
GSLKGLKKGEGQFVLEBMTIHCPFLTSSNLRALTSRLTCKNKVATSPPEEWK
NLNLKLYLTISRNNLKEPLTSLASLNALSKLTIQICMLSELPEGLGLSLTEL
VERNNMLKCLPEGLQHLTLTSLIKRGCPOLIIRCEKGIGBDWHKISHIPNVIYI"
1..3136
/locus_tag="CB3A14.5"
/notes="corresponds to sequence in BAC CB3A14 in Genbank
Accession Number AY303170"
3137..6824
/notes="missing in BAC CB3A14 in Genbank Accession Number
AY303170; amplified from genomic DNA in 3 independent PCR
products"
/replace=""
ORIGIN
Query Match 60.9%; Score 1805.8; DB 8; Length 6824;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
QY 426 AACAGTTTGTGTAATGAATGCAATGTTATGGAAGAGAGAGAGAGAGT 485
Db 1102 ACCAGGTTCTGATTAATGCAACCGAGTTATGGAAGAGAGAGAGAGAGT 1161
QY 486 AGTGAATTCCTGATTAATGAATGCAATGTTATGGAAGAGAGAGAGAGT 545
Db 1162 AGTGAATTCCTGATTAATGAATGCAATGTTATGGAAGAGAGAGAGAGT 1221
QY 546 TGGTATGGGGGAGTATGGAAGAGAGAGAGAGAGAGAGAGAGAGT 605
Db 1222 TGGTATGGGGGAGTATGGAAGAGAGAGAGAGAGAGAGAGAGAGT 1281
QY 606 AATGAGATTCCTCAATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAG 665
Db 1282 TACTAGATTCCTCAATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAGAG 1341

```

QY	666	GTGTAAAGGAAATTGTAAGATCTATGGAAGAAAGC---ACTGGGTGCATGAGCTT	722
Db	1342	GTATATAAGCAATTGTGAATCTATTGAAGGAAGGCCTACTTGGTGAATGAGACTT	1401
QY	723	GGCTCCACTTCAAAAAGACTTCGGGACTTCGTGATGAAAAAAATTTGTCTGCTT	782
Db	1402	GGCTCCACTTCAAAAAGACTTCGAGAGTTCGTGAATGAAAAAATCTTGTGCTT	1461
QY	783	AGATGATGTTGGAAATGAAGATCAAGATAGTGGCTAAGTTAAGACAAGTCTGAAGT	842
Db	1462	AGATGATGTTGGAAATGAAGATCAAGAGTGGCTAATTTAAGAGCAGTCTGAAGT	1521
QY	843	TGAGACAGTGGCGCTTCTGTTCTTACCACTACTGCTTGAAAAAGTTGATCAATAT	902
Db	1522	TGAGACAGTGGGTGCTTCTGTTCTTACCACTACTGCTTGAAAAAGTTGATCAATAT	1581
QY	903	GGGAACATTTGCACACCATATGAAATTTGCAAAATTTGTCACAAAGAAATTTGGTGGTT	962
Db	1582	GGGAACATTTGCACACCATATGAAATTTGCAAAATTTGTCACAAAGAAATTTGGTGGTT	1641
QY	963	CATGCAACGTGCATTTTGGGCACCAAGAAAGAAATTAATCTTAATCTTGCGCTATCGAAA	1022
Db	1642	CATGCAACGTGCATTTTGGGCACCAAGAAAGAAATTAATCTTAATCTTGCGCAATCGGAAA	1701
QY	1023	GGAGTTTGTGAAAAAATGTGGTGGTGGTCCCTTAGCAGCTAAAACCTCGGAAGTATTTT	1082
Db	1702	GGAGTTTGTGAAAAAATGTGGTGGTGGTCCCTTAGCAGCTAAAACCTCGGAAGTATTTT	1761
QY	1083	GGCGTTTAAAGAGAGAAAGAACAGTGGGGAACATGTGAGATATGTGAGATTTGGAATTT	1142
Db	1762	GTGCTTCAAGAGAGAGAAAGAACAGTGGGGAACATGTGAGAGACAGTCCGATTTGGAATTT	1821
QY	1143	GCCTCAAGAGAAAGTTTATTTCTGCTGCTGCCCTGAGACTTAAGTTACATCACTTCCACT	1202
Db	1822	GCCTCAAGATGAAGTTTATTTCTGCTGCTGCCCTGAGGTTATGTTACATCACTTCCACT	1881
QY	1203	TGATTTGAGACATATCTTACATATTTGTCAGTATTTCCCAAGATACCAATATGAAAA	1262
Db	1882	TGATTTGAGAACATATCTTATTTGGTATTTGGCGGTGTTCCCAAGATATGCAAAATGAAAA	1941
QY	1263	GGGAATCTAATCTCTCTGGAATGGGCATATGGTTTTATTTATCGAAGAAACTTGGGA	1322
Db	1942	AGAAAACTAATCTCTCTGGAATGGGCATATGGTTTTATTTATCGAAGAAACTTGGGA	2001
QY	1323	GCTAGAGATGTAGGTAATGGAATGAAATTAATTAATCTTGAAGTCTTCTTCCAGA	1382
Db	2002	GCTAGAGATGTGGCCATATGAAATGAAATTAATTAATCTTGAAGTCTTCTTCCAGA	2061
QY	1383	GATTGAAGTTAAATCTGGTCAAACTTATTTCAAGATGATGATCTTCAATGATCTGGC	1442
Db	2062	GATTGAAGTTAAAGATGTGTAATACTTATTTCAAGATGATGATCTTCAATGATTTGGC	2121
QY	1443	AAACATCTCTAATTTTCGGAACACATCAAGACAAATTCGGAATAATTTGATGAAAA	1502
Db	2122	AAACATCTCTGTTTTCAGCAAAACATCAAGACAAATTCGGAATAATTTAACAACAG	2181
QY	1503	TTACATACATATGATATGATTCATTTGGTTTCACTAAAGTGTATCTTCACTCTTCCCA	1562
Db	2182	TTACACACATATGATATGATTCATTTGGTTTCCGGAAGTGTATTTTTCACATCTTCCCC	2241
QY	1563	CTTGACAGAAATTTGTCCTGTTGAGGGTCTTAATCTAATGACATTAATAAGCAATT	1622
Db	2242	CTTGAAAAAGTTAATCTGTTAAGAGTGCCTTAATCTAAGTATTCGACATTTAATAAGTT	2301
QY	1623	ACCGTCTTCCATGAGAGATCTAATCAATTAAGATACCTAAACCTTGCTGGCAATACAG	1682
Db	2302	ACCATCTTCCATGAGAGATCTAATCAATTAAGATACCTGAACCTGATATGCG---AGTGG	2358
QY	1683	TATTCGTATGCTTCCAAACACAGTATATGCAAGCTTCAAAATCTGAGACTCTGTGATCTACA	1742
Db	2359	CATGCTATGCTTCCAAACACAGTATATGCAAGCTTCAAAATCTGCAAACTCTGTATCTACA	2418
QY	1743	TGCGCTCATTCACCTTTGTTGTTCCAAAAAACAAGCAACTGTGATCTTCCAAA	1802

Db	2419	ATATTGCACCAAGCTTTGTTGTTTGGCCAAAAGAAACAGTAACTTGTAAGTCTCCGAAA	2478
OY	1803	TCCTTTACCTTGAGTGGTGTCTATATGATATGACTTGTATSCAACCAAGATATAGATCTTTGAC	1862
Db	2479	TCCTTTACTTGATATGATGACGAGTCATTTGATGATGATCCTTGATGATGATGATGATGATGAC	2538
OY	1863	ATGCCCTTAAGACTCTAAAGTATGATTTGTGTGTGGGAATTCAGAGAAAAGTTGTCAACTTGG	1922
Db	2539	ATGCCCTTAAGACTCTAGGTCAATTTGTGTGTGAAA---GGAGAAAGAGTTATCAACTTGG	2595
OY	1923	TGAATTTAGAAACCTGGAATCTCTATGCGTCAATTTGAATACCGATCTTGAGAGAGTAA	1982
Db	2596	TGAACCTAGAAACCTTAATCTCTATGCGTCAATTTAAATCTCGATCTTGAGAGAGTAA	2655
OY	1983	GAATGATATGAGTCAAAAGAGGCAATTTATCTGCAAAAAGAAAATCTGCAATCTTTTAA	2042
Db	2656	GAATGATATGAGAGCCAAAAGAGGCAATTTATCTGCAAAAAGGGAATCTGCAATCTTTTAA	2715
OY	2043	CATGAAATGGAGTACGATGAACGTCCACGTAATATATGAATCAGAAAAAGTTGAAGTCT	2102
Db	2716	CATAGATTTGGAAATTAACCTTGG---GACCAACATATATATGAATCAGMAAGTTAAAGTCT	2772
OY	2103	TGAAGCTCTCAACACACACTCCATCTGCACTGTTTAAACATACAGGGGCTTCAGAGGAAT	2162
Db	2773	TGAAGCCCTCAACACACACTCCATCTGCACTCTTTTAAAAATCTATGCGTTCAAGAGGAAT	2832
OY	2163	CCGCTCTCCCAAGCTGAGTGAATCACTCAGTTTGGAAAAATGTTGTCTCTATTTGAAATCAT	2222
Db	2833	CCATCTCCCAAGAGTGAATGAATCACTCAGTATATGAATAAATAATTTGTCTCTATTTCAATTAG	2892
OY	2223	CAGTTGCAAAAACTGCTCATGCTTACCAACCCCTTGTGTAGCTGCTGCTTAAAGTCT	2282
Db	2893	CAATTCAGAAACCTGCTCATGCTTACCAACCCCTTGTGTAGCTGCTGCTTAAAGTCT	2952
OY	2283	AGAATTGTGAGAGGGGGCTGCGGAAGTGGAGTATGTTG-----A	2321
Db	2953	AGAATTCACTGGGGGGCTGCGGAGTGGAGTATGTTGAAGAGTGAATATGATGTTCA	3012
OY	2322	TTCTGGAATCCCTTCAAGAAAGAGTTTCCATCTCTGAGAAAATTAAATATACCGAATT	2381
Db	3013	TTCTGGAATCCCTTCAAGAAATTAAGTTTCCATCTCTGAGAAAATTGAATATGCGACTT	3072
OY	2382	TGATTAATCTGAAGAGATTTGCTGAAGAAAGAAAGAGAACCAATGCCCTGTGCTTGAGA	2441
Db	3073	TGATTAATCTGAAGAGATTTGCTGAAGAAAGAAAGAGAACCAATGCCCTGTGCTTGAGA	3132
OY	2442	GATGAGATTTAAATGTTGCCCTATGTTTGTATTCACACCTTCTCTCTGCAAGAAATT	2501
Db	3133	GATGATTAATTCACAGAGGCC-----TTTTCTGACCCCTTCT-----	3169
OY	2502	GGTAGATTAGTGGGAGCAAGTCAGATGCAATATAGTTTCAGTTCCATATCTAATCTCATGGC	2561
Db	3170	-----TCTAATCTTAGGCC	3183
OY	2562	TCCTTACTTCCTCTCAAAATTCGCTATTAACAAGAGATGCTTCACTCCCAAGAGATGTT	2621
Db	3184	TCCTTACTTCCTCTCAAAATTTGCTATATATTAAGTAGTACTTCAATCCCAAGAGAGATGTT	3243
OY	2622	CAAAAGCTTGCAAAATCTCAAAATCTTGAATATCTCTTTTACTTCAATCTTAAAGAGCT	2681
Db	3244	CAAAAACCTTGCAAAATCTCAAAATCTTGAACAAATCTCTGGTGCATATATCTCAAGAGCT	3303
OY	2682	GCTTACCAAGCTGGCTATGCTCAATGCTTTGAAGCATCTGGAATTCATATGTTGTATGTC	2741
Db	3304	GCTTACCAAGCTGGCTATGCTCAATGCTTTGAAGAGCTTAAATTCATATTTGTGTGCGC	3363
OY	2742	ACTAGAGAGTCTCCCGAGAGAGGTGTGAAGGTTTAATTTCACTCACAGATTTATTCAT	2801
Db	3364	ACTAGAGAGTCTCCCGTAGAGAGAGGCTGAAGGTTTAATTTCACTCACAGATTTATTTGT	3423
OY	2802	AACATATCTGGAATGCTTCAATATGTTTAAACCGAGAGGATTTGCACACCTTAACAGCCCTCAC	2861

Db 3424 TGAACCTGTAACATGCTAAATGTTTACAGAGGATTCAGACCTTAACAACCTTCAC 3483
Qy 2862 AATTTATCATGTTGATGTTTGTCCAACTGCGCAAGCGGTGTGAGAAAGGAATGGAA 2921
Db 3484 AAGTTTAAATTCGGGATGTCACACATGATCAACGGGTGAGAAAGGAATGAGAGA 3543
Qy 2922 AGACTGTACAAATTCCTACATTCCTGCTGTGTATTTAT 2964
Db 3544 AGACTGGACAAATTTCTCACTTCTAATGTAATATATAT 3586

RESULT 13
AX814114
LOCUS AX814114 7349 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 37 from Patent EP134979.
ACCESSION AX814114
VERSION AX814114.1 GI:39103416
KEYWORDS
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1
AUTHORS van der Voessen, E.A. and Allefs, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
JOURNAL Patent: EP 1334979-A 37 13-AUG-2003;
Kweek-en Researchbedrijf Agricola B.V. (NL)
FEATURES
source location/Qualifiers
1..7349
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
/note="BAC SPB4-Genomic fragment"

ORIGIN

Query Match 60.9%; Score 1805.8; DB 6; Length 7349;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
Qy 426 AACAGTTTTGTTGAATGAACCAAGTTTATGAGAGACAAAGAAAGACGAGAT 485
Db 3749 ACCAGTTCTGATTAACCGAACCGCAGGTATGAGAGACAAAGAAAGATGAGAT 3808
Qy 486 AGTGAATTCCTGATTAACAATGTAGCAATGCCCAACCTTCAGTCTCCCAATAC 545
Db 3809 AGTGAATTCCTAATTAACAATGTAGTGCACCAACCTTCAGTCTCCCAATAC 3868
Qy 546 TGTATGGGGGACAGAGAAAGACATCTTGCCCAATGCTTCAATGATCAAGAGT 605
Db 3869 TGTATGGGGGATTAAGAAAGACATCTTGCCCAATGCTTCAATGATCAAGAGT 3928
Qy 606 AATTGAGATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTTATGAGAGAG 665
Db 3929 TACTGAGATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTTATGAGAGAG 3988
Qy 666 GTTATTAAGAAATGTAGATCTATTTGAAGAAAGTCACTTGGTGCATGAGACT 722
Db 3989 GTTATTAAGCAATGTAGATCTATTTGAAGAGGCACTAATTGGTGAATGAGACT 4048
Qy 723 GGCCTCCATTTAAAGAAAGCTTCGGGACTTCTGATATGAGAAAAAATATTTGCTGCTT 782
Db 4049 GGCCTCCATTTAAAGAAAGCTTCGGGACTTCTGATATGAGAAAAAATATTTGCTGCTT 4108
Qy 783 AGATGATGTTGATGAATGAAGATTAAGTGGGCTAAGTTAAGACAGCTTGAAGGT 842
Db 4109 AGATGATGTTGATGAATGAAGATTAAGTGGGCTAATTTAAGACAGCTTGAAGGT 4168
Qy 843 TGAAGCAATGGCGCTTCTGTCTTAACCACTACCTGCTTGAAGAAAGGTGATCAATTA 902
Db 4169 TGAAGCAATGGCGCTTCTGTCTTAACCACTACCTGCTTGAAGAAAGGTGATCAATTA 4228

Qy 903 GGGAACTTGAACCATTAATGAATTTGCTCAAGAAAGATTTGTTGTT 962
Db 4229 GGGAACTTGAACCATTAATGAATTTGCTCAAGAAAGATTTGTTGTT 4288
Qy 963 CATGCAACGTGCAATTTGGGCAACAAGAAATTAATCTTAATCTTGTGCTATCGAAA 1022
Db 4289 CATGCAACGTGCAATTTGGGCAACAAGAAATTAATCTTAATCTTGTGCTATCGAAA 4348
Qy 1023 GGAATTTGAAAAAATGTGTGTGTGCTCTTGACGCTTAAACCTTTGGAGGTATTT 1082
Db 4349 GGAATTTGAAAAAATGTGTGTGTGCTCTTGACGCTTAAACCTTTGGAGGTATTT 4408
Qy 1083 GCGCTTTAAGAGAAAGAAAGACAGTGGGAAACATGTAGAGATGAGATTTGGAAT 1142
Db 4409 GCGCTTTAAGAGAAAGAAAGACAGTGGGAAACATGTAGAGATGAGATTTGGAAT 4468
Qy 1143 GCGCTTAAGAAAGAAAGTTCTATTCCTGCTGCTGAGACTTAAGTACATCACTTCAC 1202
Db 4469 GCGCTTAAGAAAGAAAGTTCTATTCCTGCTGCTGAGACTTAAGTACATCACTTCAC 4528
Qy 1203 TGATTTGAGCAATGCTTTACATTTGTGAGATTTCCCAAGAAAGTCCGAAATGAGAAA 1262
Db 4529 TGATTTGAGCAATGCTTTGAGATTTGTGAGATTTCCCAAGAAAGTCCGAAATGAGAAA 4588
Qy 1263 GGGAAATCTAATCTCTCTGATGAGACATGGTTTATTTATTCGAAAGAAAGTGA 1322
Db 4589 AGAAAGCTAATCTCTCTGATGAGACATGGTTTATTTATTCGAAAGAAAGTGA 4648
Qy 1323 GCTAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1382
Db 4649 GCTAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4708
Qy 1383 GATTGAAGTTAAATCTGGTCAAACTTATTTCAAGAGCAATGATGATGATGATGATG 1442
Db 4709 GATTGAAGTTAAATCTGGTCAAACTTATTTCAAGAGCAATGATGATGATGATGATG 4768
Qy 1443 AACATCTAATTTTCCGCAAGACATCAAGCAGCAATATCCGAAATATTTGAGAAAA 1502
Db 4769 AACATCTAATTTTCCGCAAGACATCAAGCAGCAATATCCGAAATATTTGAGAAAA 4828
Qy 1503 TTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1562
Db 4829 TTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4888
Qy 1563 CTTCAGAAAGTTGCTGCTGAGGAGGCTTAATCTAAGTGAATTAAGAGAT 1622
Db 4889 CTTCAGAAAGTTGCTGCTGAGGAGGCTTAATCTAAGTGAATTAAGAGAT 4948
Qy 1623 ACCGCTTCCATGAGATCTAGTACATTTAAGATCACTTAACCTTGTGGCAATAG 1682
Db 4949 ACCGCTTCCATGAGATCTAGTACATTTAAGATCACTTAACCTTGTGGCAATAG 5005
Qy 1683 TATTGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGCAACCTTGATCTTAA 1742
Db 5006 TATTGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGCAACCTTGATCTTAA 5065
Qy 1743 TGCGTCAATCACTTGTGTTGTTGCAAAAGAAACAAGCAATCTGAGTCTTGA 1802
Db 5066 ATATTCACCAAGCTTGTGTTGTTGCAAAAGAAACAAGCAATCTGAGTCTTGA 5125
Qy 1803 TCTTTTACTTGAATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATG 1862
Db 5126 TCTTTTACTTGAATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATG 5185
Qy 1863 ATGCTTAAGATCTAAGTGAATTTGTGTGGGAATTCAGAGAAAGTGTCACTGG 1922
Db 5186 ATGCTTAAGATCTAAGTGAATTTGTGTGGGAATTTGTGTGGGAATTTGTGTGG 5242
Qy 1923 TGAATTAAGAACTGATCTGATGCTCAATGCAATCAAGCACTTGAAGAGTGA 1982
Db 5243 TGAATTAAGAACTGATCTGATGCTCAATGCAATCAAGCACTTGAAGAGTGA 5302
Qy 1983 GAATGATATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCATTTTAA 2042

QY 606 AATTGAGCATTTTCATCCCAAAATATGAGATTGTGCTCGAAGATTTTAAATGAGAAGG 665
|
|
|
Db 3929 TACTGAGCATTTTCATCCAAATATGAGATTGTGCTCGAAGATTTTGAATGAGAAGG 3988
|
|
|
QY 666 GTTGTAAAGAAATTTGAGATCTATTTGAGAAAAGTC---ACTTGCGGACATGACATT 722
|
|
|
Db 3989 GTTAAATAAAGCAATTTGAGATCTATTTGAGAGAAGGCCATTACTTGGTGAATGACATT 4048
|
|
|
QY 723 GGCTCCACTTCAAAAAGAGCTTCGGGACCTTGCTGAATGAGAAAAAATTTTGTGCTGCTT 782
|
|
|
Db 4049 GGCTCCACTTCAAAAAGAGCTTCGGGACCTTGCTGAATGAGAAAAAAGTACTTGTGCTT 4108
|
|
|
QY 783 AGATGATGTTTGGATGAGATCAAGATTAAGTGGGCTAAGTTAAGACAGATCTTGAAGGT 842
|
|
|
Db 4109 AGATGATGTTTGGATGAGATCAAGATTAAGTGGGCTAATTTAAGAGCAGCTTTGAAGGT 4168
|
|
|
QY 843 TGGAGCAATGGCGCTTCTGTTCTAAACAATACTGCTTTGAAAAGTTGATCAATTAT 902
|
|
|
Db 4169 TGGAGCAATGGCGCTTCTGTTCTAAACAATACTGCTTTGAAAAGTTGATCAATTAT 4228
|
|
|
QY 903 GGGAAATGTCACACCATATGAATTTGTCATCAAGAAATGTTGGTGTGTT 962
|
|
|
Db 4229 GGGAAATGTCACACCATATGAATTTGTCATCAAGAAATGTTGGTGTGTT 4288
|
|
|
QY 963 CATGCAACGTGATTTGGGCACCAAGAAATTAATCTTAACTTGTGGCTATCGGAAA 1022
|
|
|
Db 4289 CATGCAACGTGATTTGGGCACCAAGAAATTAATCTTAACTTGTGGCAATGGAAA 4348
|
|
|
QY 1023 GGAAGATTGGAAAAATGTTGTTGTTGCTTACAGCTTAAATCTTTGAGAGTATTTT 1082
|
|
|
Db 4349 GGAAGATTGGAAAAATGTTGTTGTTGCTTACAGCTTAAATCTTTGAGAGTATTTT 4408
|
|
|
QY 1083 GCGCTTTAAGAGAGAAAGAACAGATGGGACATGTGAGAGATAGTGAATTTGGAATT 1142
|
|
|
Db 4409 GTGCTTCAAGAGAGAAAGAACAGATGGGACATGTGAGAGAGCTCCGATTTGGAATT 4468
|
|
|
QY 1143 GCGCTCAAGAGAAATTTATTTCTGCTGCTGCTGAGACTTATGATCACTTCCACT 1202
|
|
|
Db 4469 GCGCTCAAGAGAAATTTATTTCTGCTGCTGCTGAGACTTATGATCACTTCCACT 4528
|
|
|
QY 1203 TGATTTGAGACAAATCTTAACTATTTGACAGTATTTCCAAAGATATCCGAAATGGAATA 1262
|
|
|
Db 4529 TGATTTGAGACAAATCTTAACTATTTGACAGTATTTCCAAAGATATCCGAAATGGAATA 4588
|
|
|
QY 1263 GGGAAATCTAAATCTCTCTGATGCGACATGCTTTATTTTATGAAAAGAACTTGA 1322
|
|
|
Db 4589 AGAAAGCTAAATCTCTCTGATGCGACATGCTTTATTTTATGAAAAGAACTTGA 4648
|
|
|
QY 1323 GCTAGAGAAATGATGATTAATGAAATGGAATGATTAATTAAGTCTTTCTTCAAGA 1382
|
|
|
Db 4649 GCTAGAGAAATGATGATTAATGAAATGGAATGATTAATTAAGTCTTTCTTCAAGA 4708
|
|
|
QY 1383 GATTGAATTAATCTGATGCAAACTTATTTCAAGATGATGATCACTCAATGATCGGC 1442
|
|
|
Db 4709 GATTGAATTAATGATGATTAATCTTATTTCAAGATGATGATCACTCAATGATGATG 4768
|
|
|
QY 1443 AAATCTCTATTTTTCGAGACACATCAAGCAGCAATATCCGAGAAATTAATTTGAGAAA 1502
|
|
|
Db 4769 AAATCTCTGTTTTCAGCAACACATCAAGCAGCAATATCCGAGAAATTAATTAACAG 4828
|
|
|
QY 1503 TTATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1562
|
|
|
Db 4829 TTATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4888
|
|
|
QY 1563 CTTCAGAAAGTTTCTGCTGATGAGGATGATGATGATGATGATGATGATGATGATGATG 1622
|
|
|
Db 4889 CTTCAGAAAGTTTCTGCTGATGAGGATGATGATGATGATGATGATGATGATGATGATG 4948
|
|
|
QY 1623 ACCGTTTCCATTTGAGATCTAAGTAACTTTAAGATGATGATGATGATGATGATGATG 1682
|
|
|
Db 4949 ACCGTTTCCATTTGAGATCTAAGTAACTTTAAGATGATGATGATGATGATGATGATG 5005
|
|
|
QY 1683 TATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1742
|
|
|

Db 5006 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5065
|
|
|
QY 1743 TGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1802
|
|
|
Db 5066 ATATTTGACCAAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5125
|
|
|
QY 1803 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1862
|
|
|
Db 5126 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5185
|
|
|
QY 1863 ATGCTTAAAGCTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1922
|
|
|
Db 5186 ATGCTTAAAGCTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5242
|
|
|
QY 1923 TGAATTAAGAACTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1982
|
|
|
Db 5243 TGAATTAAGAACTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5302
|
|
|
QY 1983 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2042
|
|
|
Db 5303 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5362
|
|
|
QY 2043 CATGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2102
|
|
|
Db 5363 CATGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5419
|
|
|
QY 2103 TGAAGCTCTCAAAACACATCTCAATCTGATGTTTAAATCAATGAGGCTTCAAGAGAT 2162
|
|
|
Db 5420 TGAAGCTCTCAAAACACATCTCAATCTGATGTTTAAATCAATGAGGCTTCAAGAGAT 5479
|
|
|
QY 2163 CCGTCTCCAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2222
|
|
|
Db 5480 CCAATCTCCAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5539
|
|
|
QY 2223 CAGTTGCAAAATCTGCTCATGCTTACCAACCTTGTGATGATGATGATGATGATGATGATG 2282
|
|
|
Db 5540 CCACTTCAAGAACTGCTCATGCTTACCAACCTTGTGATGATGATGATGATGATGATGATG 5599
|
|
|
QY 2283 AGAGTTGATGAGAGGAGTCTGCGGAGTGAATGATGATGATGATGATGATGATGATGATG 2321
|
|
|
Db 5600 AGAGTTGATGAGAGGAGTCTGCGGAGTGAATGATGATGATGATGATGATGATGATGATG 5659
|
|
|
QY 2322 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2381
|
|
|
Db 5660 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5719
|
|
|
QY 2382 TGGTAAATCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2441
|
|
|
Db 5720 TGGTAAATCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5779
|
|
|
QY 2442 GATAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2501
|
|
|
Db 5780 GATAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5816
|
|
|
QY 2502 GGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2561
|
|
|
Db 5817 GGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5830
|
|
|
QY 2562 TCTTATCTTCCCTCAAAATGCTATTAACAAGAGATGCTTCACTCCAGAGAGATGTT 2621
|
|
|
Db 5831 TCTTATCTTCCCTCAAAATGCTATTAACAAGAGATGCTTCACTCCAGAGAGATGTT 5890
|
|
|
QY 2622 CAAAGCTTGAAGATCTCAAAATCTGAAATCTGTTTAACTTCAATCTTAAAGAGT 2681
|
|
|
Db 5891 CAAAGCTTGAAGATCTCAAAATCTGAAATCTGTTTAACTTCAATCTTAAAGAGT 5950
|
|
|
QY 2682 GCTTACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2741
|
|
|
Db 5951 GCTTACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6010
|
|
|
QY 2742 ACTAGAGATCTTCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2801
|
|
|

Db 6011 ACTAGAGAGTCTCCCTGAGGAGGCGTGAAGTTTATCTTCACTACAGAGTTATTTGT 6070
Qy 2802 AACATAGTGTGAATAGTCTACATATGTTTACCGGAGGATTTGACAGCACTTACAGCCCTCAG 2861
Db 6071 TGAACACTGTATACATCTTAAATTTTACACAGAGGATTTGACAGCACTTACAGCACTTAC 6130
Qy 2862 AAATTATCAGTTGAGTTTGTTCACACCTGCGCAAGCGGTGTGAGAGGATGAGAGA 2921
Db 6131 AAGTTTAAATTCGGGGAGTGTCCACAACCTGATCAAGCGGTGTGAGAGGATGAGAGA 6190
Qy 2922 AGACTGTGACAAATTTGCTCACTTCTCGTGTGTTTATTTAT 2964
Db 6191 AGACTGACAAATTTCTCACTTCTCAATGTGATATATAT 6233

RESULT 15

LOCUS AY426266 3641 bp DNA linear PLN 16-DEC-2003
DEFINITION Solanum tarijense blight resistance protein T118 gene, partial cds.
ACCESSION AY426266
VERSION AY426266.1 GI:39636815
KEYWORDS

SOURCE Solanum tarijense
ORGANISM Solanum tarijense

REFERENCE 1 (bases 1 to 3641)
AUTHORS Van Der Vossen, E., Sikkema, A., Hekkert Bt, B.L., Gros, J.,
Stevens, P., Muskens, M., Mouters, D., Pereira, A., Sikkema, W. and
Allefs, S.

TITLE An ancient R gene from the wild potato species Solanum
bulbosum confers broad-spectrum resistance to Phytophthora
infestans in cultivated potato and tomato

JOURNAL Plant J. 36 (6), 867-882 (2003)
PUBMED 14675451
2 (bases 1 to 3641)

REFERENCE van der Vossen, E. and Allefs, S.
Direct Submission

JOURNAL Submitted (03-OCT-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands

FEATURES
Source location/Qualifiers
1..3641

/organism="Solanum tarijense"

/mol_type="genomic DNA"

/db_xref="taxon:257458"

/chromosome="VIII"

/map="CT88-CT64"

join(<1..421,1217..>3641)

/product="Blight resistance protein T118"

/note="confers broad-spectrum resistance to Phytophthora
infestans in potato and tomato"

/codon_start=1

/product="Blight resistance protein T118"

/protein_id="AB29076.1"

/db_xref="GI:39636815"

/translation="MAEAFIVLLNNTSPFQELGILLGRENPNISRFITQAV
LEDQERQKDKAKIKNLQKMAAAYKVDLLDECKARLEQSLGRHHPAIVFRK
IGRIKEMMETLDAKERDTPHHEKLEIQRVARPETGPAVLEPQVGRKEDIEY
KILINVSNALELVLPIGWGGLKTTLAQMVNDORVTHFPKIMI CVSDPDEK
RLITITGNTIRSSLDVQDLASFOKLOQLNGRYLLVDVNNEDQKMDNRALV
KVAGASAVITTTLEKVGSIIMGTLOPQNLISODQWLLFIORAYRHOEISPNV
AIGETIVKSSGVPLAAKTLQGLRFRKREKREHVRDREIMNIPDEMSILPLRIS
YTHLPDLRQCFAICAVPKOTKMEKKVVISLMAHGLSRNLIEDVGENEWNEL
YLRFQDEIVRYGNTYFKMDLIHLATVLSMAHGLSRNLIEDVGENEWNEL
SEVSVSPSLQKRVSLRVNLVSKEEELPSIGDVLHRYMDLSNIEIRSLPQ
LCKONLOTLLOCTRLCCPKOTSXGSLRNLLHGCHLTPRPRIQTLCKTL
GQPVKRGVQLGELISINLYGSIKISHLRYNDKAKRANISAKENIHLISMDK
DDEPRHRESEVEYLBALRPHSNITCTIFGFGIRLPDMNHSVLKNYILITSGC
KNCKLPFGDLPCLESILQYRGSAYEEVDIVDESGFTRLRPSLRDLCTCKD
NLKGLVKGEGEGPVLMEIRYCPITLSSNLKALTSLNISNKAATSPDEMFPS
LANKYINISHPKMLKEPLTSLASLNALKSILQWCCALBSIPREGVGLSTLTLIV

ORIGIN

KFCMKLCPBGLQHLTALTRVKIMGEPQLIKRC"

Query Match 60.6%; Score 1797.2; DB 8; Length 3641;

Best Local Similarity 84.6%; Pred. No. 0; Matches 216; Conservative 0; Mismatches 293; Indels 93; Gaps 5;

Qy 426 AACAGTTTGTGTTGATGACCAAGTTTATGSAAGACAAAGAAAGACGAGAT 485
Db 1212 ACCAGTCTCTGTTTAACTGACCAAGTTTATGSAAGGACAAAGAAAGATGAGAT 1271
Qy 486 AGTAAATCTGTATAAACAAATGTTAGCAATGCCAAACACTTCAGTCTCCAAATCT 545
Db 1272 AGTAAATCTGTATAAACAAATGTTAGCAATGCCCTAGAGCTTCAGTCTCCAAATCT 1331
Qy 546 TGTATGAGGAGGACATGAAAGACACTCTGCCAAATGCTCTCATATGATGAGAGT 605
Db 1332 TGTATGAGGAGGACATGAAAGACACTCTGCCAAATGCTCTCATATGATGAGAGT 1391
Qy 606 AATTGAGCATTTCCATCCCAAAATATGGAATTTGTCTCGGAAGATTTTATGAGAGAG 665
Db 1392 TACTGAGCATTTTATCCCAAAATATGGAATTTGTCTCGGAATTTTATGAGAGAG 1451
Qy 666 GTTATTAAGGAAATGTGATCTATTTAGAAAGAAAGTCACTTGCGATGACCTGGC 725
Db 1452 GTTATTAAGGAAATGTGATCTATTTAGAAAGAAAGTCTTGATGTCAGAGACTGGC 1511
Qy 726 TCCACTTCAAAAGAAAGCTCGGACCTTGCTGTAATGAGAAAGAAATTTGCTGCTTATGA 785
Db 1512 TTTCAATTCAGAAAGAGCTTACGAGTTGTGAATGAGAAAGAAATTTGCTGCTTATGA 1571
Qy 786 TGATGTTGGAATAGATCAAGATTAAGTGGGCTTAAGTAAAGACAGCTTGAAGTTGG 845
Db 1572 TGATGTTGGAATAGATCAAGATTAAGTGGGCTTGAAGTGGATTTGAAGTTGG 1631
Qy 846 AGCAAGTGGGCTTCTGTTTCAACCACTACTGCTTGAAGAAAGTGGATCAATTAAGG 905
Db 1632 AGCAAGTGGGCTTCTGTTTCAACCACTACTGCTTGAAGAAAGTGGATCAATTAAGG 1691
Qy 906 AACCTTCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
Db 1692 AACCTTCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1751
Qy 966 GCAAGTGCATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGGCTATCGAAAGAA 1025
Db 1752 ACAGCGTCATATGACATCAAGAAAGAAATTAATCTTGGCTATCGAAAGAA 1811
Qy 1026 GATTGTGAAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1085
Db 1812 AATTGTGAAAGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1871
Qy 1086 CTTTAAGAGAGAGAAAGACAGTGGAAACATGTGAGAGATGTGAGATTTGGAAATGCC 1145
Db 1872 CTTCAAGAGAGAGAAAGAGAGATGGAAACATGTGAGAGATGTGAGATTTGGAAATGCC 1931
Qy 1146 TCAGAGAGAAAGTTCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205
Db 1932 TCAGAGAGAAAGTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1991
Qy 1206 TTTGAGCAATGCTTTATCATATTTGTCAGATTTCCAAAGGATACGAAATGAGAAAGG 1265
Db 1992 TTTGAGCAATGCTTTGCGATTTGTCAGATTTCCAAAGGATACGAAATGAGAAAGG 2051
Qy 1266 AAATCTATCTCTCTCTGATGAGCAATGTTTATTTTATTCGAAAGAAAGCTTGAGCT 1325
Db 2052 GAAAGTATCTCTCTCTGATGAGCAATGCTTTTATTCGAAAGAAAGCTTGAGCT 2111
Qy 1326 AGAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
Db 2112 AGAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2171
Qy 1386 TGAAGTTAAATCTGTCMAAATTATTTCAAGATGATGATCTCATGATGATGATGATGAT 1445

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2005, 12:53:05 ; Search time 1434 Seconds

(without alignments)
12248.168 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967

Sequence: 1 atggcgtgaagcttcctcctca.....ctcgtgtcttattattatag 2967

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 16Dec04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	100.0	3193	12	ADK98516 S Bulboca
2	2541.8	85.7	3595	12	ADK98518 S Bulboca
3	2541.8	85.7	5028	12	ADK98524 S Bulboca
4	2309	77.8	3347	12	ADK98520 S Bulboca
5	2077.2	70.0	2913	10	ADK98520 S Bulboca
6	2077.2	70.0	2913	12	ADK98520 S Bulboca
7	1880.8	63.4	3971	10	ADK98520 S Bulboca
8	1880.8	63.4	3971	12	ADK98520 S Bulboca
9	1805.8	60.9	3592	10	ADK98520 S Bulboca
10	1805.8	60.9	3592	12	ADK98520 S Bulboca
11	1805.8	60.9	5191	12	ADK98520 S Bulboca
12	1805.8	60.9	7349	10	ADK98520 S Bulboca
13	1771.6	59.7	3260	10	ADK98520 S Bulboca
14	1771.6	59.7	3260	12	ADK98520 S Bulboca
15	1735.2	58.5	3899	12	ADK98520 S Bulboca
16	1735.2	58.5	3899	10	ADK98520 S Bulboca
17	1599.2	53.9	3222	12	ADK98522 S Bulboca
18	232.4	7.8	4149	8	ADA70126 Rice gene
19	217.6	7.3	1028	3	AAA39996 Rice gene
20	208.8	7.0	4465	2	AAT42135 I2C-2 gen

21	208.2	7.0	3801	3	AAA59332 Nucleotid
22	208.2	7.0	6658	2	AAT79882 Tomato im
23	202.6	6.8	4163	2	AAV44230 Lettuce r
24	202.6	6.8	4208	2	AAV44188 Lettuce r
25	202.6	6.8	4208	6	ABK67786 Lettuce p
26	201	6.8	4163	6	ABK67828 Lettuce p
27	200.8	6.8	1662	2	AAV44194 Lettuce r
28	200.8	6.8	1662	6	ABK67791 Lettuce p
29	196.6	6.6	2353	2	AAV44189 Lettuce r
30	196.6	6.6	2353	6	ABK67787 Lettuce p
31	177.8	6.0	4948	2	AAT42134 I2C-1 gen
32	145.2	4.9	3879	8	ADA69439 Rice gene
33	143.6	4.8	2988	8	ADA71057 Rice gene
34	143.4	4.8	518	3	AAZ58279 Rice resi
35	143.2	4.8	5910	2	AAV66798 Rice bact
36	127.6	4.3	517	3	AAZ58273 Maize res
37	121	4.1	647	3	AAA39999 Rice dise
38	121	4.1	4001	10	AAL54262 DNA Seq I
39	118	4.0	629	10	ADC72492 DNA Seq I
40	117	3.9	510	3	AAZ58280 Rice resi
41	104	3.5	644	3	AAZ51886 N. tabacu
42	102.8	3.5	515	3	AAZ58277 Rice resi
43	93.6	3.2	1036	2	AAV44191 Lettuce r
44	93.6	3.2	1036	6	ABK67788 Lettuce p
45	90.4	3.0	505	3	AAZ58282 Sorghum r

ALIGNMENTS

RESULT 1

ADK98516

ID ADK98516 standard; cDNA: 3193 BP.

XX

AC ADK98516;

XX

DT 03-JUN-2004 (first entry)

XX

DE S Bulbocactanum Sbull cDNA sequence Seg1.

XX

KW plant disease resistance polypeptide; solanaceous plant; potato;

KW late blight disease; fungus; Phytophthora infestans;

KW conferring pathogen resistance; Sbull; gene; ss.

XX

OS Solanum bulbocactanum.

XX

EH Key Location/Qualifiers

FT	CDS	52..3018
FT	FT	/*tag= a
FT	FT	/product= "S Bulbocactanum Sbull protein"
XX	PN	WO2004020594-A2.
XX	PD	11-MAR-2004.
XX	PF	28-AUG-2003; 2003WO-US027045.
XX	PR	29-AUG-2002; 2002US-0407100P.
XX	PR	20-AUG-2003; 2003US-00647268.
XX	PA	(USDA) US SEC OF AGRIC.
XX	PA	(DRYC-) DRY CREEK LAB.
XX	PI	Osumi T, Belknap WR, Rockhold DR, Maccree MM;
XX	PI	WPI; 2004-239179/22.
XX	DR	P-PSDB; ADK98517.
XX	PT	New isolated Solanum bulbocactanum late blight resistance nucleic acid
XX	PT	molecule encoding a plant disease resistance polypeptide; useful for
XX	PT	conferring pathogen resistance to Phytophthora infestans in plants.
XX	PS	Claim 1; SEQ ID NO 1; 103bp; English.

XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a plant disease resistance polypeptide. The preferred plant is a
CC solanaceous plant that is potato. The resistance is to late blight
CC disease, caused by the fungus *Phytophthora infestans*. The invention is
CC useful for conferring pathogen resistance in plants using a *Solanum*
CC bulbocastanum late blight resistance gene. The present sequence is the S
CC bulbocastanum cDNA sequence of the invention.

SQ Sequence 3193 BP, 1031 A; 543 C; 671 G; 948 T; 0 U; 0 Other;

Query Match 100.0%; Score 2967; DB 12; Length 3193;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGCTGAAGCTTCTTCAAGTTCCTTTAGCAATCTGACTTGTTCATCCAAAGGGGAA 60
DB 52 ATGGCTGAAGCTTCTTCAAGTTCCTTTAGCAATCTGACTTGTTCATCCAAAGGGGAA 111
QY 61 CTTCGATTGATCTTGGTTTAAAGATGAGTCGAAAAGCTTCAAAGCACTTTACTCA 120
DB 112 CTTCGATTGATCTTGGTTTAAAGATGAGTCGAAAAGCTTCAAAGCACTTTACTCA 171
QY 121 ATCCAAAGCTGTCTGAAGATGCTCAGAAAGCAATTTGAAGCAAGCAATGAAAT 180
DB 172 ATCCAAAGCTGTCTGAAGATGCTCAGAAAGCAATTTGAAGCAAGCAATGAAAT 231
QY 181 TGGTTGCGAAGAACTGAATGCTGCTGCTCATATGAGGCTGATGACATTTGGAGAGATGATA 240
DB 232 TGGTTGCGAAGAACTGAATGCTGCTGCTCATATGAGGCTGATGACATTTGGAGAGATGATA 291
QY 241 ACTGAGGACCAATTTAGACAGAGAAAGAAACAAATATGGGTGTATCATCCAAACGTTATC 300
DB 292 ACTGAGGACCAATTTAGACAGAGAAAGAAACAAATATGGGTGTATCATCCAAACGTTATC 351
QY 301 ACTTTTGTCTACAGATTTGGGAAAAAGATGAAAAAGATTATGAGAAACTATGATGTAAAT 360
DB 352 ACTTTTGTCTACAGATTTGGGAAAAAGATGAAAAAGATTATGAGAAACTATGATGTAAAT 411
QY 361 GCAGCGAAGCAATTAAGTTTCATTTGATGAAGAAAGTATATGAGAGCAAGTTGTCTACA 420
DB 412 GCAGCGAAGCAATTAAGTTTCATTTGATGAAGAAAGTATATGAGAGCAAGTTGTCTACA 471
QY 421 CGCCAAACAGGTTTGTTTTGAATGAAACCAAGTTTATGGAAGAGCAAAAGAAAGAC 480
DB 472 CGCCAAACAGGTTTGTTTTGAATGAAACCAAGTTTATGGAAGAGCAAAAGAAAGAC 531
QY 481 GAGATAGTGAAGAAATCTGATTAACCAATGTTAGCAATGCCAAACACTTCCAGTCTCCCA 540
DB 532 GAGATAGTGAAGAAATCTGATTAACCAATGTTAGCAATGCCAAACACTTCCAGTCTCCCA 591
QY 541 ATACTGGTATGGGGGACCTAGAAAGACAGCTCTGCCCCAAATGGTCTTCAATGATCAG 600
DB 592 ATACTGGTATGGGGGACCTAGAAAGACAGCTCTTCCCCAAATGGTCTTCAATGATCAG 651
QY 601 AGAGTAATATGACATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATAGAG 660
DB 652 AGAGTAATATGACATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATAGAG 711
QY 661 AAGAGTTGTAATAAGAAATTTGTAGATCTTATGAAAGAAAGTCACTTGGTGGAGTGGAC 720
DB 712 AAGAGTTGTAATAAGAAATTTGTAGATCTTATGAAAGAAAGTCACTTGGTGGAGTGGAC 771
QY 721 TTGGCTCCACTTCAAAAGAGCTTCGGGACCTTCGTAATGGAAGAAATATTTTGTCTGTC 780
DB 772 TTGGCTCCACTTCAAAAGAGCTTCGGGACCTTCGTAATGGAAGAAATATTTTGTCTGTC 831
QY 781 TTGATGATGTTTGGATGAAGATCAAGATPAAGTGGCTAAGTTTAAACAAGTCTTGAAG 840
DB 832 TTGATGATGTTTGGATGAAGATCAAGATPAAGTGGCTAAGTTTAAACAAGTCTTGAAG 891
QY 841 GTTGAGACAGTGGCGCTTCTGTTCTAACAATCTGTCTTGAAAAGTTTGAATCAATT 900
```

```
DB 892 GTTGAGACAGTGGCGCTTCTGTTCTAACAATCTGTCTTGAAAAGTTTGAATCAATT 951
QY 901 ATGGGAACATTTGCAACCATATGAATTTGTCATCAAGAAAGATTTGGTGTGTG 960
DB 952 ATGGGAACATTTGCAACCATATGAATTTGTCATCAAGAAAGATTTGGTGTGTG 1011
QY 961 TTTCATGCAAGTGTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTTGGCTATGGA 1020
DB 1012 TTTCATGCAACGTGCAATTTGGGACCAAGAAAGAAATTAATCTTAATCTTTGGCTATGGA 1071
QY 1021 AAGAGATTTGGAAGAAATGATGATGATGCTCTAGAGCTTAAACCTTGGAGATTT 1080
DB 1072 AAGAGATTTGGAAGAAATGATGATGATGCTCTAGAGCTTAAACCTTGGAGATTT 1131
QY 1081 TTGCGCTTTAAGAGAGAAAGACAGTGGGAAACATGTGAGAGATTAAGATTTGGAAA 1140
DB 1132 TTGCGCTTTAAGAGAGAAAGACAGTGGGAAACATGTGAGAGATTAAGATTTGGAAA 1191
QY 1141 TTGCGCTAAGAGAAAGTGTCTATCTGCTGCTGAGCTTGAAGTTCATCACTTCCA 1200
DB 1192 TTGCGCTAAGAGAAAGTGTCTATCTGCTGCTGAGCTTGAAGTTCATCACTTCCA 1251
QY 1201 CTTCGATTGAGACATGCTTTTACATATTTGTCAGATATCCCAAGAGATCCGAATGGA 1260
DB 1252 CTTCGATTGAGACATGCTTTTACATATTTGTCAGATATCCCAAGAGATCCGAATGGA 1311
QY 1261 AAGGGAATCTAATCTCTCTGAGATGCGACATGCTTTTATTTATGCAAGAACTTG 1320
DB 1312 AAGGGAATCTAATCTCTCTGAGATGCGACATGCTTTTATTTATGCAAGAACTTG 1371
QY 1321 GAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1372 GAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
QY 1381 GAGATGGAATTAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGAT 1440
DB 1432 GAGATGGAATTAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGAT 1491
QY 1441 GCAACATCTCTATTTTTCGGAACACATCAAGAGCAATTCGGAAGAAATTTGTAAGA 1500
DB 1492 GCAACATCTCTATTTTTCGGAACACATCAAGAGCAATTCGGAAGAAATTTGTAAGA 1551
QY 1501 AATTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1552 AATTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1611
QY 1561 CACTTGCAAGATTTGTCTGTTGAGGGTGTATTAATCTAAGTACATTAAGACAG 1620
DB 1612 CACTTGCAAGATTTGTCTGTTGAGGGTGTATTAATCTAAGTACATTAAGACAG 1671
QY 1621 TTACCGCTTCCATTTGAGAGATCTAGTACATTTAAGTATCTTAACCTTGTGGCAATCT 1680
DB 1672 TTACCGCTTCCATTTGAGAGATCTAGTACATTTAAGTATCTTAACCTTGTGGCAATCT 1731
QY 1681 AGTATTCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGAGACCTTGAATCTA 1740
DB 1732 AGTATTCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGAGACCTTGAATCTA 1791
QY 1741 CATGCTGTCATTCATCTTGTGTTTGCAGAAAGAAACAGCAAACTTGTGTGCTTGA 1800
DB 1792 CATGCTGTCATTCATCTTGTGTTTGCAGAAAGAAACAGCAAACTTGTGTGCTTGA 1851
QY 1801 AATCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1852 AATCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
QY 1861 ACATGCTTTAAGACTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
DB 1912 ACATGCTTTAAGACTCTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1971
QY 1921 GGTGAATTAAGAACTGAAATCTTAATGCTCAATTTGAATCAAGCATTTTGAAGAGTG 1980
DB 1972 GGTGAATTAAGAACTGAAATCTTAATGCTCAATTTGAATCAAGCATTTTGAAGAGTG 2031
```

```

OY 1981 AAGATGATATGATGACAAAAGACCAATTATCTGCAAAAAGAAATCTGCATTCCTTA 2040
DB 2032 AAGATGATATGATGACAAAAGACCAATTATCTGCAAAAAGAAATCTGCATTCCTTA 2091
OY 2041 AGCATGAAAATGGGATGACGATGACGTCACCTATATATGATATCAAAAAAGTTGAAGTG 2100
DB 2092 AGCATGAAAATGGGATGACGATGACGTCACCTATATATGATATCAAAAAAGTTGAAGTG 2151
OY 2101 CTGGAAGCTTCCAAACCACTCCCAATCTGACTTGTGTTAAACAATGAGGGCTTCAGAGA 2160
DB 2152 CTGGAAGCTTCCAAACCACTCCCAATCTGACTTGTGTTAAACAATGAGGGCTTCAGAGA 2211
OY 2161 ATCCGCTCCCAAGCTGATGATCACTCAAGTTTGAAGAAATGTGTCTATGAAATC 2220
DB 2212 ATCCGCTCCCAAGCTGATGATCACTCAAGTTTGAAGAAATGTGTCTATGAAATC 2271
OY 2221 ATCAGTTGCCAAAACCTGCTCATGCTTACCACTTGTGAGCTGCTTGTGTAAGT 2280
DB 2272 ATCAGTTGCCAAAACCTGCTCATGCTTACCACTTGTGAGCTGCTTGTGTAAGT 2331
OY 2281 CTAGAGTTGTGAGAGGGGCTTCGCGAAGTGAGTATGTTGATTCGATTCCTTCAAGA 2340
DB 2332 CTAGAGTTGTGAGAGGGGCTTCGCGAAGTGAGTATGTTGATTCGATTCCTTCAAGA 2391
OY 2341 AGAAGTTTCCATCTCTGAGAAAACCTTAAATATACGCGAATTTGATATCTGAAAGGATTG 2400
DB 2392 AGAAGTTTCCATCTCTGAGAAAACCTTAAATATACGCGAATTTGATATCTGAAAGGATTG 2451
OY 2401 CTGAAAAAGAGAGAGAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTTGC 2460
DB 2452 CTGAAAAAGAGAGAGAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTTGC 2511
OY 2461 CCTATGTTGTTATTCCAACCTTTCTCTGTCAAGAAATGTTGTTAGTGGGAGCAAG 2520
DB 2512 CCTATGTTGTTATTCCAACCTTTCTCTGTCAAGAAATGTTGTTAGTGGGAGCAAG 2571
OY 2521 TCAGATGCAATGAGTTTCAAGTTCATATCTATCATGGCTCTTACTCTCCCAAT 2580
DB 2572 TCAGATGCAATGAGTTTCAAGTTCATATCTATCATGGCTCTTACTCTCCCAAT 2631
OY 2581 CGCTATTAACAAAGAGATGCTTCACTCCGAGAGAGATGTTCAAAAGCCTTGCAATCTC 2640
DB 2632 CGCTATTAACAAAGAGATGCTTCACTCCGAGAGAGATGTTCAAAAGCCTTGCAATCTC 2691
OY 2641 AAATATCTGATATCTCTTTTACTTCAATCTTAAAGAGCTGCTTACCAAGCTGCTAGT 2700
DB 2692 AAATATCTGATATCTCTTTTACTTCAATCTTAAAGAGCTGCTTACCAAGCTGCTAGT 2751
OY 2701 CTCAATGCTTTGAAGCATCTGGAATTCATAGTTGTTATGCACTGAGAGCTCCCGAG 2760
DB 2752 CTCAATGCTTTGAAGCATCTGGAATTCATAGTTGTTATGCACTGAGAGCTCCCGAG 2811
OY 2761 GAAGGTGGAAGGTTTATTTCACTCAACAGTTATCATTAACACTGTTGAATGCTA 2820
DB 2812 GAAGGTGGAAGGTTTATTTCACTCAACAGTTATCATTAACACTGTTGAATGCTA 2871
OY 2821 CAATGTTTACCGGAGGATGACGACCTTAACAGCCCTCACAAAATTTATCAGTTAGTTT 2880
DB 2872 CAATGTTTACCGGAGGATGACGACCTTAACAGCCCTCACAAAATTTATCAGTTAGTTT 2931
OY 2881 TGTCCAAACATGCGCAACGCGTGTGAGAAAGGATAGAGAAAGATGCTATCAAAATTTCT 2940
DB 2932 TGTCCAAACATGCGCAACGCGTGTGAGAAAGGATAGAGAAAGATGCTATCAAAATTTCT 2991
OY 2941 CACATTTCTCTGTGTATTTATTTAG 2967
DB 2992 CACATTTCTCTGTGTATTTATTTAG 3018

```

RESULT 2
ADK98518
ID ADK98518 standard; DNA; 3595 BP.

```

XX AC ADK98518;
XX DT 03-JUN-2004 (first entry)
XX DE S Bulbocastanum Sbul1 gene genomic DNA sequence SeqID3.
XX KW plant disease resistance polypeptide; solanaceous plant; potato;
XX KW late blight disease; fungus; Phytophthora infestans;
XX KW conferring pathogen resistance; Sbul1; gene; de.
XX OS Solanum bulbocastanum.
XX FH Key Location/Qualifiers
XX FT CDS 57..3432
XX FT /tag= a
XX FT /product= "S Bulbocastanum Sbul1 protein"
XX FT /tag= b
XX PN Intron
XX PD 11-MAR-2004.
XX PF 28-AUG-2003; 2003WO-US027045.
XX PR 29-AUG-2002; 2002US-0407100P.
XX PR 20-AUG-2003; 2003US-00647268.
XX PA (USDA ) US SEC OF AGRIC.
XX PA (DRYC-) DRY CREEK LAB.
XX PI Osumi T, Belknap WR, Rockhold DR, Maccree MW;
XX DR WPI: 2004-239179/22.
XX DR P-PSDB; ADK98519.
XX PT New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX PT molecule encoding a plant disease resistance polypeptide, useful for
XX PT conferring pathogen resistance to Phytophthora infestans in plants.
XX PS Claim 1; SEQ ID NO 3; 103pp; English.
XX CC This invention relates to a novel isolated nucleic acid molecule encoding
XX CC a plant disease resistance polypeptide. The preferred plant is a
XX CC solanaceous plant that is potato. The resistance is to late blight
XX CC disease, caused by the fungus Phytophthora infestans. The invention is
XX CC useful for conferring pathogen resistance in plants using a Solanum
XX CC bulbocastanum late blight resistance gene. The present sequence is the S
XX CC bulbocastanum gene sequence of the invention.
XX SQ Sequence 3595 BP; 1139 A; 614 C; 737 G; 1105 T; 0 U; 0 Other;

Query Match 85.7%; Score 2541.8; DB 12; Length 3595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 428 CAGGTTTGTGTTGAATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 487
DB 896 CAGGTTTGTGTTGAATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 955
OY 488 TGAATATCTGATTAACAATGTTGCAATGCGCAAAACCTTCCAGTCTCCCAATCTTG 547
DB 956 TGAATATCTGATTAACAATGTTGCAATGCGCAAAACCTTCCAGTCTCCCAATCTTG 1015
OY 548 GTATGGGGGAGCTAGAAAGACGACTTGGCCCAATGTTCTTCAATGATCAGAGATTA 607
DB 1016 GTATGGGGGAGCTAGAAAGACGACTTGGCCCAATGTTCTTCAATGATCAGAGATTA 1075
OY 608 TTGAGCAATTTCCATCCCAAAATATGATTTGTGTCTGGAAAGATTTTATATGAAAGAGT 667
DB 1076 TTGAGCAATTTCCATCCCAAAATATGATTTGTGTCTGGAAAGATTTTATATGAAAGAGT 1135

```

QY 668 TATATAAGAAATTTAGATCTATTAAGAAAAAGTCACTGGGCGATGCACTGGCGCTC 727
| | | | |
Db 1136 TATATAAGAAATTTAGATCTATTAAGAAAAAGTCACTGGGCGATGCACTGGCGCTC 1195
| | | | |
QY 728 CACTTCAAAAGAAAGCTTGGGGAAGCTGCTGTAATGGAAGAAAAATATTTGCTGCTTATGATG 787
| | | | |
Db 1196 CACTTCAAAAGAAAGCTTGGGGAAGCTGCTGTAATGGAAGAAAAATATTTGCTGCTTATGATG 1255
| | | | |
QY 788 ATGTTGGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGACAAGTCTTGAAGTTGGAG 847
| | | | |
Db 1256 ATGTTGGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGACAAGTCTTGAAGTTGGAG 1315
| | | | |
QY 848 CAAAGTGGCGCTTCTGTTCTAACCACTACTGCTGTTGAAAAAGTTGGATCAATATGAGAA 907
| | | | |
Db 1316 CAAAGTGGCGCTTCTGTTCTAACCACTACTGCTGTTGAAAAAGTTGGATCAATATGAGAA 1375
| | | | |
QY 908 CATTGCAACCATATGAATTTGTCAATTTGTCTCAAGAAAGATTTGTTGTTGTTCTATGC 967
| | | | |
Db 1376 CATTGCAACCATATGAATTTGTCAATTTGTCTCAAGAAAGATTTGTTGTTGTTCTATGC 1435
| | | | |
QY 968 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGGCTATCGGAAGAGAGA 1027
| | | | |
Db 1436 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGGCTATCGGAAGAGAGA 1495
| | | | |
QY 1028 TTGTGAAAAAATGTGTGTGTGCTCTAGACGCTTAAAATCTTGGAGATATTTGGCT 1087
| | | | |
Db 1496 TTGTGAAAAAATGTGTGTGTGCTCTAGACGCTTAAAATCTTGGAGATATTTGGCT 1555
| | | | |
QY 1088 TTAAGAGAGAAAGAAAGACAGTGGGAAACATGTGAGATAGTGAATTTGAAATTTGGCTC 1147
| | | | |
Db 1556 TTAAGAGAGAAAGAAAGACAGTGGGAAACATGTGAGATAGTGAATTTGAAATTTGGCTC 1615
| | | | |
QY 1148 AAGAAAGAAAGTTCTATTTCTGCTGCTGAGACTTAAGTTACATCACTTGCACCTTGAAT 1207
| | | | |
Db 1616 AAGAAAGAAAGTTCTATTTCTGCTGCTGAGACTTAAGTTACATCACTTGCACCTTGAAT 1675
| | | | |
QY 1208 TGAAGCATGCTTATCATATTTGTGAGATATCCCAAGATACCGAAATGGAAGAGGAA 1267
| | | | |
Db 1676 TGAAGCATGCTTATCATATTTGTGAGATATCCCAAGATACCGAAATGGAAGAGGAA 1735
| | | | |
QY 1268 ATCTAATCTCTCTGATGAGCACTGAGTTTATTTATCGAAAGAAACTTGGAGCTAG 1327
| | | | |
Db 1736 ATCTAATCTCTCTGATGAGCACTGAGTTTATTTATCGAAAGAAACTTGGAGCTAG 1795
| | | | |
QY 1328 AGAATGTAAGTAATGAAGTATGAATTAATCTTGAAGTCTTCTTCCAGAGATG 1387
| | | | |
Db 1796 AGAATGTAAGTAATGAAGTATGAATTAATCTTGAAGTCTTCTTCCAGAGATG 1855
| | | | |
QY 1388 AAGTTAATCTGATCAAACTTAATTTCAAGATGATGATCTCATGATCTGGCAAT 1447
| | | | |
Db 1856 AAGTTAATCTGATCAAACTTAATTTCAAGATGATGATCTCATGATCTGGCAAT 1915
| | | | |
QY 1448 CTCTAATTTTGGGCAAGCACTACGAGCAATATCCGAGAAATTAATGTAAGAAATTA 1507
| | | | |
Db 1916 CTCTAATTTTGGGCAAGCACTACGAGCAATATCCGAGAAATTAATGTAAGAAATTA 1975
| | | | |
QY 1508 TACATTAAGATGCTCATTTGCTTCTAATAGTGTATCTTCTACTCTTCTTCCACTG 1567
| | | | |
Db 1976 TACATTAAGATGCTCATTTGCTTCTAATAGTGTATCTTCTACTCTTCTTCCACTG 2035
| | | | |
QY 1568 AGAAGTTTGTCTGTTGAGGCTGCTTAATCTAAGTGAATTAATCAAGAGTTACCGT 1627
| | | | |
Db 2036 AGAAGTTTGTCTGTTGAGGCTGCTTAATCTAAGTGAATTAATCAAGAGTTACCGT 2095
| | | | |
QY 1628 CTTCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGTCTGAGATATCTATGAT 1687
| | | | |
Db 2096 CTTCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGTCTGAGATATCTATGAT 2155
| | | | |
QY 1688 GTAGTCTTCAACCAAGATTAAGAGTTCAGAAATCTGAGACTCTTGAATCTAATGCT 1747
| | | | |
Db 2156 GTAGTCTTCAACCAAGATTAAGAGTTCAGAAATCTGAGACTCTTGAATCTAATGCT 2215
| | | | |
QY 1748 GTATTCATCTTGTGTGTTGCCAAAGAAACAAGCAAACTTGGTATGCTTCAAAATCTTT 1807
| | | | |
| | | | |
Db 2216 GTATTCATCTTGTGTGTTGCCAAAGAAACAAGCAAACTTGGTATGCTTCAAAATCTTT 2275
| | | | |
QY 1808 TACTTGATGTTGCTATGATGATTAAGCTTGTATGCCAACAAGATAGATCTTTGACATGCC 1867
| | | | |
Db 2276 TACTTGATGTTGCTATGATGATTAAGCTTGTATGCCAACAAGATAGATCTTTGACATGCC 2335
| | | | |
QY 1868 TTAAGACTTAAGATTAATTTGTGTGGGAATTCAGAAAGAAAGTTGCACTTGTGTAAT 1927
| | | | |
Db 2336 TTAAGACTTAAGATTAATTTGTGTGGGAATTCAGAAAGAAAGTTGCACTTGTGTAAT 2395
| | | | |
QY 1928 TACGAAACCTGAATCTGATGCTCAATTTGAATCAAGCATCTTGAAGAGTGAAGATG 1987
| | | | |
Db 2396 TACGAAACCTGAATCTGATGCTCAATTTGAATCAAGCATCTTGAAGAGTGAAGATG 2455
| | | | |
QY 1988 ATATGATGCAAAAGAAAGCCAAATTTATCTGCAAAAGAAATCTGCATCTTTAAGATGA 2047
| | | | |
Db 2456 ATATGATGCAAAAGAAAGCCAAATTTATCTGCAAAAGAAATCTGCATCTTTAAGATGA 2515
| | | | |
QY 2048 AATGAGATGACGATGAAGCTCCACGTATATATGAAATGGAAGATGGAAGTCTTGAG 2107
| | | | |
Db 2516 AATGAGATGACGATGAAGCTCCACGTATATATGAAATGGAAGATGGAAGTCTTGAG 2575
| | | | |
QY 2108 CTCTCAAAACCACTGCAATCTGAATTTGTTTAAATCAATCAAGGCTTCAAGAAATCCGCT 2167
| | | | |
Db 2576 CTCTCAAAACCACTGCAATCTGAATTTGTTTAAATCAATCAAGGCTTCAAGAAATCCGCT 2635
| | | | |
QY 2168 TCCGAGCTGATGAATCACTCAAGTTTGAAGAAATGTGTCTCATATGAATCAATCACT 2227
| | | | |
Db 2636 TCCGAGCTGATGAATCACTCAAGTTTGAAGAAATGTGTCTCATATGAATCAATCACT 2695
| | | | |
QY 2228 GCAAAAACCTGCTGATGCTTACCAACCTTTGAGAGCTGCTTGTCTTAAAAAGCTAGAT 2287
| | | | |
Db 2696 GCAAAAACCTGCTGATGCTTACCAACCTTTGAGAGCTGCTTGTCTTAAAAAGCTAGAT 2755
| | | | |
QY 2288 TGTGAGAGGGGCTCTGGGAAAGTGAATGTTGATTTGTGATTTCCCTAACAAGAAAGT 2347
| | | | |
Db 2756 TGTGAGAGGGGCTCTGGGAAAGTGAATGTTGATTTGTGATTTCCCTAACAAGAAAGT 2815
| | | | |
QY 2348 TTCCATCTGAGAGAAACTTAATATAGCGAATTTGTTGATTCGAAAGATGCTGAAA 2407
| | | | |
Db 2816 TTCCATCTGAGAGAAACTTAATATAGCGAATTTGTTGATTCGAAAGATGCTGAAA 2875
| | | | |
QY 2408 AGAAGAGAGAGAGCAATGCTGCTGTGTTGAAGATTAAGATTAATGTTGCCCTATG 2467
| | | | |
Db 2876 AGAAGAGAGAGAGCAATGCTGCTGTGTTGAAGATTAAGATTAATGTTGCCCTATG 2935
| | | | |
QY 2468 TTGTTAATCCAAACCTTTCTTCTGTCAAGAAATTTGTTAGTGTGGGACAACTCAGATG 2527
| | | | |
Db 2936 TTGTTAATCCAAACCTTTCTTCTGTCAAGAAATTTGTTAGTGTGGGACAACTCAGATG 2995
| | | | |
QY 2528 CAATAGGTTTCAAGTCTCATATCTAATCTCATGCTCTTACTTCCCTCCAAATTTGCTATA 2587
| | | | |
Db 2996 CAATAGGTTTCAAGTCTCATATCTAATCTCATGCTCTTACTTCCCTCCAAATTTGCTATA 3055
| | | | |
QY 2588 ACAAGAGAGAGTCTTCACTCCAGAGAGATGTTCAAAAAGCTTGGCAATCTCAATACT 2647
| | | | |
Db 3056 ACAAGAGAGAGTCTTCACTCCAGAGAGATGTTCAAAAAGCTTGGCAATCTCAATACT 3115
| | | | |
QY 2648 TGAATATCTCTTTTATCTTCAATCTTAAGAGCTGCTTCAAGCTGCTGCTATGCTCAAG 2707
| | | | |
Db 3116 TGAATATCTCTTTTATCTTCAATCTTAAGAGCTGCTTCAAGCTGCTGCTATGCTCAAG 3175
| | | | |
QY 2708 CTTTGAAGCATCTGAAATTCATATGTTTATGACTAGAGAGTCTCCCGAGAGAGGTG 2767
| | | | |
Db 3176 CTTTGAAGCATCTGAAATTCATATGTTTATGACTAGAGAGTCTCCCGAGAGAGGTG 3235
| | | | |
QY 2768 TGAAGGTTTAATTTCACTCAACAGTTATTCATATACTATCTGTAATGCTCAATGTT 2827
| | | | |
Db 3236 TGAAGGTTTAATTTCACTCAACAGTTATTCATATACTATCTGTAATGCTCAATGTT 3295
| | | | |
QY 2828 TACCGAGGAGTTGAGACCTTAACAGGCTTCAAAAATTTATCAATGATTTTGTCCAA 2887
| | | | |
| | | | |

Db 3396 TACCGAGGATTCGACGACCTTAACAGCCCTCAAAATTATCACTGAGTTTGTCCAA 3355
Qy 2888 CACTGCGCCAGCGGTGTGAGAGGAGATAGAGAGTGTGACAAATTTGCTCACTTC 2947
Db 3356 CACTGCGCCAGCGGTGTGAGAGGAGATAGAGAGTGTGACAAATTTGCTCACTTC 3415
Qy 2948 CTGCTGTGTTTATTTATTTAG 2967
Db 3416 CTCGTGTGTTTATTTATTTAG 3435

RESULT 3
ADK98524
ID ADK98524 standard; DNA; 5028 BP.
XX
AC ADK98524;
DT 03-JUN-2004 (first entry)
DE S Bulbocastanum Sbul protein-related chimeric transgene SeqID9.
XX plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
XX conferring pathogen resistance; gene; ds; transgenic; Ubi 3 promoter.
OS Solanum bulbocastanum.
OS Chimeric.

XX Key Location/Qualifiers
FH 1029..4404
FT /*tag= a
CT /*product= "S Bulbocastanum Sbul protein"
FT 1460..1871
FT intron /*tag= b

XX MO2004020594-A2.
XX 11-MAR-2004.
XX 28-AUG-2003; 2003WO-US027045.
XX 29-AUG-2002; 2002US-0407100P.
XX 20-AUG-2003; 2003US-00647268.
XX (USDA) US SEC OF AGRIC.
PA (DRYC-) DRY CREEK LAB.
XX
PI Osumi T, Belknap WR, Rockhold DR, Maccree NM;
XX
XX WPI: 2004-239179/22.
DR P-PSDB; ADK98525.
XX

FT New isolated Solanum bulbocastanum late blight resistance nucleic acid
FT molecule encoding a plant disease resistance polypeptide, useful for
FT conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Claim 1; SEQ ID NO 9; 103bp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum
XX bulbocastanum late blight resistance gene. The present sequence is that
XX of a chimeric transgene (Sbul gene with a potato Ubi1 promoter sequence)
XX of the invention.

XX Sequence 5028 BP; 1647 A; 847 C; 958 G; 1576 T; 0 U; 0 Other;
Query Match 85.7%; Score 2541.8; DB 12; Length 5028;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 428 CAGGTTTTTGTGTAATGAAACCAAGTTATGGAAGACAAAGAAAGACGATAG 487
Db 1868 CAGGTTTTTGTGTAATGAAACCAAGTTATGGAAGACAAAGAAAGACGATAG 1927
Qy 488 TGAATAATCCTGATTAACAATTTAGCAATGCCCAACCTCCAGTCTCCCAATACTG 547
Db 1928 TGAATAATCCTGATTAACAATTTAGCAATGCCCAACCTCCAGTCTCCCAATACTG 1987
Qy 548 GTATGGGGGACTAGAAAAGCACTCTTGCCCAATAGCTTTCGAATGATCAGAGATGA 607
Db 1988 GTATGGGGGACTAGAAAAGCACTCTTGCCCAATAGCTTTCGAATGATCAGAGATGA 2047
Qy 608 TTGACATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTATGAGAAAGCT 667
Db 2048 TTGACATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTATGAGAAAGCT 2107
Qy 668 TGAATTAAGAAATTTGTAGAAATCTATTTGAGAAAGTCACTTGTTGATGAGACTTGCTC 727
Db 2108 TGAATTAAGAAATTTGTAGAAATCTATTTGAGAAAGTCACTTGTTGATGAGACTTGCTC 2167
Qy 728 CACTTCAAAAAGAGCTTCGGGACTTGCTGATGAGAAAAAATATTTGCTCTTAGATG 787
Db 2168 CACTTCAAAAAGAGCTTCGGGACTTGCTGATGAGAAAAAATATTTGCTCTTAGATG 2227
Qy 788 ATGTTTGAATGAAGATCAAGATTAAGTGAGCTTAAGTAAACAATCTTGAAGTTGAG 847
Db 2228 ATGTTTGAATGAAGATCAAGATTAAGTGAGCTTAAGTAAACAATCTTGAAGTTGAG 2287
Qy 848 CAACTGGCGCTTCGTGTTCTAACCACTACTGCTTTGAAAAGTTGATCAATTTATGGAA 907
Db 2288 CAACTGGCGCTTCGTGTTCTAACCACTACTGCTTTGAAAAGTTGATCAATTTATGGAA 2347
Qy 908 CATTGCAACCATGAATGTCAAATTTGTCTCAAGAAGATTGTTGTTGTTTCATGC 967
Db 2348 CATTGCAACCATGAATGTCAAATTTGTCTCAAGAAGATTGTTGTTGTTTCATGC 2407
Qy 968 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTATCTTGTGGCTATCGGAAAGAGA 1027
Db 2408 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTATCTTGTGGCTATCGGAAAGAGA 2467
Qy 1028 TTGTGAAAAAATGTGTGTGTGCTCTGACAGCTAAACCTTTGAGAGTATTTTGGCCT 1087
Db 2468 TTGTGAAAAAATGTGTGTGTGCTCTGACAGCTAAACCTTTGAGAGTATTTTGGCCT 2527
Qy 1088 TTAAGAGAGAAAGAACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGCTC 1147
Db 2528 TTAAGAGAGAGAAAGAACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGCTC 2587
Qy 1148 AAGAGAAAGTTCTATTTCTGTGCTGCCCTGAGACTTATACATCACCTTCACCTGAT 1207
Db 2588 AAGAGAAAGTTCTATTTCTGTGCTGCCCTGAGACTTATACATCACCTTCACCTGAT 2647
Qy 1208 TGAACAAATGCTTTACATATTGTGCAATTTCCAAAGGATACCGAAATGGAAGGAA 1267
Db 2648 TGAACAAATGCTTTACATATTGTGCAATTTCCAAAGGATACCGAAATGGAAGGAA 2707
Qy 1268 ATCTAATCTCTCTGATGAGCAATGCTTTATTTATGGAAGAACTTGGAGTAG 1327
Db 2708 ATCTAATCTCTCTGATGAGCAATGCTTTATTTATGGAAGAACTTGGAGTAG 2767
Qy 1328 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1387
Db 2768 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2827
Qy 1388 AAGTTAAATCTGTGCAAACTTATTTCAAGATGATGATCTATTCATGATTTGGCAAT 1447
Db 2828 AAGTTAAATCTGTGCAAACTTATTTCAAGATGATGATCTATTCATGATTTGGCAAT 2887
Qy 1448 CTTATTTTGGGCAAGACATCAAGACGAAATATCCGAAATATATGAGAAATTTACA 1507
Db 2888 CTTATTTTGGGCAAGACATCAAGACGAAATATCCGAAATATATGAGAAATTTACA 2947
Qy 1508 TACATATGATGTCATTTGTTCACTAAAGTGTATCTTCTACTCTCTTCCACTTGC 1567

This invention relates to a novel isolated nucleic acid molecule encoding a plant disease resistance polypeptide. The preferred plant is a solanaceous plant that is potato. The resistance is to late blight disease, caused by the fungus *Phytophthora infestans*. The invention is useful for conferring pathogen resistance in plants using a *Solanum bulbocastanum* late blight resistance gene. The present sequence is the *S bulbocastanum* Sbul 2 gene sequence which was used in the exemplification of the invention.

Sequence 3347 BP; 1070 A; 577 C; 693 G; 1007 T; 0 U; 0 Other;

Query Match 77.8%; Score 2309; DB 12; Length 3347;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2773; Conservative 0; Mismatches 190; Indels 330; Gaps 2;

```
QY 1 ATGGCTGAAGCTTCTCAAGTCTGTAGCATCTGACCTGTTCATCCAGGGGAA 60
DB 57 ATGGCTGAAGCTTCTCAAGTCTGTAGCATCTGACCTGTTCATCCAGGGGAA 116
QY 61 CTGGATTTGATTTCTTTTAAAGATGATTCGAAAGCTTCAAGACGTTTACTACA 120
DB 117 GTTGATTTGATTTCTTTTAAAGATGATTCGAAAGCTTCAAGACGTTTACTACA 176
QY 121 ATCCAGCTGTCTGAAAGATGCTCAGAAAGCAATTGAAGACAGCAATGAAAT 180
DB 177 ATCCAGCTGTCTGAAAGATGCTCAGAAAGCAATTGAAGACAGCAATGAAAT 236
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGACCTTGGAGGANTGAA 240
DB 237 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGACCTTGGAGGANTGAA 296
QY 241 ACTGAGCAGCAATTTAGACAGAAAGAACTATGAGTGTATCATCCAAAGCTTATC 300
DB 297 ACTGAGCAGCAATTTAGACAGAAAGAACTATGAGTGTATCATCCAAAGCTTATC 356
QY 301 ACTTTTCTCAAGATTTGGGAAAAGATGAAAAGATTATGAGAAACTATGATGTAAT 360
DB 357 GCTTCCCTCAAGATTTGGGAAAAGATGAAAAGATTATGAGAAACTATGATGTAAT 416
QY 361 GCACGCGAAGCAATTAATTTTCAATTTGATGAAAGATATAGAGACAGATGCTTACA 420
DB 417 GCACGCGAAGCAATTAATTTTCAATTTGATGAAAGATATAGAGACAGATGCTTACA 476
QY 421 CGCCAAA----- 427
DB 477 CGCCAAAAGGTGCTCATCTTATGATTTTCTAAAAAAGCCTTATATCATGAAT 536
QY 428 ----- 427
DB 537 CATGTGTGTTGGGATTTTCTAATCTAAATGTTGCTCAAGTCTAAGTAGATAGTG 596
QY 428 ----- 427
DB 597 ATCCAGATTGGATATATTAATATATTAATCTAAATTTGTTGCGAAATTTTAAACAGAT 656
QY 428 ----- 427
DB 657 AAAGCTGAGTTGTTTGAACATTAATAATTAACAATATATATGGAATTCAAAAAA 716
QY 428 ----- 427
DB 717 GTGCATATATGCTGCTGCTCTCAAGCTTATCATGTCTCTTATATGCAAAATTCCTC 776
QY 428 ----- 427
DB 777 TTGCTTTTCTGACTCTACTAGAGCTTGAACAGGTTTGTATTAAGAACCAACA 836
QY 454 GTTATGAGAGACAAAGAAAGACAGATAGTGAATCTCGATTAACATAGTTAGC 513
DB 837 GTTATGAGAGACAAAGAAAGACAGATAGTGAATCTCGATTAACATAGTTAGC 896
QY 514 AATGCCCAACACTTCAGTCTCCCAATACTTGGTATGGGGGAGCTAGAAAGACGACT 573
```

```
DB 897 GATGCCCAACACTTCAGTCTCCCAATACTTGGTATGGGGGAGCTAGAAAGACGACA 956
QY 574 CTTCGCCCAATATGCTTCAATGATCAGAGATATTTGATGCAATTCACCAAAATATAG 633
DB 957 CTTCGCCCAATATGCTTCAATGATCAGAGATATTTGATGCAATTCCTTCCAAATATAG 1016
QY 634 ATTTGTCTCGAAGATTTTATGAGAAAGGTTGATTAAGAAATTTGAAATCTAAT 693
DB 1017 ATTTGTCTCGAAGATTTTATGAGAAAGGTTGATTAAGAAATTTGAAATCTAAT 1076
QY 694 GAAAGAAAGTCACTTGTGGATGAGACTTGGCTCCACTTCAAAAGAACTTGGGACTTG 753
DB 1077 GAAAGAAAGTCACTTGTGATGATGAGACTTGGCTCCACTTCAAAAGAACTTGGGACTTG 1136
QY 754 CTGAATGAGAAATATTTGCTGCTCTTATGATGATGTTGGAATGGAATCAAGATTAAG 813
DB 1137 CTGAATGAGAAATATTTGCTGCTCTTATGATGATGTTGGAATGGAATCAAGATTAAG 1196
QY 814 TGGGCTAAGTTAAGACAACTTTGAGGTTGAGCAAGTGCGCTTGTCTTAACACT 873
DB 1197 TGGGCTAAGTTAAGACAACTTTGAGGTTGAGCAAGTGCGCTTGTCTTAACACT 1256
QY 874 ACTGCTCTGAAAAGTTGGATCAATTTAGGAAACATTGCAACCATATGATTTGCAAT 933
DB 1257 ACTGCTCTGAAAAGTTGGATCAATTTAGGAAACATTGCAACCATATGATTTGCAAC 1316
QY 934 TTGTCTCAAGAAATTTGGTGTGTTGTCATGCAAGTGATTTGGGACCAAGAAAGAA 993
DB 1317 TTGTCTCAAGAAATTTGGTGTGTTGTCATGCAAGTGATTTGGGACCAAGAAAGAA 1376
QY 994 ATTAATCTTAATCTTGTGCTATCGAAGAGATTTGAAAATATGTTGTGTGTGCT 1053
DB 1377 ATTAATCTTAATCTTGTGCTATCGAAGAGATTTGAAAATATGTTGTGTGTGCT 1436
QY 1054 CTGACAGCTAATACTTTGAGATTTTGGCTTTAAGAGAAAGAAAGCAAGTGGGAA 1113
DB 1437 CTGACAGCTAATACTTTGAGATTTTGGCTTTAAGAGAAAGAAAGCAAGTGGGAA 1496
QY 1114 CAGTGAAGATGATGATTTGGAAATTTGCTCAAGAAAGATTTGATTTGCTGCTGCC 1173
DB 1497 CAGTGAAGATGATGATTTGGAAATTTGCTCAAGAAAGATTTGATTTGCTGCTGCC 1556
QY 1174 CTGACAGCTAATCACTTCACTTCACTTGAATTTGAGACATGCTTATATTTGCA 1233
DB 1557 CTGACAGCTAATCACTTCACTTGAATTTGAGACATGCTTATATTTGCA 1616
QY 1234 GATTTCCCAAGATCCGAATGGAATGGAATCTAATCTCTCTGTGATGCAAT 1293
DB 1617 GATTTCCCAAGATCCGAATGGAATGGAATCTAATCTCTCTGTGATGCAAT 1676
QY 1294 GCTTTATTTTATCGAAGAACTTGGAGCTGAGAAATGATGATTAAGATTAAGAT 1353
DB 1677 GCTTTATTTTATCGAAGAACTTGGAGCTGAGAGATTAAGATTAAGATTAAGAT 1736
QY 1354 GAATTTACTTGAAGGCTTCTTCAAGAGATGGAATTAATCTGCTCAAACTTATTT 1413
DB 1737 GAATTTACTTGAAGGCTTCTTCAAGAGATGGAATTAATCTGCTCAAACTTATTT 1796
QY 1414 AAGATGATATCTCATATGATCTGGCAACATCTCTAATTTTGGCAAGCAATCAAGC 1473
DB 1797 AAGATGATATCTCATATGATTTGGCTATCTCTAATTTTGGCAAGCAATCAAGC 1856
QY 1474 AGCAATATCGAGAAATTAATTTAGAAATTAATCAATATGATGATTTGCTGCT 1533
DB 1857 AAGCAATATCGAGAAATTAATTTAGAAATTAATCAATATGATGATTTGCTGCT 1916
QY 1534 AAGTGTATCTTCTAATCTCTTCCACTTGCAGAAATTTGCTGTTGAGGCTGCT 1593
DB 1917 AAGTGTATCTTCTAATCTCTGCTCTCACTTCAAAAGTTTGTCTGTTAAGGCTGCT 1976
QY 1594 AATCTAAGTACATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 1653
DB 1977 AATCTAAGTACATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 2036
```

QY	1654	AGATACCTAACTCTGCTGGCAATACTAGTATTCGTAGTCTTCCAAACCAAGTATGCAAG	1713
Db	2037	AGATACCTAACTCTGCTGACATATAATAATTCGAGCTTCCAAAGCAAGTATGCAAG	2098
QY	1714	CTTCAAAATCTGACACTCTGATCTCACTGCGCTGATCTCACTTGTGTGGTGCAAA	1773
Db	2097	CTTCAAAATCTGACACTCTGATCTGACTTGTGTGTCACAGCTTCTGTGGTGCAAA	2156
QY	1774	GAACCAAGCAACTTGGTAGTCTTGGAATCTTTTACTTGATGGTTGCTAGATGACT	1833
Db	2157	GAACCAAGCAACTTGGTAGTCTCGGAATCTTTTACTTGATCGTTGCAAGATGACT	2216
QY	1834	TGTATGCCCAAGAGATAGGATCTTTGACATCCCTTAAGACTCTAAGTAGATTTGTGCTG	1893
Db	2217	TGTATGCCCAAGAGATAGGATCTTACATATCCCTTAAGACTCTAAGATGCTTGCAATG	2276
QY	1894	GGAATTCAGACAGAAAATTGTCAACTGGTGAATTACGAAACCTGAATCTGATGGCTCA	1953
Db	2277	GGAATTCAGACAGAAAATTGTCAACTGGTGAATTACGAAACCTGAATCTGATGGCTCA	2333
QY	1954	ATTGAATCAAGCATCTTGAGAGATGAAGATGATAGATGCAAAAGAACCAATTTA	2013
Db	2334	ATTGAATCAAGCATCTTGAGAGATGAAGATGATAGATGCAAAAGAACCAATTTA	2393
QY	2014	TCTGCAAAAGAAAATCTGCAATCTTTAAGCATGAATGGATGACGATGACGTCCACGT	2073
Db	2394	TCTTCAAAAGAAAATCTGCAATCTTTAAGTATGATATGGATGAAAGATGACGTCCACAT	2453
QY	2074	ATATATGATCAGAAAAGTTGAAGTCTTGAAGCTTCAACCACTCCATATGACT	2133
Db	2454	AGATATGATCAGAAAAGTTGAAGTCTTGAAGCTTCAACCACTCCATATGACT	2513
QY	2134	TGTTTAAACATCAGGGCTTCAGAGGAATCCGCTCCCAAGCTGAATGAATCACTCAGTT	2193
Db	2514	TGTTTAAACATTTATTTGGCTTCAGAGGAATCCGCTCCCAAGCTGAATGAATCACTCAGTT	2573
QY	2194	TTGAAAAATGTTGTCTCTATTGAATCATCAGTTGCAAAAACCTGCTCATGCTTACACCC	2253
Db	2574	TTGAAAAATGTTGTCTCTCTGAAATCAGCATTTGCAAAAACCTGCTCATGCTTACACCC	2633
QY	2254	TTTGGTAGCTGCTGTGCTTAAAAAGCTTACAGTTGGAGGGGGCTGGGGAAGTGGAG	2313
Db	2634	TTTGGTAGACTGCTGTGCTTAAATAGCTTACAGTTTAGAGTGGGTCTGCAAGAGTGGAG	2693
QY	2314	TATGTGATCTCGAATTCCTTACAGAAAGAGTTTCAATCTCTGAAAAACTTAATATA	2373
Db	2694	TATATGTATCTCGAATTCCTTACAGAAAGAGTTTCAATCTCTGAAAAACTTAATATA	2753
QY	2374	CGGCAATTTGGTATCTGAAAGGATTCCTGAAAAAGAAAGAAAGCAATGCCCTGTG	2433
Db	2754	GGCCAATTTGTATATCTGAAAGGATTTGTGAAAAAGAAAGAAAGCAATGCCCTGTG	2813
QY	2434	CTTGAAGAGATAGAGATTTAATGTTGGCCATGTTGTTTATTCCAACCCTTTCTTCTGTC	2493
Db	2814	CTTGAAGAGATAGAGATTTAATCTGGTGCCTATGTTTGTATTCGAAACCTTTTCTTCTGTC	2873
QY	2494	AAGAAATTTGTAAGTTAGTGGGGCAAGTCAGATGCAATAGGTTTCAAGTTCCATATCTAAT	2553
Db	2874	AACAAATTTGTAAGTTAGTGGGGCAAGTCCAGATGCAATAGGCTTCAAGTTCCATATCTAAT	2933
QY	2554	CTCATGCTCTTATCTTCCCTCCAAATTCGCTATTAACAAAGAAAGATGCTTCACTCCAGAA	2613
Db	2934	CTCATGCTCTTATCTTCAATTTAGCTATTAATCTGAAAGCTTCACTCACTCCAGAA	2993
QY	2614	GAGATGTTCAAAAACCTTGCAGAAATCTCAAAATCTGAATATCTCTTTTAACTTCAATCTT	2673
Db	2994	GAGATGTTCAAAAACCTTGCAGAAATCTCAAAATCTGAATATCTTAACTTCAAGAAATCTC	3053
QY	2674	AAAGAGCTGCTTACAGGCTGGGCTAAGTCTCAAGCTTTGAAGATCTGGAAATTCATATCT	2733
Db	3054	AAAGAGCTGCTTACCAACTGGCTAAGCTTAAAGCTTTGAAGATCTGGAAATTTGAAGAT	3113

QY	2734	TGTTATGACATAGAGAGCTCCCGAGAGAGTGAAGGTTAAATTTCACTCAACAG	2793
Db	3114	TGTTATGACATAGAGAGCTCCCGAGAGAGTGAAGGTTAAATTTCACTCAACAA	3173
QY	2794	TTATTCATACATACCTGTAAGATCTACAAATGTTTACCGAGAGGATTCAGACCTTAACA	2853
Db	3174	TTATTCATACATACCTGTAAGATCTACAAATGTTTACCGAGAGGATTCAGACCTTAACA	3233
QY	2854	GCCCTCACAAAATTTATCAGTTGAGTTTGTGTCACACCTGGCCAAAGCGGTGTGAAGAGGA	2913
Db	3234	GCCCTCACAAAATTTATCAGTTGAGGATTTGTTCACACCTGGCCAAAGCATGTGAAGAGGA	3293
QY	2914	ATAGAGAGAAGACTGGTACAAAAATTTCTCACATTTCTCGTGTGTTATTTATTA	2966
Db	3294	ATAGAGAGAAGACTGGTACAAAAATTTCTCACATTTCTCGTGTGTTATTTATTTA	3346

RESULT 5

ADFI17759

ID ADFI17759 standard; DNA; 2913 BP.

AC ADFI17759;

DT 12-FEB-2004 (first entry)

DE Solanum bulbocastanum Rpi-b1b DNA sequence.

KW gene; ds; Rpi-b1b; Rpi-b1b gene cluster; growth regulant; oomycete infection; introgression breeding; plant; late blight.

OS Solanum bulbocastanum.

XX

XX

FH Key

FT Location/Qualifiers

FT 1..2913

FT CDS

FT /*tag= a

XX /product= "Rpi-b1b protein"

PN RPI1334979-A1.

PD 13-AUG-2003.

XX

XX

PF 08-FEB-2002; 2002EP-00075565.

PD

PF 08-FEB-2002; 2002EP-00075565.

PR

PR 08-FEB-2002; 2002EP-00075565.

XX

XX

PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

XX

PI Van Der Vossen EAG, Allefs JHM;

XX

PI WPI; 2003-714439/68.

DR

DR P-FSDB; ADFI17765.

XX

XX

PT

PT

PT

PT

PS

Example 5; SEQ ID NO 35; 86pp; English.

This invention relates to novel isolated polynucleotides that confer resistance against late blight caused by the oomycete pathogen *Phytophthora infestans*, which threatens both tomato and potato crops. Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes leucine-rich repeat (LRR) proteins identified in *Solanum bulbocastanum*, and which cause disease resistance to bacteria, fungi, nematodes etc. These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be described as plant growth regulators. They are useful in providing resistance to *Phytophthora infestans*, especially in *Solanum tuberosum* (potato) plants to protect against oomycete infection or to demonstrate disease susceptibility. Resistance can be conferred by transformation of existing potato and tomato cultivars with the gene, a procedure that is more straightforward and faster than conventional introgression breeding. This polynucleotide sequence is the *Solanum bulbocastanum* Rpi-b1b DNA of the invention.

XX Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;
SQ Query Match 70.0%; Score 2077.2; DB 10; Length 2913;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 2495; Conservative 0; Mismatches 388; Indels 105; Gaps 8;

QY 1 ATGCTGAAGCTTCTCAAGTTCGTGTAAACAATCGAATCTGATCTGTTTCAATCAAGGGAA 60
DB 1 ATGCTGAAGCTTCTCAAGTTCGTGTAAACAATCGAATCTGATCTGTTTCAATCAAGGGAA 60
QY 61 CTGTGATGCTTTTGGGTTTCAAGATGATGATCCAAAGCTTCAAGCATGTTTCTACA 120
DB 61 CTGTGATGCTTTTGGGTTTCAAGATGATGATCCAAAGCTTCAAGCATGTTTCTACA 120
QY 121 ATCCAGCTGCTAGAGATGCTCAGAAAGCAATGGAAGCAAGCAAGCAATGAAAT 180
DB 121 ATCCAGCTGCTAGAGATGCTCAGAAAGCAATGGAAGCAAGCAAGCAATGAAAT 180
QY 121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAACTCAACCAACCTCTGAAAT 180
DB 121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAACTCAACCAACCTCTGAAAT 180
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGATCTTGAAGATGAA 240
DB 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGATCTTGAAGATGAA 240
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGATCTTGAAGATGAA 240
DB 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATGATCTTGAAGATGAA 240
QY 241 ACTGAGGCAACCAATTAAGACAGAAAGCAATATGAGGCTTATCATCCAAAGTATC 300
DB 241 ACTGAGGCAACCAATTAAGACAGAAAGCAATATGAGGCTTATCATCCAAAGTATC 300
QY 241 ACCAAGGCCACA---AGATTCCTCCAGCTGATATGAGGCTTATCATCCAAAGTATC 297
DB 241 ACCAAGGCCACA---AGATTCCTCCAGCTGATATGAGGCTTATCATCCAAAGTATC 297
QY 301 ACTTTTGTCTCAAGATTTGGGAAAAGATGAAAAAGATTATGAGAAACTTGATGAT 360
DB 301 ACTTTTGTCTCAAGATTTGGGAAAAGATGAAAAAGATTATGAGAAACTTGATGAT 360
QY 298 CTTTTCGCTCAAGATTCGAGGAAAAGATGAGCCAAAGTGAAGAACTTAAAGCAAT 357
DB 298 CTTTTCGCTCAAGATTCGAGGAAAAGATGAGCCAAAGTGAAGAACTTAAAGCAAT 357
QY 361 GCACGCGAAGCAATTAAGTTCATTTGATGAAAGCACTATGAGAGCAAGTGTACA 420
DB 361 GCACGCGAAGCAATTAAGTTCATTTGATGAAAGCACTATGAGAGCAAGTGTACA 420
QY 358 GCTAGAGAAAGAAAGATTTTCAATTGCAAGAAAATTTGAGAGAGCAAGCTTTGA 417
DB 358 GCTAGAGAAAGAAAGATTTTCAATTGCAAGAAAATTTGAGAGAGCAAGCTTTGA 417
QY 421 CGCCAAACAGGTTTGTGTTTGAATGAACCAAGTTTATGAGAAAGCAAGAAAGAC 480
DB 421 CGCCAAACAGGTTTGTGTTTGAATGAACCAAGTTTATGAGAAAGCAAGAAAGAC 480
QY 418 CGGAAACAGGTTCTGATTAACGAACCGCAGGTTTATGAGAAAGCAAGAAAGAT 477
DB 418 CGGAAACAGGTTCTGATTAACGAACCGCAGGTTTATGAGAAAGCAAGAAAGAT 477
QY 481 GAGATAGTGAATTCCTGATTAACAATGTTGACATGCTCCAAACCTTCCAGTCTCCA 540
DB 481 GAGATAGTGAATTCCTGATTAACAATGTTGACATGCTCCAAACCTTCCAGTCTCCA 540
QY 478 GAGATAGTGAATTCCTGATTAACAATGTTGACATGCTCCAAACCTTCCAGTCTCCA 537
DB 478 GAGATAGTGAATTCCTGATTAACAATGTTGACATGCTCCAAACCTTCCAGTCTCCA 537
QY 541 ATACTTGTATGAGGAGGAGCTAGAAAGCAGCTCTGCTCCAAATGCTTCAATGATCAG 600
DB 541 ATACTTGTATGAGGAGGAGCTAGAAAGCAGCTCTGCTCCAAATGCTTCAATGATCAG 600
QY 538 ATACTTGTATGAGGAGGAGCTAGAAAGCAGCTCTGCTCCAAATGCTTCAATGATCAG 597
DB 538 ATACTTGTATGAGGAGGAGCTAGAAAGCAGCTCTGCTCCAAATGCTTCAATGATCAG 597
QY 601 AGAGTAAATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAG 660
DB 601 AGAGTAAATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAG 660
QY 598 AGAGTAAATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAG 657
DB 598 AGAGTAAATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAG 657
QY 661 AAGAGTTGATTAAGAAATTTGATCTATTTGAGAAAGTCT---ACTTGTGAGCATG 717
DB 661 AAGAGTTGATTAAGAAATTTGATCTATTTGAGAAAGTCT---ACTTGTGAGCATG 717
QY 658 AAGAGTTGATTAAGAAATTTGATCTATTTGAGAAAGTCT---ACTTGTGAGCATG 717
DB 658 AAGAGTTGATTAAGAAATTTGATCTATTTGAGAAAGTCT---ACTTGTGAGCATG 717
QY 718 GACTTGCTCAGCTTCAAAAGAGCTTGGGAGCTGCTGATGAGAAATTTATGCTC 777
DB 718 GACTTGCTCAGCTTCAAAAGAGCTTGGGAGCTGCTGATGAGAAATTTATGCTC 777
QY 718 GACTTGCTCAGCTTCAAAAGAGCTTGGGAGCTGCTGATGAGAAATTTATGCTC 777
DB 718 GACTTGCTCAGCTTCAAAAGAGCTTGGGAGCTGCTGATGAGAAATTTATGCTC 777
QY 778 GTCTTAATGATGTTTGAATGAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
DB 778 GTCTTAATGATGTTTGAATGAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
QY 778 GTCTTAATGATGTTTGAATGAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
DB 778 GTCTTAATGATGTTTGAATGAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
QY 838 AAGGTTGAGCAAGTGGGCTTCTGTTCTAACAATCTCTCTTGAAGAGTGTGATCA 897
DB 838 AAGGTTGAGCAAGTGGGCTTCTGTTCTAACAATCTCTCTTGAAGAGTGTGATCA 897
QY 898 ATTATGGAATGATGCAACCATATGATGATGATGATGATGATGATGATGATGATG 957
DB 898 ATTATGGAATGATGCAACCATATGATGATGATGATGATGATGATGATGATGATG 957
QY 958 TTGTTTCATGCAACGTCATTTGGGACCAAGAAATTAATCTTGTGCTATC 1017
DB 958 TTGTTTCATGCAACGTCATTTGGGACCAAGAAATTAATCTTGTGCTATC 1017

DB 958 TTGTTTCATGCAACGTCATTTGGGACCAAGAAATTAATCTTGTGCTATC 1017
QY 1018 GGAAGAGATTTGAAAAATGAGTGTGCTCTAGACGCTTAAATCTTGAAGT 1077
DB 1018 GGAAGAGATTTGAAAAATGAGTGTGCTCTAGACGCTTAAATCTTGAAGT 1077
QY 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGACATGTGAGAGATGATGATTTGG 1137
DB 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGACATGTGAGAGATGATGATTTGG 1137
QY 1138 AAATTGCTTCAAGAGAAAGTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
DB 1138 AAATTGCTTCAAGAGAAAGTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
QY 1198 CCACTTAATTTGAGACAAATGCTTACATTTGTCAGATGATGATGATGATGATGATG 1257
DB 1198 CCACTTAATTTGAGACAAATGCTTACATTTGTCAGATGATGATGATGATGATGATG 1257
QY 1258 GAAAAAGAAATCTAATCTCTCTGATGAGCAATGCTTATTTATGAAAGAAAC 1317
DB 1258 GAAAAAGAAATCTAATCTCTCTGATGAGCAATGCTTATTTATGAAAGAAAC 1317
QY 1318 TTGAGCTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
DB 1318 TTGAGCTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
QY 1378 CAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
DB 1378 CAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
QY 1438 CTGGCAACATCTCTATTTTGGGCAAGACATCAAGACAGCAATCCGAAATTAATGTA 1497
DB 1438 CTGGCAACATCTCTATTTTGGGCAAGACATCAAGACAGCAATCCGAAATTAATGTA 1497
QY 1498 GAAAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
DB 1498 GAAAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
QY 1558 TCCCACTTGAAGAGTGTGCTGTTGAGGAGTGTATGATGATGATGATGATGATG 1617
DB 1558 TCCCACTTGAAGAGTGTGCTGTTGAGGAGTGTATGATGATGATGATGATGATG 1617
QY 1618 CAGTTACGCTCTTCAATGAGATCTAGTACATTAATGATGATGATGATGATGATG 1677
DB 1618 CAGTTACGCTCTTCAATGAGATCTAGTACATTAATGATGATGATGATGATGATG 1677
QY 1678 AAGTTACATCTTCCATTTGAGAGATCTAGTACATTAATGATGATGATGATGATG 1737
DB 1678 AAGTTACATCTTCCATTTGAGAGATCTAGTACATTAATGATGATGATGATGATG 1737
QY 1675 AGTGGCATGCTGATGCTTCCAAAGCAGTATGCAAGCTTCAAAATCTGCAAACTCTGAT 1734
DB 1675 AGTGGCATGCTGATGCTTCCAAAGCAGTATGCAAGCTTCAAAATCTGCAAACTCTGAT 1734
QY 1738 CTACATGCTGCTCATTCATTTGTTTGTGTTGCTTGTGCTTGTGCTTGTGCTTGT 1797
DB 1738 CTACATGCTGCTCATTCATTTGTTTGTGTTGCTTGTGCTTGTGCTTGTGCTTGT 1797
QY 1798 CGAAATCTTTTACCTTGAATGCTGATGATGATGATGATGATGATGATGATGATG 1857
DB 1798 CGAAATCTTTTACCTTGAATGCTGATGATGATGATGATGATGATGATGATGATG 1857
QY 1795 CGAAATCTTTTACCTTGAATGCTGATGATGATGATGATGATGATGATGATGATG 1854
DB 1795 CGAAATCTTTTACCTTGAATGCTGATGATGATGATGATGATGATGATGATGATG 1854
QY 1858 TTGACATGCTTGAAGCTTGAAGTATGATGATGATGATGATGATGATGATGATG 1917
DB 1858 TTGACATGCTTGAAGCTTGAAGTATGATGATGATGATGATGATGATGATGATG 1917
QY 1918 CTTGTTGATTTAAGAAACCTGATTTCTATGCTGCTCAATTTGAAATCTGCTGAG 1977
DB 1918 CTTGTTGATTTAAGAAACCTGATTTCTATGCTGCTCAATTTGAAATCTGCTGAG 1977
QY 1912 CTTGTTGATTTAAGAAACCTGATTTCTATGCTGCTCAATTTGAAATCTGCTGAG 1971
DB 1912 CTTGTTGATTTAAGAAACCTGATTTCTATGCTGCTCAATTTGAAATCTGCTGAG 1971
QY 1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2037
DB 1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2037
QY 1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2031
DB 1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2031
QY 2038 TTAAGCATGAAATGGAATGATGATGATGATGATGATGATGATGATGATGATG 2097
DB 2038 TTAAGCATGAAATGGAATGATGATGATGATGATGATGATGATGATGATGATG 2097
QY 2032 TTAAGCATGAAATGGAATGATGATGATGATGATGATGATGATGATGATGATG 2088
DB 2032 TTAAGCATGAAATGGAATGATGATGATGATGATGATGATGATGATGATGATG 2088

Oy	2098	GGGCTGGAAGCCTCCAAACCAACTCCATTCGACTGTGTTTAACAATCAAGGGCGTTCAGA	2157
Db	2089	GAGCTTGAAAGCCCTCAACCAACAATCCAAATCGAAGCTTCTTTAAAAATCTAATGGCTTCAGA	2148
Oy	2158	GGAAATCCGCTGCCCAAGCTGAGTAGATCACTCAGTGTGTTGAAAATAATGTGTCTATTGAA	2217
Db	2149	GGAAATCATCTCCAGAGTAGATGAAATCACTCAGATATTGAAAATATTGTCTATTCTTA	2208
Oy	2218	ATCATCATGTTGCMAAAACTGCTCATGCTTACCACCCCTTGGAGCTGCTCTGTTAAA	2277
Db	2209	ATTAGCAACCTTGAGAAATCGCTCAATGCTTACCAACCCCTTGGAGATCTGCTGTAGAA	2268
Oy	2278	AAGCTAGAGTGTGGAGGGGGGTCTGCGGAAGTGAATGTTG-----	2320
Db	2269	AAGTCTAGAGTTACACTCGGGGGGTCTCGGATGTGGAGTATGTTGAAGAAATGGAATTTGAT	2328
Oy	2321	----ATTCTGATTCCTTACAGAAAGAAAGTTTCATCTCTGAGAAAATTAAATATACGC	2376
Db	2329	GTTTCATTCGTGATTCCTCCACAAAGAAATTAAGTTTCCATCTTGAGAAAATTGATATATGC	2388
Oy	2377	GAAATTTGGTAAATCTGAAAAGATTTGCTGAAAAAGAGAGAAAGCAATGCGCTGTGCTT	2436
Db	2389	GACTTTGGTAGCTGAAAAGATTTGCTGAAAAAGAGAGAAAGCAATTCCTGTGCTT	2448
Oy	2437	GAAAGATAGAGATTTAAATGTTGGCCCTATGTTTGTATTCCAACCTTTCTCTGTCAAG	2496
Db	2449	GAAAGATAGATTAATTCACGAGTGCCC-----TTTTCTGACCCCTTCT-----	2490
Oy	2497	AAATTGTAGTTAGTGGGAGACAAGTCAGATGCAATAGGTTTCAGTTCATATCTAATCTC	2556
Db	2491	-----TCTAATCTT	2499
Oy	2557	ATGAGCTTACTTCCCTCCAAATTCGCTATAACAAAGAAATGTTTCACTCCAGAAAGAG	2616
Db	2500	AGGGCTCTTACTCTCCCTCAGAAATTTGCTATATATAAGTAGCTACTTCAATCCAGAAAGAG	2559
Oy	2617	ATGTTCAAAGACCTTGCMAATCTCAAAATCTTGAATATCTCTTTTACTTCAATCTTAA	2676
Db	2560	ATGTTCAAAGAACCTTGCMAATCTCAAAATCTTGAATATCTCTGGGTGCAATATCTCAAA	2619
Oy	2677	GAGCTGCTTACCAAGCTGTGCTAGTCTGAATGCTTTGAAAAGTCTAAAAATTTCAATTGTGT	2679
Db	2620	GAGCTGCTTACCAAGCTGTGCTAGTCTGAATGCTTTGAAAAGTCTAAAAATTTCAATTGTGT	2679
Oy	2737	TATGACTAGAGAGTCTCCCGAGAGAGGTGTGAAGAATTAAATTCACTCAACAAGTTA	2796
Db	2680	TGCGCACTAGAGAGTCTCCCGAGAGAGGTGTGAAGAATTAAATTCACTCAACAAGTTA	2739
Oy	2797	TCCATAATATCTGTGAAATGCTACATGTTTACCGAGAGGATTTGACGACACTTACAGGC	2856
Db	2740	TTTGTGTGAACCTGTAAATGCTAAATGTTTACAGAGGATTTGACGACACTTACAGACC	2799
Oy	2857	CTCACAAAATTTATCAGTTGAGTTTGTGTCACAACCTGGCCCAAGCGGTGTGAGAAAGGAAATA	2916
Db	2800	CTCACAAGTAAAAATTCGGGAGATGTGCCACAATGATCAAGCGGTGTGAGAAAGGAAATA	2859
Oy	2917	GGAGAAAGCTGTACAAATTTGCTCACATCTCGATGTGTTATTTAT	2964
Db	2860	GGAGAAAGCTGTACAAATTTTCTCACATCTCTAATGTGAATATATAT	2907

[illegible]

421 GCCCAACAGGTTTGTGTTGAATGAACCAAGTTTATGAAAGACAAAGAAAGAC 480
418 CCGGAAACAGTTCGTGTATTAACCGAACCGAGTTTATGAAAGACAAAGAAAGAT 477
481 GAGATAGGAAATCCGTGATTAACAAATGTACAAATGCCAAACCTTCAGTCTCCCA 540
478 GAGATAGGAAATCCGTGATTAACAAATGTAGAGGCCCAACCTTCAGTCTCCCA 537
541 ATACTTGGATGGGGGACCTAGAAAGACAGCTTTGCCCAATGGTCTTCAATGATCAG 600
538 ATACTTGGATGGGGGACCTAGAAAGACAGCTTTGCCCAATGGTCTTCAATGATCAG 597
601 AGAGTATAGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAATAG 660
598 AGAGTATAGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAATAG 657
661 AGAGTATAGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAATAG 717
658 AGAGTATAGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAATAG 717
718 GACTTGGCTCAGCTTCAAAAGAGCTTGGGACCTTGTGATGAGAAATATTTGCTC 777
718 GACTTGGCTCAGCTTCAAAAGAGCTTGGGACCTTGTGATGAGAAATATTTGCTC 777
778 GTCTTAGATGATGTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 837
778 GTCTTAGATGATGTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 837
838 AAGTTTGAAGCAAGTGGCGCTTCTGTCTAACCACTACTGCTTGAAGAGTTGATCA 897
838 AAGTTTGAAGCAAGTGGCGCTTCTGTCTAACCACTACTGCTTGAAGAGTTGATCA 897
838 AAGTTTGAAGCAAGTGGCGCTTCTGTCTAACCACTACTGCTTGAAGAGTTGATCA 897
898 ATTATGGGAACTTGAACATATGATTTGTCAAAATTTGTCTCAAGAGATTTGTTG 957
898 ATTATGGGAACTTGAACATATGATTTGTCAAAATTTGTCTCAAGAGATTTGTTG 957
958 TTGTTTCATGCACTGTCATTTTGGGACCAAGAAAGAAATTAATCTTATCTTGTGCTATC 1017
958 TTGTTTCATGCACTGTCATTTTGGGACCAAGAAAGAAATTAATCTTATCTTGTGCTATC 1017
1018 GGAAGAGAGATTTGTAAGAAATGTGTGTGTGTCTTACAGCTTAAACCTTTGAGGT 1077
1018 GGAAGAGAGATTTGTAAGAAATGTGTGTGTGTCTTACAGCTTAAACCTTTGAGGT 1077
1078 ATTTCGCTTTAAGAGAGAAAGAAAGACAGTGGGAACTGTGAGATGATGAGATTTG 1137
1078 ATTTCGCTTTAAGAGAGAAAGAAAGACAGTGGGAACTGTGAGATGATGAGATTTG 1137
1138 AAATTCCTCAAGAGAAAGTTCTATTCTGCTGCTGCTGAGACTTATGTTACATCAGCTT 1197
1138 AAATTCCTCAAGAGAAAGTTCTATTCTGCTGCTGCTGAGACTTATGTTACATCAGCTT 1197
1138 AAATTCCTCAAGAGAAAGTTCTATTCTGCTGCTGCTGAGACTTATGTTACATCAGCTT 1197
1198 CCACTTGAATTTGAGACATGCTTTTACATATTTGTGAGATTTCCCAAGAGATCCGAATG 1257
1198 CCACTTGAATTTGAGACATGCTTTTACATATTTGTGAGATTTCCCAAGAGATCCGAATG 1257
1258 GAAAAGGAGAAATCTATCTCTCTGAGAGAGACAGTGGTATTTATTTATCCAAAGAAAC 1317
1258 GAAAAGGAGAAATCTATCTCTCTGAGAGAGACAGTGGTATTTATTTATCCAAAGAAAC 1317
1318 TTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1318 TTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1318 ATGAGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1378 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
1378 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437
1438 CTGGGAAACATCTCTATTTTTCGGGAGACATCAACAGCAATATCCGGAATTAATTA 1497
1438 TTGGGAAACATCTCTATTTTTCGGGAGACATCAACAGCAATATCCGGAATTAATTA 1497
1498 GAAAATTCATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557

1498 CACAGTTACACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
1558 TCCGACTTGCAGAGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
1558 TCCGACTTGCAGAGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
1558 CCCCCCTGGAAGATTTATCTGTTAAGAGTCTTAATCTTAAGTATGATGATGATGAT 1617
1618 CAGTTACCGCTCTTCCATGAGATCTAGATCTAATTAAGATCTAATCTTGTCTGCAAT 1677
1618 AAGTTACATCTTCCATGAGATCTAGATCTAATTAAGATCTAATCTTGTCTGCAAT 1674
1678 ACTAGTATTCGATGCTTCCCAACCAAGTATGCAAGCTTCAAAATCTGAGACTTGTAT 1737
1678 ACTAGTATTCGATGCTTCCCAACCAAGTATGCAAGCTTCAAAATCTGAGACTTGTAT 1737
1675 AGTGCAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1734
1738 CTAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797
1735 CTAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
1798 CGAAATCTTTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857
1795 CGAAATCTTTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
1858 TTGACATGCTTTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
1855 TTGACATGCTTTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
1918 CTGCTGATTAATGCAAAACCTGATATCTATGCTTCAATTTGAATACCATCTTGAAGA 1977
1912 CTGCTGATTAATGCAAAACCTGATATCTATGCTTCAATTTGAATACCATCTTGAAGA 1971
1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2037
1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
2038 TTAAGCATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
2032 TTAAGCATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
2088 GTGCTTGAAGCTTCCAAACCACTGATGATGATGATGATGATGATGATGATGATGAT 2157
2089 GTGCTTGAAGCTTCCAAACCACTGATGATGATGATGATGATGATGATGATGATGAT 2148
2158 GGAATCCGCTCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
2149 GGAATCCGCTCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2208
2218 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2277
2209 ATTAGCAATCTTCAAGAACTGCTCATGCTTACCACTTTGATGATGATGATGATGAT 2268
2278 AGCTAGAGTGTGAGAGGGGCTGCGGAAGTGAATGATGATGATGATGATGATGATGAT 2320
2269 AGCTAGAGTGTGAGAGGGGCTGCGGAAGTGAATGATGATGATGATGATGATGATGAT 2328
2321 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2376
2329 GTTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2388
2377 GAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2436
2389 GAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2448
2449 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2490
2497 AAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2556
2491 AAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2499
2557 ATGCTCTTACCTTCCCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2616

```
Db 2500 AGGGCTTACTTCCCTCAGAAATTGCTATATAAAGTAGTACTTCAATCCAGAGAG 2559
QY 2617 ATGTTGAAAAAGCTTGCAAAATCTCAAAATCTGTAATATCTTTTACTTCAATCTTAA 2676
Db 2560 ATGTTGAAAAAGCTTGCAAAATCTCAAAATCTGTAATATCTTTTACTTCAATCTTAA 2619
QY 2677 GAGCTGCTACAGAGCTGGCTAGTCTCAGAGCTTTGAACATCTGGAATTCATAGTCT 2736
Db 2620 GAGCTGCTACAGAGCTGGCTAGTCTCAGAGCTTTGAACATCTGGAATTCATAGTCT 2679
QY 2737 TATGACATGAGAGTCTCCCGAGAGAGTGTGAAGTTTAAATTCATCTCACAGATTA 2796
Db 2680 TCGGCTCTAGAGAGTCTCCCTGAGAGAGGCTGTGAAGTTTAAATTCATCTCACAGATTA 2739
QY 2797 TCCATACATCTCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTAATCTGTA 2856
Db 2740 TTTGTTGAACTGTGAACATGTCTAAATGTTTAAATTCATCTCACAGATTA 2799
QY 2857 CTCACAAATTTATCAAGTTGATTTTGTCCACACAGTGGCCAGAGCTGTGAAGAGGAATA 2916
Db 2800 CTCACAAATTTATCAAGTTGATTTTGTCCACACAGTGGCCAGAGCTGTGAAGAGGAATA 2859
QY 2917 GGAGAAAGCTGTGACAAATTTCTCAATCTCTGCTGTGTTTAT 2964
Db 2860 GGAGAAAGCTGTGACAAATTTCTCAATCTCTGCTGTGTTTAT 2907
```

RESULT 7

ADFL17763

ID ADF17763 standard; DNA; 3971 BP.

XX ADF17763;

DT 12-FEB-2004 (first entry)

DE S_bulbocastanum RGC3-b1b coding DNA containing an intronic sequence.

XX gene; ds; RGC3-b1b; Rpi-b1b gene cluster; growth regulant;
KM oomycete infection; introgression breeding; plant; late blight.

XX Solanum bulbocastanum.

FH Key Location/Qualifiers

FT CDS

FT CDS

FT CDS

FT CDS

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

FT intron

Db 2174 TCAGATGAAAGTCTATTCGCTGCGCTGAGGCTTAGTACATCATCTTCCACTTGA 2233
Qy 1206 TTGAGACAAATGCTTACATATTTGACAGTATTTCCAAAGATACCAAAATGAAAGG 1265
Db 2234 TTGAGACAAATGCTTACATATTTGACAGTATTTCCAAAGATACCAAAATGAAAGG 2293
Qy 1266 AAATCTAATCTCTCTGAGTGGACATGCTTTTATTTTATGAAAGAACTTGGAGCT 1325
Db 2294 AAATCTAATCTCTCTGAGTGGACATGCTTTTATTTTATGAAAGAACTTGGAGCT 2353
Qy 1336 AGAGAAATGAGTATGAGTATGAGTATGAGTATTAATTAATTAATTAATTAATTAAT 1385
Db 2354 AGAGAAATGAGTATGAGTATGAGTATGAGTATTAATTAATTAATTAATTAATTAAT 2413
Qy 1386 TGAAGTAAATCTGCTCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAC 1445
Db 2414 TGAAGTAAATCTGCTCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAC 2473
Qy 1446 ATCTCTAATTTTGGGACACATCAAGACCAATATCCGAGAAATTAATTAATTAATTA 1505
Db 2474 ATCTCTAATTTTGGGACACATCAAGACCAATATCCGAGAAATTAATTAATTAATTA 2533
Qy 1506 CATACATATGATGATCTATGCTTTCACTAAAGTATCTTTTCTCTTCCACTT 1565
Db 2534 TGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
Qy 1566 GCAGAAATTTGCTGCTGAGGAGCTTAATCTAATGATGATCAATTAATTAATTAATTA 1625
Db 2594 GCAGAAATTTGCTGCTGAGGAGCTTAATCTAATGATGATCAATTAATTAATTAATTA 2653
Qy 1626 GTCTTCCATGAGATCTAATGATCAATTAATTAATTAATTAATTAATTAATTAATTA 1685
Db 2654 ATCTTCCATGAGATCTAATGATCAATTAATTAATTAATTAATTAATTAATTAATTA 2713
Qy 1686 TCGTATGCTTCCAAACCAATTAATGATCAATTAATTAATTAATTAATTAATTAATTA 1745
Db 2714 TCGTATGCTTCCAAACCAATTAATGATCAATTAATTAATTAATTAATTAATTAATTA 2773
Qy 1746 CTGCTATTCATCTGCTGCTGAGGAGCTTAATCTAATGATGATCAATTAATTAATTA 1805
Db 2774 TTGGAATCTCTCTCTGCTGAGGAGCTTAATCTAATGATGATCAATTAATTAATTA 2833
Qy 1806 TTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
Db 2834 TTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2890
Qy 1866 CCTTAAGCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1925
Db 2891 CCTTAAGCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2947
Qy 1926 ATTGAGAAACCTGAATCTCTAATGATGATGATGATGATGATGATGATGATGATGAT 1985
Db 2948 ACTTAAATTAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3007
Qy 1986 TGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
Db 3008 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3067
Qy 2046 GAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
Db 3068 GAGTTGGAGCTTGAATGAAA---ACATGATATGATGATCA-----GAAATCTTGA 3115
Qy 2106 AGCTCTGAAACCACTGCAATCTGATCTGTTTAAATCAATGAGGCTTCAAGGAAATCG 2165
Db 3116 AGCTCTGAAACCACTGCAATCTGATCTGTTTAAATCAATGAGGCTTCAAGGAAATCG 3175
Qy 2166 TCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2225
Db 3176 TCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3235
Qy 2226 TTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2285
Db 3236 TTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3295

Qy 2286 GTTGTGAGGAGGCTCTGCGAAGTGAAGTGAATGTTGATTTCTGATTTCCCTACAGAAAG 2345
Db 3296 GTTACACACCGGCTAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGAT 3352
Qy 2346 GTTTCATCTCTGAGAAATCTTAATATACGGAATTTGGTAACTGAAAGATCTGTGA 2405
Db 3353 GTTTCATCTCTGAGAAATCTTAATATGAGGACTTGTATCTTAATCAAAAGATCTGAA 3412
Qy 2406 AAAGGAGAGAAAGCAATGCGCTGCTGAGAGATGAGATTAATGTTGCGCTAT 2465
Db 3413 AAAGGAGAGAAAGCAATGCGCTGCTGAGAGATGAGATTAATGTTGCGCTAT 3472
Qy 2466 GTTGTATTTCCAAACCTTCTCTGCTGCAAAAATTTGATGATGAGGAGCAAACTGAG 2525
Db 3473 GTTGTATTTCCAAACCTTCTCTGCTGCAAAAATTTGATGATGAGGAGCAAACTGAG 3526
Qy 2526 TGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2585
Db 3527 TGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3586
Qy 2586 TAAACAAAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGAATCTCAATTA 2645
Db 3587 TAAACAAAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGAATCTCAATTA 3646
Qy 2646 CTGGAATATCTCTTTTACTTCAATCTTAAGAGCTGCTCAAGCTGCTGATGCTCA 2705
Db 3647 CTGGAATATCTCTTTTACTTCAATCTTAAGAGCTGCTCAAGCTGCTGATGCTCA 3706
Qy 2706 TGCCTTGAAGATCTGGAATTAATGATGATGATGATGATGATGATGATGATGATGAT 2765
Db 3707 TGCCTTGAAGATCTGGAATTAATGATGATGATGATGATGATGATGATGATGATGAT 3766
Qy 2766 TGTGAAGGTTTAAATTTTCACTCAACAGTTATCCATTAATCTGTGAATGCTCAATG 2825
Db 3767 GGTGAAGGTTTAAATTTTCACTCAACAGTTATCCATTAATCTGTGAATGCTCAATG 3826
Qy 2826 TTTACCGGAGGATTTGAGCACTTAACAGCTTCAAAATTTATCAGTTGATGTTGCTC 2885
Db 3827 TTTACCGGAGGATTTGAGCACTTAACAGCTTCAAAATTTATCAGTTGATGTTGCTC 3886
Qy 2886 AACACTGCGCAAGCGGTGTGAAGGAAATGAGAAAGATGTTCAAAATTTGCTCAAT 2945
Db 3887 AATGATATTAAGCGGTGTGAAGGAAATGAGAAAGATGTTCAAAATTTGCTCAAT 3946
Qy 2946 TCTCTGCTGTTTATTTATTTG 2967
Db 3947 TCCATATTTGACTCTATATGAG 3968

RESULT 8
ADH51535
ID ADH51535 standard; DNA; 3971 BP.
XX
AC ADH51535;
XX
XX 25-MAR-2004 (first entry)
DE
DE S bulbocactanum RGC3-b1b gene SegID52.
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW de; RGC3-b1b.
OS Solanum bulbocactanum.
XX
XX US2003221215-A1.
XX
XX 27-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
PR

XX (KME-) KMEK EN RESEARCHBEDRIJF AGRICO BV.
XX Allefs JHM, Van Der Vossen EAG;
XX WPI, 2004-010903/01.
XX
XX New isolated or recombinant Rpi-blb nucleic acids and proteins, useful
XX PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX PT with resistance against oomycete infection.
XX
XX Claim 6; SEQ ID NO 52; 98pp; English.
XX
XX This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
XX protein which may provide a plant or its progeny with at least partial
XX resistance against an oomycete infection caused by Phytophthora
XX infestans. The invention may be useful for the development of compounds
XX with a fungicide activity. The DNA sequence of the invention encodes an
XX Rpi-blb protein comprising 970 amino acids. The nucleic acid, vector,
XX cell, protein or binding molecule is useful for providing a plant or its
XX progeny with resistance against an oomycete infection such as late blight
XX (a disease of major importance to production of Solanaceae such as potato
XX and tomato cultivars). The present sequence is that of the S
XX bulbocactanum RG3-blb gene which is related to the invention.
XX
XX Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;

Query Match 63.4%; Score 1880.8; DB 12; Length 3971.
Best Local Similarity 85.5%; Pred. No. 0;
Matches 2173; Conservative 0; Mismatches 342; Indels 27; Gaps 6;

QY 426 AACAGGTTTGTGTAATGAACCAAGTTATGAGAGACAAAGAAAGACGAGAT 485
Db 1454 ACCAGGTTCTGTGTTAACTGAACCAAGTTATGAGAGACAAAGAAAGATGAGAT 1513
QY 486 AGTGAATCTCTGAATGAACCAAGTTATGAGAGACCAAGTTATGAGAGAT 545
Db 1514 AGTGAATCTCTGAATGAACCAAGTTATGAGAGACCAAGTTATGAGAGAT 1573
QY 546 TGTATGAGGAGGAGTGAAGAGACGCTTGTCCCAATGCTTCAATGATGAGAGT 605
Db 1574 TGTATGAGGAGGAGTGAAGAGACGCTTGTCCCAATGCTTCAATGATGAGAGT 1633
QY 606 AATTGAGATTTCATCCCAATATGAGATTGTGTCTCGAGAGATTATGAGAGAG 665
Db 1634 AACTGAGGTTTCTATCCCAATATGAGATTGTGTCTCGAGAGATTATGAGAGAG 1693
QY 666 GTTGAATAAGGAATGTGAGATCTATGAGAAAGTCACTGTGTGAGATGAGAGT 725
Db 1694 GTTGAATAAGGAATGTGAGATCTATGAGAAAGTCACTGTGTGAGAGATGAGT 1753
QY 726 TCCACTTCAAAGAGGCTTGGGACTGTGATGAGAGAAATATTTGCTGCTTGA 785
Db 1754 TCCACTTCAAAGAGGCTTGAAGGTTGCTGAATGAGAAAGATCTTCTTGTGTTAGA 1813
QY 786 TGAATGTTGAATGAATGATCAAGTAAAGTGGCTAAGTTAAGACAGTCTTGAAGTGG 845
Db 1814 TGAATGTTGAATGAATGATCAAGTAAAGTGGCTAATTTAAGAGAGTCTTGAAGTGG 1873
QY 846 AGCAAGTGGGCTTCTGTTCTAACCACTACCTGCTTGAAGAGTTGAGATTTAGG 905
Db 1874 AGCAAGTGGGCTTCTGTTCTAACCACTACCTGCTTGAAGAGTTGAGATTTAGG 1933
QY 906 AACATTGCAACATGATGATGATGATTTGCTCAAGAGATGTTGTTGTTGTTCAAT 965
Db 1934 AACATTGCAACATGATGATGATGATTTGCTCAAGAGATGTTGTTGTTGTTCAAT 1993
QY 966 GCAAGCGATTTGGGACCAAGAAAGAAATTTAATCTTGTGTGCTATCGAAAGGA 1025
Db 1994 GCAAGCGATTTGGGACCAAGAAAGAAATTTAATCTTGTGTGCTATCGAAAGGA 2053
QY 1026 GATTTGAAAAAAATGTTGTGTGTGCTCTGAGAGCTAAATCTTGAAGATTTTGGG 1085

Db 2054 GATTTGAAAAAAATGTTGTGTGTGCTCTGAGAGCTAAATCTTGGAGATTTTGGG 2113
QY 1086 CTTTAAG 1145
Db 2114 CTTCAAG 2173
QY 1146 TCAAG 1205
Db 2174 TCAAG 2233
QY 1206 TTTGAG 1265
Db 2234 TTTGAG 2293
QY 1266 AATCTTATGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
Db 2294 AATCTTATGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2353
QY 1326 AG 1385
Db 2354 AG 2413
QY 1386 TGAAGTTAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1445
Db 2414 TGAAGTTAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2473
QY 1446 ATCTTATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
Db 2474 ATCTTGTGTTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2533
QY 1506 CATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
Db 2534 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
QY 1566 GCAGAGTTTGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1625
Db 2594 GCAGAGTTTGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2653
QY 1626 GTCTTCCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1685
Db 2654 ATCTTCCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2713
QY 1686 TCGTATGCTTCCAAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1745
Db 2714 TCGTATGCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2773
QY 1746 CTGTCAATTCATTTGTTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1805
Db 2774 TTGCACTCTCTTCTGTTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2833
QY 1806 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
Db 2834 TTTTACTGATG--GCTGTTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 2890
QY 1866 CCTTAAG 1925
Db 2891 CCTTAAG 2947
QY 1926 ATTTAAG 1985
Db 2948 ACTTAAG 3007
QY 1986 TGAATGATGAG 2045
Db 3008 AGATGAG 3067
QY 2046 GAAATGAG 2105
Db 3068 GAGTTGGAG 3115
QY 2106 AGCTTCAACCACTCCATCTGATGATGATGATGATGATGATGATGATGATGAT 2165

```

Db 3116 AGCCCTCAACCACTCCCAATCTGAAATATTAGAAATCAATGCGCTCGAGAAATCCG 3175
Qy 2166 TCTCCCAAGATGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 2225
Db 3176 TCTCCCAAGATGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 3235
Qy 2226 TTGCAAAATGCTCATGCTTACACACCTTGGTGGAGTGCCTTGTCTAAAAAGTCTAGA 2285
Db 3226 TTGTAATAAATGCTCATGCTTACACACCTTGGTGGAGTGCCTTGTCTAAAAAGTCTAGA 3295
Qy 2286 GTTGTGAGGGGGGTGTCGGGAAGTGAATGTTGATTTGCGATTCCCTCAAGAAAGAG 2345
Db 3286 GTTGTGAGGGGGGTGTCGGGAAGTGAATGTTGATTTGCGATTCCCTCAAGAAAGAG 3352
Qy 2346 GTTTCATCTCTGAGAAAACTTAATATACGGGAATTGGTATCTGAAGAAGTGTCTGAA 2405
Db 3346 GTTTCATCTCTGAGAAAACTTAATATACGGGAATTGGTATCTGAAGAAGTGTCTGAA 3412
Qy 2406 AAAGGAAGAGAAAGCAATGCTGCTGCTGAGAGATAGAGATTAATGTTGCCCTAT 2465
Db 3413 AAAGGAAGAGAAAGCAATGCTGCTGCTGAGAGATAGAGATTAATGTTGCCCTAT 3472
Qy 2466 GTTGTATATCCAACTCTTCTCTGTCTGAAGAAATGGTATGAGGGAACAGTCA 2525
Db 3473 GTTGTATATCCAACTCTTCTCTGTCTGAAGAAATGGTATGAGGGAACAGTCA 3526
Qy 2526 TGCAATAGATTTGCTGCTCATATCTAATCTCATAGGCTCTTACCTCCCAATTCGCTA 2585
Db 3527 TGCAATAGATTTGCTGCTCATATCTAATCTCATAGGCTCTTACCTCCCAATTCGCTA 3586
Qy 2586 TAAACAAGAGATGCTTCACTCCCAAGAGAGATGTTCAAAAGCCTTGCAAAATCTCAATA 2645
Db 3587 TAAAGTAAAGATCTTCACTCCCAAGAGAGATGTTCAAAAGCCTTGCAAAATCTCAATA 3646
Qy 2646 CTGGAATATCTCTTTTACTTCAATCTTAAAGAGTGCCTTACAGCCTGCTAGTCTCAA 2705
Db 3647 CTGGAATATCTCTTTTACTTCAATCTTAAAGAGTGCCTTACAGCCTGCTAGTCTCAA 3706
Qy 2706 TGCTTTGAAGATCGAATTCATAGTTGATATGACATAGAGATCTCCCGAGGAAGG 2765
Db 3707 TGCTTTGAAGATCGAATTCATAGTTGATATGACATAGAGATCTCCCGAGGAAGG 3766
Qy 2766 TGTGAAAGTTAATTTCACTCAACAGATTTTCAATATCATATGTAATGCTACATAG 2825
Db 3767 GGTGAAAGTTAATTTCACTCAACAGATTTTCAATATCATATGTAATGCTACATAG 3826
Qy 2826 TTTAACCGAGGAGATTCAGACACTTAACAGCCCTCAAAATTTATCAGTTGAGTTTGTCC 2885
Db 3827 TTTAACCGAGGAGATTCAGACACTTAACAGCCCTCAAAATTTATCAGTTGAGTTTGTCC 3886
Qy 2886 AACACTGCGCCAAAGCGGTGTGAGAGAGGAATAGAGAAATCTGTACAAATTTGCTCACT 2945
Db 3887 AATAGTATTCAGAGCGGTGTGAGAGAGGAATAGAGAAATCTGTACAAATTTGCTCACT 3946
Qy 2946 TCCTCGTGTGTTTATTTATAG 2967
Db 3947 TCCATATTTGACTCTATATGAG 3968

```

```

RESULT 9
ADF17760
ID ADF17760 standard; DNA; 3592 BP.
AC ADF17760;
XX
XX 12-FEB-2004 (first entry)
DE Solanum bulbocastanum Rpi-b1b genomic DNA.
XX
XX gene; ds; Rpi-b1b; Rpi-b1b gene cluster; growth regulator;
KW oomycete infection; introgression breeding; plant; late blight.
XX
XX Solanum bulbocastanum.
OS

```

```

XX Key Location/Qualifiers
FH 1..3592
FT CDS /*tag= a
FT /product= "Rpi-b1b protein"
FT /note= "This coding sequence contains one intron"
FT /transl_except= (pos: 1107..1108, aa: Gly)
FT intron 428..1106
FT /*tag= b
FT /number= 1
XX
XX EP1334979-A1.
XX
XX 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Van Der Vossen ENG, Allefs JHM;
XX
XX WPI: 2003-714439/68.
XX
XX P-PSDB; ADF17765.
XX
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes and tomatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX
XX Example 5; SEQ ID NO 36; 86bp; English.
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b genomic
XX DNA of the invention.
XX
XX Sequence 3592 BP; 1129 A; 659 C; 734 G; 1070 T; 0 U; 0 Other;
XX
XX Query Match 60.9%; Score 1805.8; DB 10; Length 3592;
XX Beest Local Similarity 84.2%; Pred. No. 0;
XX Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
Qy 426 AACAGTTTGTGTTGTAATGAAACCAAGTTTATGAAAGAGACAAAGAAAAGACGAGAT 485
Db 1102 ACCAGTTTCTGTATTAACCGACCGCAGGTTTATGAAAGAGACAAAGAAAAGATGAGAT 1161
Qy 486 AGTGAATAATCCTGATAAACAATGTAGCAATGCCAACAACCTTCAGTCTCTCCCAATACT 545
Db 1162 AGTGAATAATCCTGATAAACAATGTAGTATGCCCAACAACCTTTCAGTCTCTCCCAATACT 1221
Qy 546 TGTATAGGGGGGACTAGAAAGAGACTCTGCGCAATAGTCTTCAATATGATGAGAGT 605
Db 1222 TGTATAGGGGGGATTAAGAAAACGACTCTGCGCAATAGTCTTCAATATGATGAGAGT 1281
Qy 606 AATTGACATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTTAATGAGAAG 665
Db 1282 TACTGACATTTCCATTCAAAATATGATTTGTGTCTCGGAAGATTTTAATGAGAAG 1341
Qy 666 GTTGATTAAGGAATTTGAAATCTATTTGAAGAAAGTGC--ACTTGTGCGATGAGCTT 722
Db 1342 GTTATATAAGCAATGTAGAAATCTATTTGAAGAAAGCCACTTGTGTGATGAGACTT 1401

```

QY	723	GGCTCCACTTCAAAAGAGCTTCGGGACCTTGCTGTAATGAGAAAAAATATTTGCTGCTT	782
Db	1402	GGCTCCACTTCAAAAGAGCTTCAGGAGTTGCTGAATGAGAAAAAGATCTTGCTGCTT	1461
QY	783	AGATGATGTTTGGAAATGAAAGATCAAGATTAAGTGGCTTAAGTTAAGACAAGCTTTGAAGGT	842
Db	1462	AGATGATGTTTGGAAATGAAAGATCAAGAGTGGCTTAATTTAAGACAGCTTTGAAGGT	1521
QY	843	TGAGAGCAAGTGGCTGCTGTTCTTAACCACTAGTCTTGAGAAAAGGTGGATCAATTAAT	902
Db	1522	TGAGAGCAAGTGGCTGCTGTTCTTAACCACTAGTCTTGAGAAAAGGTGGATCAATTAAT	1581
QY	903	GGGAACATTGGCAACCAATTAATGTAATGTCAAATTTGTCTCAAGAAAGATTTGTTGTTGT	962
Db	1582	GGGAACATTGGCAACCAATTAATGTAATGTCAAATTTGTCTCAAGAAAGATTTGTTGTTGT	1641
QY	963	CANGCACGTGCATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGCGCTATCCGAAA	1022
Db	1642	CANGCACGTGCATTTGGACACCAAGAAAGAAATTAATCAACCTTGTCGAATCCGAAA	1701
QY	1023	GGAGATTGTGAAAAATGTGTGTGTGCTCTAGCAGCTAAACTCTTGAGAGTTATTT	1082
Db	1702	GGAGATTGTGAAAAAATGTGTGTGTGCTCTAGCAGCCAAACTCTTGAGAGTTATTT	1761
QY	1083	GGCTTTTAAGAGAGAAAGAAACAGTGGAAACATGTGAGAGATGTGAGATTTGAAATT	1142
Db	1762	GGCTTTCAAGAGAGAAAGAAAGCAGTGGAAACATGTGAGAGACAGTCCATTTGGAAATT	1821
QY	1143	GGCTTCAGAGAAAGTTCTATTTGCTGCTGCGCTGAGACTTAAGTTACATCACCTTCACT	1202
Db	1822	GGCTTCAGAGATGAAGTTCTATTTGCTGCTGCGCTGAGGCTTAAGTTACATCACTTCACT	1881
QY	1203	TGATTTGAGACAAATGCTTTTACATATTTGTGCAATTTCCAAAGATACCGAAATGAGAAA	1262
Db	1882	TGATTTGAGAACAAATGCTTTGTGATTTGTGCGGTGTTCCCAAGAGATGCCAAATGAGAAA	1941
QY	1263	GGGAAATCTAATCTCTCTGAGAGGACATGTTTTATTTTAAGAAAGAACTTGA	1322
Db	1942	AGAAAGATATCTCTCTGAGTGGCGCAGTGGTTTTCTTTTACAAAGAGAAACATGGA	2001
QY	1323	GCTAGAGATGTAGTAAATGAAGTGAATGAATTAATTGAGGCTTTTCTTCCAGA	1382
Db	2002	GCTAGAGAGTGTGGGCATGAAGTGAAGAAATTAATTGAGGCTTTTCTTCCAGA	2061
QY	1383	GATTGAAGTTAAATCTGTGCAAACTTATTTCAAGATGCAATCTCATTCATGATCTGGC	1442
Db	2062	GATTGAAGTTAAAGATGTAAACTTATTTCAAGATGCAATCTCATTCAGATTTGGC	2121
QY	1443	AACATCTTAATTTTTGCGCAAGACATCAAGCAGCAATATCCGAGAAATATTTGAGAAA	1502
Db	2122	AACATCTCTGTTTTACAGCAACACATCAAGCAGCAATATCCGTAATTAATTAACACAG	2181
QY	1503	TTTACATACATATGATGTCCATTGGTTTCACTTAAAGTGTATCTTCTTCTTCCCA	1562
Db	2182	TTTACACACATATATGTCCATTGGTTTCCCGAAGGTGTGTTTTTACACTCTTCCCCC	2241
QY	1563	CTTGCAAGAGTTTGTCTGCTGAGGGGCTTAATCTAAGTGCATAAACTTAAGACGTT	1622
Db	2242	CTTGCAAAAATTTTATCTCGTTAAGATGCTTAACTTAACTGATGTGCAATTAATTAAGTT	2301
QY	1623	ACCGTCTTCAATGAGATCTAGTACATTTAAGATACCTAAACTTGTCTGGCAATACAG	1682
Db	2302	ACCATCTTCAATGAGATCTAGTACATTTAAGATACCTTAACCTGTATGCG---AAGTGG	2358
QY	1683	TATTCGAATCTTCCAAACAGATTAGCAAGCTTCAAAATCTGCAAGCTCTTGATCTACA	1742
Db	2359	CATGCGTATGCTTCCAAAGCAGTTATGCAAGGCTTAAATCTGCAACTCTTGATCTACA	2418
QY	1743	TGCGCTGTCAATCACTTTGTTGTTGCAAAAGAAACAAGCAAACTTGGTAGTCTTGAAA	1802
Db	2419	ATATGCAACCAAGCTTTGTTGTTTGGCAAAAGAAACAAGTAACTTGGTAGTCTTCCAAA	2478

|||||
Db 3484 AAGTTAAAAATTCGGGATGTCACAACTGATCAAGCGTGTGAGAGGGAATGAGAGA 3543
OY 2922 AGACTGTACAAAATTGCTCATCTCGTGTGTTTAT 2964
Db 3544 AGACTGCGCAAAATTTCTCACATTCCTAATGTGAATATAT 3586

RESULT 10
ADH51532
ID ADH51532 standard; DNA; 3592 BP.
XX
XX ADH51532;
AC
XX ADH51532;
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum Rpi-b1b gene SegID49.
XX
XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KM de.
XX
OS Solanum bulbocastanum.
XX
XX US2003221215-A1.
XX
XX 27-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PI Allefs JTHM, Van Der Vossen BAG;
DR WPI; 2004-010903/01.
XX
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
XX Claim 6; SEQ ID NO 49; 98bp; English.
XX
XX This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector, or
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of the S
CC bulbocastanum Rpi-b1b gene which is related to the invention.
XX
XX Sequence 3592 BP; 1129 A; 659 C; 734 G; 1070 T; 0 U; 0 Other;

Query Match 60.9%; Score 1805.8; DB 12; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;

OY 426 AACGAGTTTGTGTAATGACCAAGTTTATGGAAGAGCAAAAGAAAGAGAGAT 485
Db 1102 ACCAGGTTCTGTATTAACCGAACCGAGTTTATGGAAGAGCAAAAGAAAGATGAT 1161
OY 486 AGTGAATTCGATTAACATGTTAGCAATGCCCAACACTTCAGTCCCTCCAAATCT 545
Db 1162 AGTGAATTCGATTAACATGTTAGTATGCCCAACACTTCAGTCCCTCCAAATCT 1221
OY 546 TGGTATGGGGGAGTACGAGAAAGCACTCTTGCCCAATGCTTTCATGATCAGAGAGT 605
|||||

Db 1222 TGGTATGGGGGAGTACGAGAAACGACTCTTGCCCAATGCTTTCATGATCAGAGAGT 1281
OY 606 AATTGACATTTCCATCCCAAAATATGGAATTTGTCTCGGAGATTTTAATGAGAGAG 665
Db 1282 TACTGAGCATTTCCATTCGAAAAATATGATTTGTCTCGGAGAAATTTGATGAGAGAG 1341
OY 666 GTTGATAAAGAAATTTGTAGATCTATTTGAAGAAAGTC--ACTGTGCGATGACTT 722
Db 1342 GTTAATAAAGCAATTTGATGAAATCTATTTGAAGAGGACCACTACTCTGTGATGACTT 1401
OY 723 GGTCCCACTTCAAAAGAGCTTGGGACTTCTGTAATGAGAAAAAATTTGCTGCTT 782
Db 1402 GGTCCCACTTCAAAAGAGCTTCAAGAGTGTCTGAATGAGAAAAAGATGCTGTGCTT 1461
OY 783 AGATGATGTTTGAATGAAAGATCAAGATTAAGTGGGCTAAGTTAAGACAGCTTGAAGGT 842
Db 1462 AGATGATGTTTGAATGAAAGATCAAGATTAAGTGGGCTAAGTTAAGACAGCTTGAAGGT 1521
OY 843 TGGAGCAAGTGGCGCTTCTGTTCTAACCACTACTCGTCTTGAAAAAGTTGGATCAATAT 902
Db 1522 TGGAGCAAGTGGCTTCTGTTCTAACCACTACTCGTCTTGAAAAAGTTGGATCAATAT 1581
OY 903 GGGAACTTGGCAACCATATGATTTGCAATTTGTCTCAAGAGAAATTTGTTGTTGTT 962
Db 1582 GGGAACTTGGCAACCATATGATTTGCAATTTGTCTCAAGAGAAATTTGTTGTTGTT 1641
OY 963 CATGCAACGTGCAATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGCGCTATCGGAA 1022
Db 1442 CATGCAACGTGCAATTTGGACCAAGAAAGAAATTAATCTTAATCTTGCGCAATCGGAA 1701
OY 1023 GGAATTTGTGAAAAATGTGTGTGTGCTCTAGACACTTAAACCTTTGGAGGTATTTT 1082
Db 1702 GGAATTTGTGAAAAATGTGTGTGTGCTCTAGACACTTAAACCTTTGGAGGTATTTT 1761
OY 1083 GCGCTTTAAGAGAGAGAAAGACATGTGGAAACATGTGAGATGTGAGATTTGAAATT 1142
Db 1762 GTGCTTCAAGAGAGAAAGAGAGATGGAACATGTGAGAGACAGTCCGATTTGGAATTT 1821
OY 1143 GCCCTCAAGAAAGAAAGTCTATTTCTGCGCTGCGCTGAGACTTATGACCATCACTTCCACT 1202
Db 1822 GCTTCAAGAGAAAGTCTATTTCTGCGCTGCGCTGAGACTTATGACCATCACTTCCACT 1881
OY 1203 TGATTTGAGCAATGCTTTATCATATTTGTGAGATTTCCAAAGAGTACCGAAATGAGAAA 1262
Db 1882 TGATTTGAAACAATGCTTTGCTATTTGTGGGTGTTCCAAAGAGTACCGAAATGAGAAA 1941
OY 1263 GGGAAATCTAATCTCTCTGATGAGCAATGTTTATTTATGAAAGAAACCTTGA 1322
Db 1942 AGAAATCTAATCTCTCTGATGAGCAATGTTTATTTATGAAAGAAACATGGA 2001
OY 1323 GCTAGAGAAATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1382
Db 2002 GCTAGAGAAATGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 2061
OY 1383 GATTGAAGTTAATCTGTGCAAACTTATTTCAAGATCATGATCTCAATGATCTGCGC 1442
Db 2062 GATTGAAGTTAAGATGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 2121
OY 1443 AACATCTTAATTTGGCAAGACATCAAGCAAGCAATATTCGAGAAATTAATTTAGAAAA 1502
Db 2122 AACATCTCTGTTTTCAGCAAAACATCAAGCAAGCAATATTCGAGAAATTAATTAACACAG 2181
OY 2182 TTACACACATATATATGTCATGTTGCTTGGCAAGTGTGTTTTTTCACCTCTCCCC 2241
OY 1563 CTTCGAGAAATTTGTCTGTTGAGGCTTAAATCTAAGTACATTAACCTTAAGCAGTT 1622
Db 2242 CTTCGAGAAATTTATCTGTTAAGAGTCTTAATCTAAGTATTCGACATTTAATAAGTT 2301
OY 1623 ACCGTTTCAATTTGAGATCTAAGTACATTTAAGATCTAATCTTGTCTGCAATATCTAG 1682
Db 2302 ACCATCTTCAATTTGAGATCTAAGTACATTTAAGATCTAATCTTGTCTGCAATATCTAG 2358
|||||

```

QY 1683 TATTGGAGTCTCCAAACCAAGTTATGCAAGCTTCAAAATCTGCAGACTCTTGATCTACA 1742
Db 2359 CAGCGTAGTCTTCCAAAGCAATTAAGCAAGCTTCAAAATCTGCAGACTCTTGATCTACA 2418
QY 1743 TGGCTGTCACTTCTGTTGTTGGCAAAAGAAACAAGCAACTGTGTAGTCTTGAAA 1802
Db 2419 ATATTGACCAAGCTTGTGTTGTTGGCAAAAGAAACAAGCAACTGTGTAGTCTTGAAA 2478
QY 1803 TCTTTACTTGAATGTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
Db 2479 TCTTTACTTGAATGTGTGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 2538
QY 1863 ATGCTTAAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
Db 2539 ATGCTTAAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2595
QY 1923 TGAATTAAGCAAACTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1982
Db 2596 TGAATTAAGCAAACTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 2655
QY 1983 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
Db 2656 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2715
QY 2043 CATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
Db 2716 CATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2772
QY 2103 TGAAGCTCTCAAAACCAAGCTCAAGTCTGATGATGATGATGATGATGATGATGATGAT 2162
Db 2773 TGAAGCTCTCAAAACCAAGCTCAAGTCTGATGATGATGATGATGATGATGATGATGAT 2832
QY 2163 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
Db 2833 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2892
QY 2223 CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTGTGATGATGATGATGATGATGATGAT 2282
Db 2893 CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTGTGATGATGATGATGATGATGATGAT 2952
QY 2283 AGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2342
Db 2953 AGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3012
QY 2322 TTCTGATTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2381
Db 3013 TTCTGATTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3072
QY 2382 TGGTATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2441
Db 3073 TGGTATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3132
QY 2442 GATAGAGATTAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2501
Db 3133 GATAGATTAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3169
QY 2502 GGTAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2561
Db 3170 GGTAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183
QY 2562 TCTTACTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2621
Db 3184 TCTTACTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243
QY 2622 CAAAAGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2681
Db 3244 CAAAAGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3303
QY 2682 GCTTACCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2741
Db 3304 GCTTACCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3363

```

```

QY 2742 ACTAGAGAGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2801
Db 3364 ACTAGAGAGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3423
QY 2802 AAACATCTGTAATGCTACAAATGTTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2861
Db 3424 TGAACATCTGTAATGCTACAAATGTTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
QY 2862 AAATTTATCAGTTGATGTTTGTCCCAACAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 2921
Db 3484 AAGTTTAAATTTGGGGAGATGTCACAACTGATCAACGGGTGTGAGAGAGAGAGAGAGAG 3543
QY 2922 AGACTGTGCAAAATTTGCTCATTTCTCGTGTTTATTTAT 2964
Db 3544 AGACTGTGCAAAATTTCTCATTTCTTAATGTGAATATATAT 3586

RESULT 11
ADH51533
ID ADH51533 standard; DNA, 5191 BP.
XX
AC ADH51533;
XX
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum Rpi-b1b partial gene SeqID50.
XX
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
XX
OS Solanum bulbocastanum.
XX
EN US2003221215-A1.
XX
PD 27-NOV-2003.
XX
PF 07-FEB-2003; 2003US-00360522.
XX
PR 07-FEB-2003; 2003US-00360522.
XX
PA (KWE-) KWEER EN RESEARCHBEDRIJF AGRICO BV.
XX
PI Allefs JHM, Van Der Voessen EAG;
XX
DR WPI; 2004-010903/01.
XX
PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
PS Claim 6; SEQ ID NO 50; 98bp; English.
XX
CC This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a fragment of the
CC S bulbocastanum Rpi-b1b protein which is related to the invention.
XX
SQ Sequence 5191 BP; 1673 A; 877 C; 941 G; 1700 T; 0 U; 0 Other;

Query Match 60.9%; Score 1805.8; DB 12; Length 5191;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
QY 426 AACAGTTTGTGTTGATGAAACCAAGTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAT 485

```

Db 2292 ACCAGGTTCTGTAATTAACCGAACCCGAGGTTATGGAAGAGACAAAGGAAGATGAGAT 2351
Qy 486 AGTGAATTCCTGATTAACCAATGTTAGCAATGCCCCAACACTCCAGTCCCTCCAACT 545
Db 2352 AGTGAATTCCTGATTAACCAATGTTAGCAATGCCCCAACACTCCAGTCCCTCCAACT 2411
Qy 546 TGGTATGGGGGGGACTAGGAAGAGACACTTGGCCCCAAATGCTCTTCAATGATCAGAGT 605
Db 2412 TGGTATGGGGGGGACTAGGAAGAGACACTTGGCCCCAAATGCTCTTCAATGATCAGAGT 2471
Qy 606 AATTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATGAGAAG 665
Db 2472 TACTAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATGAGAAG 2531
Qy 666 GTTGATAAAGAAATTTGTAATCTATGGAAGAAAGTC---ACTGTGGAGATGAGCTT 722
Db 2532 GTTATTAAGGCAATTTGTAATCTATGGAAGAAAGCCACTACTTGTGTGAGATGAGCTT 2591
Qy 723 GGCTCCACTTCAAAAGAGCTTCGGGACTTGTGTAATGGAAGAAATATTTGCTGCTT 782
Db 2592 GGCTCCACTTCAAAAGAGCTTCAGAGATTTGTGTAATGGAAGAAATATTTGCTGCTT 2651
Qy 783 AGATGATGTTGGAATGGAATCAAGATTAAGTGGCTAAGTTAGACAAGTCTTGAAGT 842
Db 2652 AGATGATGTTGGAATGGAATCAAGATTAAGTGGCTAAGTTAGACAAGTCTTGAAGT 2711
Qy 843 TGGAGCAAGTGGCGCTTCTGTTCTTACCACTACTGCTCTTGAAGAAAGTTGATCAATAT 902
Db 2712 TGGAGCAAGTGGCGCTTCTGTTCTTACCACTACTGCTCTTGAAGAAAGTTGATCAATAT 2771
Qy 903 GGAACATTTGCAACCATATGATGTAATGTCAAAATTTGTCTCAAGAGATTTGGTGTGTT 962
Db 2772 GGAACATTTGCAACCATATGATGTAATGTCAAAATTTGTCTCAAGAGATTTGGTGTGTT 2831
Qy 963 CATGCAACGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGCTATCGAAA 1022
Db 2832 CATGCAACGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGCTATCGAAA 2891
Qy 1023 GGAATTTGTGAAGAAATATGTTGTGTGTGCTCTAGCACTAAATCTCTTGAAGATTTT 1082
Db 2892 GGAATTTGTGAAGAAATATGTTGTGTGTGCTCTAGCACTAAATCTCTTGAAGATTTT 2951
Qy 1083 GCGCTTTAAGAGAGAAAGACAGTGGGAACTATGAGATGATGAGATTTGGAATT 1142
Db 2952 GTGCTTCAAGAGAGAGAAAGACAGTGGGAACTATGAGATGATGAGATTTGGAATT 3011
Qy 1143 GCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTAGTTACATCACTTCCACT 1202
Db 3012 GCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTAGTTACATCACTTCCACT 3071
Qy 1203 TGAATTTGACACATGCTTTACATATTTGTCAGATTTCCCAAGATCCGAATGAGAAA 1262
Db 3072 TGAATTTGACACATGCTTTGCTATTTGTGCGTGTTCCTCAAGATGCAAAATGAGAAA 3131
Qy 1263 GGGAAATCTAATCTCTCTGGAATGGCAATGTTTATTTTATGGAAGAAAGTCTGGA 1322
Db 3132 AGAAAGATTAATCTCTCTGGAATGGCAATGTTTATTTTATGGAAGAAAGTCTGGA 3191
Qy 1323 GCTAGAGATGTAGATTAATGAGATGAGATTAATTAATTAATTAATTAATTAATTAAT 1382
Db 3192 GCTAGAGATGTAGATTAATGAGATGAGATTAATTAATTAATTAATTAATTAATTAAT 3251
Qy 1383 GATTGAATTAATGCTGCTCAACTTATTTCAAGATGATGATCTCATTCATGATGCGC 1442
Db 3252 GATTGAATTAATGCTGCTCAACTTATTTCAAGATGATGATCTCATTCATGATGCGC 3311
Qy 1443 AACATCTGATTTTGGGAGAGACATCAAGAGCAATTCGAGAGAAATTAATTAATTAAT 1502
Db 3312 AACATCTGATTTTGGGAGAGACATCAAGAGCAATTCGAGAGAAATTAATTAATTAAT 3371
Qy 1503 TTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562

Db 3372 TTACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3431
Qy 1563 CTTGAGAGATTTGCTGCTGAGGGGCTTAATCTAATGATGACATTAATTAAGCAGTT 1622
Db 3432 CTTGAGAGATTTGCTGCTGAGGGGCTTAATCTAATGATGATGATGATGATGATGATGAT 3491
Qy 1623 ACCGCTTCCATGGAAGATCTAGTACATTTTAAGATACCTTAACCTTGTGCGCAATACAG 1682
Db 3492 ACCATCTTCCATGGAAGATCTAGTACATTTTAAGATACCTTGAACCTGTATGCGC---AGTGG 3548
Qy 1683 TATTGATGCTTCCCAACCGATTAATGACAGCTTCAAAATCTGAGATCTTGAATCTCA 1742
Db 3549 CATGCGATGCTTCCCAACCGATTAATGACAGCTTCAAAATCTGAGATCTTGAATCTCA 3608
Qy 1743 TGGGTCATTCACCTTGTGTTGTCGCAAAAGAAACCAACCTGATGCTTCGAAA 1802
Db 3609 ATATTGACCAAGCTTGTGTTGTCGCAAAAGAAACCAACCTGATGCTTCGAAA 3668
Qy 1803 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
Db 3669 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3728
Qy 1863 ATGCTTTAAGACTTAAGTATGATTTGTGTGGGAATTCAGAGAAAGTTGCACTTGG 1922
Db 3729 ATGCTTTAAGACTTAAGTATGATTTGTGTGGGAATTCAGAGAAAGTTGCACTTGG 3785
Qy 1923 TGAATTAAGAACTGATCTCTATGCTCAATGGAATCAAGCATCTGAGAGATGAA 1982
Db 3786 TGAATTAAGAACTGATCTCTATGCTCAATGGAATCTGGAATCTGAGAGATGAA 3845
Qy 1983 GAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
Db 3846 GAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3905
Qy 2043 CATGAATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
Db 3906 CATGAATTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3962
Qy 2103 TGAAGCTCTGAAACCACTCTCAATCTGATGTTTAAACATCAAGGGCTTCAGAGAT 2162
Db 3963 TGAAGCTCTGAAACCACTCTCAATCTGATGTTTAAACATCTGATGTTTAAACATCAAG 4022
Qy 2163 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
Db 4023 CCATCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4082
Qy 2223 CAGTTGAAAACTGCTCATGCTTTACCACTCTTGTGATGCTGCTTGTAAAGTCT 2282
Db 4083 CAATCTCAGAAACTGCTCATGCTTTACCACTCTTGTGATGCTGCTTGTAAAGTCT 4142
Qy 2283 AGATTTGTGAGAGGGGCTCTGCGGAAGTGAATGTTG-----A 2321
Db 4143 AGAGTTTCACTGGGGGCTCTGCGAGATGAGATGTTGAAGAGATGATGATGATGATGAT 4202
Qy 2322 TTCTGATATCCCTTCAAGAGAAAGTTTCAATCTGAGAGAACTTAATTAATTAATTAAT 2381
Db 4203 TTCTGATATCCCTTCAAGAGAAAGTTTCAATCTGAGAGAACTTAATTAATTAATTAAT 4282
Qy 2442 GATGAGATTAATATGTTGCTTATGTTTGTATTTCCAACTTCTCTGTGCAAGAAAT 2501
Db 4283 GATGAGATTAATATGTTGCTTATGTTTGTATTTCCAACTTCTCTGTGCAAGAAAT 4359
Qy 2502 GGTATGATGAGGGGACAGTCAAGTGAATGATGATGATGATGATGATGATGATGATGAT 2561
Db 4360 -----TCTAATCTTAAGGC 4373
Qy 2562 TCTTACTTCCCTCAAAATGCTATTAACAAAGAGATGCTTCACTCCAGAGAGATGTT 2621
Db 4374 TCTTACTTCCCTCAAAATGCTATTAATTAAGTATGATGATGATGATGATGATGATGATGAT 4433

```
OY 2622 CAAAGCCTTGAATCTCAATCTGAAATATCTCTTTACTGATCTTAAGAGCT 2681
Db 4434 CAAAACCTTGGCAATCTCAAAATATCTGCAATCTCTCGGTGCAATATCTCAAAAGAGCT 4493
OY 2682 GCCTACAGCTGGTGTAGTCTCAATGCTTTGAAAGATCTGAAATTCATAGTTGTTATGC 2741
Db 4494 GCCTACAGCTGGTGTAGTCTGAAATGCTTTGAAATTCATAGTTGTTGCGC 4553
OY 2742 ACTAGAGCTCTCCCGAGAGAGTGTGAAAGTTAATTTCACTACACAGTTATCCAT 2801
Db 4554 ACTAGAGCTCTCCCGAGAGAGTGTGAAAGTTAATTTCACTACACAGTTATTTGT 4613
OY 2802 AACATCTGTGAATCTCAATGTTTACCGAGGATTCAGACCTTAACAGCCCTCAC 2861
Db 4614 TGACACCTGTACATGCTAAATGTTTACAGAGGATTCAGACCTTAACACCTTCAC 4673
OY 2862 AAATTTATGATTTGATTTGTTCCAACTGCGCAAGCGGTGTGAAAGGAAATAGAGA 2921
Db 4674 AAGTTTAAATTCGGGGATGTCACACTGATCAAGCGGTGTGAAAGGAAATAGAGA 4733
OY 2922 AGACTGTACAAATTTGCTCAATCTCTGCTGTTTATTTAT 2964
Db 4734 AGACTGTACAAATTTGCTCAATCTCTGATGATATATAT 4776
```

RESULT 12

```
ADFI7761
ID ADFI7761 standard; DNA; 7349 BP.
```

```
AC ADFI7761;
```

```
DT 12-FEB-2004 (first entry)
```

```
DE Solanum bulbocastanum BAC SPB4 genomic DNA fragment.
```

```
KM ds; BAC SPB4; Rpi-b1b gene cluster; growth regulant; oomycete infection;
introduction breeding; plant; late blight.
```

```
OS Solanum bulbocastanum.
```

```
PN EP134979-A1.
```

```
PD 13-AUG-2003.
```

```
PF 08-FEB-2002; 2002EP-00075565.
```

```
PR 08-FEB-2002; 2002EP-00075565.
```

```
PA (KMEF-) KMEF EN RESEARCHBEDRIJF AGRICO BV.
```

```
PI Van Der Vossen ENG, Allefs JHM;
```

```
DR WPI; 2003-714439/68.
```

```
PT New resistance gene conferring resistance against an oomycete pathogen,
useful for producing plants, especially potatoes and tomatoes, resistant
against oomycete pathogens such as Phytophthora infestans.
```

```
XX Example 5; SEQ ID NO 37; 86bp; English.
```

```
XX This invention relates to novel isolated polynucleotides that confer
resistance against late blight caused by the oomycete pathogen
Phytophthora infestans, which threatens both tomato and potato crops.
Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
and which cause disease resistance to bacteria, fungi, nematodes etc.
These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
described as plant growth regulators. They are useful in providing
resistance to Phytophthora infestans, especially in Solanum tuberosum
(potato) plants to protect against oomycete infection or to demonstrate
disease susceptibility. Resistance can be conferred by transformation of
existing potato and tomato cultivars with the gene, a procedure that is
```

```
CC more straightforward and faster than conventional introgression breeding.
CC This polynucleotide sequence is the Solanum bulbocastanum BAC SPB4
CC genomic DNA fragment, present in RGC2-b1b of the invention.
```

```
XX Sequence 7349 BP; 2508 A; 1139 C; 1218 G; 2484 T; 0 U; 0 Other;
```

```
Query Match 60.9%; Score 1805.8; DB 10; Length 7349;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
```

```
OY 426 AACAGTTTGTGTTGATGATGACCAAGTTTATGAAAGACAAAGAAAGACGAGT 485
Db 3749 ACCAGTTTGTGTTATTAACCAAGTTTATGAAAGACAAAGAAAGATGAGT 3808
OY 486 AGTAAATCTGATTAACAAATGTTACCAATGCCAAACCTTCAGTCTCCCAATCT 545
Db 3809 AGTAAATCTGATTAACCAATGTTAGTGTGCCAACACTTTCAGTCTCCCAATCT 3868
OY 546 TGGTATGGGGGAGATAGAAAGACACTCTTCCCAATGCTTCAATGATCAGAGAT 605
Db 3869 TGGTATGGGGGAGATAGAAAGACACTCTTCCCAATGCTTCAATGATCAGAGAT 3928
OY 606 AATTGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTATGAAAGAG 665
Db 3929 TACTGACATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTATGAAAGAG 3988
OY 666 GTTATTAAGAAATTTGATGATCTATTTGAAAGAAAGTCT--ACTTGTGGCATGACCTT 722
Db 3989 GTTATTAAGAAATTTGATGATCTATTTGAAAGAAAGTCTTGTGATGATGACCTT 4048
OY 723 GGCTCCACTTCAAAAGAGCTTGGGACTGCTGAATGAGAAAGAAATTTGCTGCTT 782
Db 4049 GGCTCCACTTCAAAAGAGCTTGGGACTGCTGAATGAGAAAGAAATTTGCTGCTT 4108
OY 783 AGATGATTTGGAATGATGATCAAGATTAAGTGGGCTTAAGTTAAGCAAGCTTTGAAGT 842
Db 4109 AGATGATTTGGAATGATGATCAAGATTAAGTGGGCTTAAGTTAAGCAAGCTTTGAAGT 4168
OY 843 TGGAGCAAGTGGGCTTCTGTTCTACCACTACTGCTTGAAGAGTTGATCAATTTAT 902
Db 4169 TGGAGCAAGTGGGCTTCTGTTCTACCACTACTGCTTGAAGAGTTGATCAATTTAT 4228
OY 903 GGGAACTTGGCAACATATGAAATTTGCTCAAGAAAGATTTGCTGTTGTT 962
Db 4229 GGGAACTTGGCAACATATGAAATTTGCTCAAGAAAGATTTGCTGTTGTT 4288
OY 963 CATGCAAGCTGATTTGGGCAACAGAAAGAAATTAATCTTATCTTGGCTATGGAAA 1022
Db 4289 CATGCAAGCTGATTTGGGCAACAGAAAGAAATTAATCTTATCTTGGCTATGGAAA 4348
OY 1023 GGAGATTTGAAAGAAATTTGGTGTGCTCTAGAGCTTAACCTTTGAGGATTTT 1082
Db 4349 GGAGATTTGAAAGAAATTTGGTGTGCTCTAGAGCTTAACCTTTGAGGATTTT 4408
OY 1083 GGGCTTTAAGAGAGAAAGACAGTGGACATGTGAGATGAGATTTGAAAAT 1142
Db 4409 GGGCTTTAAGAGAGAAAGACAGTGGACATGTGAGATGAGATTTGAAAAT 4468
OY 1143 GGCTCAAGAAAGATTTCTGCTGCTGCTGAGAGCTTGAATTCATCACTTCCACT 1202
Db 4469 GGCTCAAGAAAGATTTCTGCTGCTGCTGAGAGCTTGAATTCATCACTTCCACT 4528
OY 1203 TGAATTTGACACATCTTATCATATTTGTCAGTATTTCCAAAGATTAACGAATGAAA 1262
Db 4529 TGAATTTGACACATCTTATCATATTTGTCAGTATTTCCAAAGATTAACGAATGAAA 4588
OY 1263 GGGAAATCTAATCTCTCTGATGACATGCTTTTATTTATGAAAGAAAGATTTGGA 1322
Db 4589 GGGAAATCTAATCTCTCTGATGACATGCTTTTATTTATGAAAGAAAGATTTGGA 4648
OY 1323 GCTAAGATGATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
Db 4649 GCTAAGATGATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4708
```


OY	1383	GATTGAAGTTAAATCTGGTCAAACTTATTTCAAGATGATATCTCATGAGATCTGGC	1442
Db	4709	GATTGAAGTTAAAGATGGTAAACTTATTTCAAGATGATATCTCATGATTTGGC	4768
OY	1443	AACATCTTATTTTCGGCAGACATCAAGACGCAATATCCGAGAAATATTTGAGAAA	1502
Db	4769	AACATCTCTGTTTTCAGCAAAACATCAAGCAGCAATATCCGTGAATATTAATAACAG	4828
OY	1503	TTACATATATATGATATGATTCATTTGGTTTCACTAAAGTGATCTTCTTCTTTCCCA	1562
Db	4829	TTACACATATATGATATGATTCATTTGGTTTCCGGAATGGTGTTTTTCACCTCTTCCCC	4888
OY	1563	CTTGCAGAAAGTTTGTCTGTGAGGGGTCTTAATATTAAGTGACATATAAATTAGCAGTT	1622
Db	4889	CTTGGAAAAGTTTATCTGTTTAAGAGTCTTAATCTAGTGATTTGCAATTTAATAGTT	4948
OY	1623	ACCGTCTTCCATTGGAGATCTTAAGTACATTTAAGATACCTAACTTGTCTGCAATCTAG	1682
Db	4949	ACCATCTTCCATTGGAGATCTTAAGTACATTTAAGATACCTGAACCTGTATGTC--AGTGC	5005
OY	1683	TATTCGTATGTCCTTCCAAACAGTTATGCAAGCTTCAAAATCGCAGATCTTGAATCTACA	1742
Db	5006	CATGGTATGTCCTTCCAAACAGTTATGCAAGCTTCAAAATCTGCAAACTTGAATCTACA	5065
OY	1743	TGGCTGTCAATTCATTTGTTGTTGGCCAAAAGAAAACAAGCAAACTTGTACTCTTCGAAA	1802
Db	5066	ATATTTGACCAAGCTTTGTTGTTGGCCAAAAGAAAACAAGTAACTTGTACTCTCCGAAA	5125
OY	1803	TCTTTTACTTGAATGGTGTGCTATGATTTGATCTTATATGCAACCAAGATAGATCTTTGAC	1862
Db	5126	TCTTTTACTTGAATGGTGTGCTATGATCTTATATGCAACCAAGATAGATCAATTGAC	5185
OY	1863	ATGCTTTAAGACTCTAAGTATGATTTGTGTGGGAATTCAGAAAGAAAAGTTGTCAACTTGG	1922
Db	5186	ATGCTTTAAGACTCTAAGTATGATTTGTGTGGGAATTCAGAAAGAAAAGTTGTCAACTTGG	5242
OY	1923	TGAATTAAGAAACCTGAATCTCTATATGCTCAATTGAATTCAGCACTTGAAGAGTGAA	1982
Db	5243	TGAATTAAGAAACCTGAATCTCTATATGCTCAATTGAATTCAGCACTTGAAGAGTGAA	5302
OY	1983	GAAATGATATGGAATGCAAAAAGAAAGCAATTTATCTGCAAAAAGAAAATCTGCATCTTTAAG	2042
Db	5303	GAAATGATATGGAATGCAAAAAGAAAGCAATTTATCTGCAAAAAGAAAATCTGCATCTTTAAG	5362
OY	2043	CATGAAATGGAGATGACGATGGAACGTCCACGTATATATGATCAGAAAAAGTTGGAAGTCT	2102
Db	5363	CATGAGTTGGAAATTAATCTTGT--GACCAATATATATGATCAGAAAGTTAAGTCT	5419
OY	2103	TGAAGCTCTCAAAACCACTCCCAATCTGATCTTGTTTAAACAATCAAGGGCTTCAAGGAT	2162
Db	5420	TGAAGCTCTCAAAACCACTCCCAATCTGATCTTGTTTAAAAATCTATGCTTCAAGGAT	5479
OY	2163	CCGATCTCCCAAGCTGATGATCACTCAGTTTGTAAAAAATTTGTCTTATTTGAATCAT	2222
Db	5480	CCATCTCCCAAGCTGATGATCACTCAGTATTTGAAAAAATTTGTCTTATTTGAATGAG	5539
OY	2223	CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTTTGTGTGAGCTGCTTGTAAAAAGCTT	2282
Db	5540	CAGTTGCAAAAACCTGCTCATGCTTACCAACCTTTTGTGTGATCTGCTTGTAAAAAGCTT	5599
OY	2283	AGACTTGTGAGGGGGGTCTGCGAAAGTGGATATGTTG-----A	2321
Db	5600	AGACTTGTGAGGGGGGTCTGCGAAAGTGGATATGTTGAGAAAGTGGATATGTTGATCTTCA	5659
OY	2322	TTCTGATATCCCTTCAAGAAAGAGTTTCCATCTCTGAGAAAATTATATATACCGAAT	2381
Db	5660	TTCTGATATCCCTTCAAGAAATTAAGTTTCCATCTCTGAGAAAATTATATATATGAGCTT	5719
OY	2382	TGTGATATCTGAAAAGATTTCTGAAAAAAGAAAGAAAGCAATGCTCTGTGCTTTGAGA	2441
Db	5720	TGTGATATCTGAAAAGATTTCTGAAAAAAGAAAGAAAGCAATTTCCCTGTGCTTTGAGA	5779

Qy	2442	GATGAGATTAAAGTTGGCCCTATGTTGATATTCACACCCCTTCTCTGTCAGAAATY	2501
Db	5780	GATATTAATTCACAGAGTCCC-----TTTTCGACCCCTTCT-----	5816
Qy	2502	GGTAGTTAGTGGGACAAAGTCAGATGCATAGATTTTCAGTTCATATCTATCTCATGGC	2561
Db	5817	-----TCTATCTTAGGGC	5830
Qy	2562	TCTTACTTCCCTCCAAATGGCTATTAACAAAGAAAGATGCTTCACTCCACAGAGAGATGT	2621
Db	5831	TCTTACTTCCCTCAGAAATTTGCTATTAATTAAGTAGTACTTCACTTCCACAGAGAGATGT	5890
Qy	2622	CAAAAGCCTTGCAAAATCTCAAAATCTGGAATTCCTTTTACTTCAATCTTAAGAAGCT	2681
Db	5891	CAAAAACCTTGCAAAATCTCAAAATCTGGAACATCTCCGGTCGAATATCTCCAAAGAGCT	5950
Qy	2682	GCCACACAGCCTGGCTAGTCTCAATGCTTTGAAAGCATCTGGAATATCATAGTTGTTATGC	2741
Db	5951	GCCACACAGCCTGGCTAGTCTGAATGCTTTGAAAAGTCTTAAATATCAATTTGTTGCGC	6010
Qy	2742	ACTAGAGAGTCTCCCCAGAGAAAGGTGTGAAGGTTTAAATTTCACTCAACAGATTATCCAT	2801
Db	6011	ACTAGAGAGTCTCCCTGAGGAAGGCTGGAAGGTTTATCTTCACTCAACAGATTATTTGT	6070
Qy	2802	AACATACTGTGAATGTGTACATATGTTTACCGGAGGATTCAGACACCTTAACAGCCCTCAC	2861
Db	6071	TGAACACTGTAACTATGTTAAATATGTTTACAGAGAGGATTCAGACACCTTAACACCCCTCAC	6130
Qy	2862	AAATTTATCAGTTGAGTTTGTCCAAACACTGGCCACAGCGGTGTGAAGAAAGGAATAGAGA	2921
Db	6131	AAAGTTTAAAAATTCGGGAGATGTCACAACTGATCTACAGCGGTGTGAAGAAAGGAATAGAGA	6190
Qy	2922	AGACTGGTACAAATTTGCTCAACTCCGCTGTTGTTAATTTAT	2964
Db	6191	AGACTGGCACAATAATTTCTCACTCTCTAATATGTAATATATAT	6233

XX	RESULT 13
ADFI17762	
ID	ADFI17762 standard; DNA; 3260 BP.
XX	
AC	ADFI17762;
DT	
XX	12-FEB-2004 (first entry)
DE	
XX	S_bulbocastanum RGCl-b1b coding DNA containing an intronic sequence
KW	gene; ds; RGCl-b1b; Rpi-b1b gene cluster; growth regulant;
KM	oomycete infection; introgression breeding; plant; late blight.
XX	
OS	Solanum bulbocastanum.
XX	
FH	Location/Qualifiers
FT	1..3260
CDS	
FT	/*tag= a
FT	/product= "RGCl-b1b protein"
FT	/note= "this coding sequence contains one intron"
FT	/transl_except= (pos: 709..710, aa: Gly)
FT	428..708
FT	/*tag= b
FT	/number= 1
FT	
FT	intron
XX	
PN	EP1334979-A1.
XX	
PD	13-AUG-2003.
XX	
XX	08-FEB-2002; 2002EP-00075565.
XX	
XX	08-FEB-2002; 2002EP-00075565.
PR	
XX	
XX	(KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX	
XX	Van Der Vossen EAG, Allefs JHM;
XX	

|||||
2366 ATATGAATCCGAAAGATTAAAGTCTGGAAGCCCTCAAAACCACTCCCAATCTGAAATA 2425
2136 TTAAACATCCAGGGCTTCAGAGAAATCCGTCTCCAGCTGGAGTAATCATCTGATT 2195
2426 TTAAATAATCATGACTCTGAGATCTGCTCCCTGAGTAATCACTCAAGTTT 2485
2196 GAAAAATGTTGCTCTAATGAATCATGATGCAAAAACTGCTATGCTTACCACTT 2255
2486 GAAAAATGTTGCTCTAATGAATCATGATGCAAAAACTGCTATGCTTACCACTT 2545
2236 TGTGAGCTGCTTGTCTTAAAAAGTCTAGAGTTGAGAGGGGCTGCGGAAGTGAATA 2315
2546 TGTGAGCTGCTTGTCTTAAAAAGTCTAGAGTTGAGAGGGGCTGCGGAAGTGAATA 2605
2316 TGT---GATTTGATTCCTTCAAGAAAGAGTTTCCATCTGAGAAAACTTAAT 2372
2606 TGTGAAAGATTCCTGATTCCTGACAAAGAAAGATTTCCATCTGAGAAAACTTCAAT 2665
2373 ACGCAATTTGGTATCTGAAGAGATGCTGAAAAAGAAAGAGAGCAATGCTTGT 2432
2666 AGTGGCTTTTGTATCTGAAGAGATTCGAAGAAATGAAGAGAGCAATGCTTGT 2725
2433 GCTTGAAGAGATGAGATTTAAATGTTGCCCTATGTTGTTATTCACCCCTTCTTGT 2492
2726 GCTTGAAGAGATGAGATTTGCGATTTGCCCTATGTTGTTATTCACCCCTTCTTGT 2785
2493 CAAAGAAATTTGATGATTAAGTGGGAGCAAGTCAATGATGATGATGATGATGAT 2552
2786 CAAAGAAATTTGATGATTAAGTGGGAGCAAGTCAATGATGATGATGATGATGAT 2842
2553 TCTGATGCTCTTATCTTCCCTCAAAATTCGATTAACAAAGAGAGTTCATCTCCAGA 2612
2843 TCTGATGCTCTTATCTTCCCTCAAAATTCGATTAACAAAGAGAGTTCATCTCCAGA 2902
2613 AGAGATGTTCAAAAGCTTGCATAATCTCAATATCTGATATCTTCTTCAATCT 2672
2903 AGAGATGTTCAAAAGCTTGCATAATCTCAATATCTGATATCTTCTTCAATCT 2962
2673 TAAAGAGCTGCTTACCAAGCTTGGCTAGTCTCAATCTTGAAGCATCTGAAATCTAAG 2732
2963 CAAAGAGCTGCTTACCAAGCTTGGCTAGTCTCAATCTTGAAGCATCTGAAATCTAAG 3022
2733 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2792
3023 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3082
2793 GTTATCATTAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2852
3083 GTTATCATTAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3142
2853 AGCCCTCAAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2912
3143 AACCTCAAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3202
2913 AATAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2964
3203 AATAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3254

RESULT 14

ADH51534

ID ADH51534 standard; DNA; 3260 BP.

AC ADH51534;

XX 25-MAR-2004 (first entry)

DE S bulbocastanum RGL1-b1b gene SeqID51.

XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
XX Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW de; RGL1-b1b.

XX Solanum bulbocastanum.
OS US2003221215-A1.
XX 27-NOV-2003.
XX 07-FEB-2003; 2003US-00360522.
XX 07-FEB-2003; 2003US-00360522.
XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX Allele JHM, Van Der Vossen EAG;
XX WPI; 2004-010903/01.
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
XX for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX with resistance against oomycete infection.
XX Claim 6; SEQ ID NO 51; 98pp; English.
XX This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
XX protein which may provide a plant or its progeny with at least partial
XX resistance against an oomycete infection caused by Phytophthora
XX infestans. The invention may be useful for the development of compounds
XX with a fungicide activity. The DNA sequence of the invention encodes an
XX Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX cell, protein or binding molecule is useful for providing a plant or its
XX progeny with resistance against an oomycete infection such as late blight
XX (a disease of major importance to production of Solanaceae such as potato
XX and tomato cultivars). The present sequence is that of the S
XX bulbocastanum RGL1-b1b gene which is related to the invention.
SQ Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;
Query Match 59.7%; Score 1771.6; DB 12; Length 3260;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 389; Indels 54; Gaps 7;
426 AACAGGTTTGTGTAATGAAACCAAGTTATGAAAGAGCAAGAGAT 485
704 AGCAGGTTTGTGTAATGAAACCAAGTTATGAAAGAGCAAGAGAT 763
486 AGTAAATCTGATTAACCAATGTTAGCAATGCCAAACACTTCCAGTCTCCCAATCT 545
764 AGTAAATCTGATTAACCAATGTTAGTATTCGAAAGAGTTCCAGTCTCCCAATCT 823
546 TGTATGGGGGACTAGAAAGAGACTCTTCCCAATGCTTCAATGATCAGAGAT 605
824 TGTATGGGGGACTAGAAAGAGAGACTCTTCCCAATGCTTCAATGATCAGAGAT 883
606 AATTGAGATTTCCATCCCAATATGATGATTTGTCTCGAAGATTTTAATGAAAGAG 665
884 TACTGAGATTTCAATCAAAAGATGATGATTTGTCTCAGATATTTGATGAAAGAG 943
666 GTTATGAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
944 GTTATGAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003
726 TCCACTTCAAAAGAGCTTGGGACTTGGCAATGAAAGAAATTAATTTGCTGCTTGA 785
1004 TCCCTCCAGAAAGCTTCAAGAGTTGTAATGAAAGAAAGATTAATTTGCTTGTGGA 1063
786 TGAATTTGAGATGATCAAGATTAAGTGGGCTAATGTTAAGACAGCTTGAAGTTGG 845
1064 TGAATTTGAGATGATCAAGATTAAGTGGGCTAATGTTAAGACAGATTTGAAGTTGG 1123
846 AGCAGTGGGCTTCTGTTTACCACTACTGCTTGAAGAAAGTTGATCAATTAATGG 905
1124 AGCTAGTGGGCTTCAATTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1183

QY	1956	TGAAATCAGACACTTTGGAGGTGAAGATGATATGATGTGAAGAAAGAACCAATTTATC	201
Db	2255	TTCAATCAACAACATCTTGAAGAGTGAATAATGATATGAGGCAAAAGAACCAATTTATC	2314
QY	2016	TGCAAAAGAAATCTGCATCTCTTTAAGACATGAATGAGATGACATGAAAGCTCACGTAT	2075
Db	2315	TGCAAAAGCAAACTCAACTCTTTTAAGCATGATGGGATA-----GACCAAAACAG	2365
QY	2076	AATATGATATGAAAAGATTTGAATGATGCTTGAAGCTCTGAAACCACTCCATTCGACTTG	2153
Db	2366	AATATGATATCGAAGAAAGTTAAAGTCTTGAAGCCTCAACCAACAATCCCAATCTGAATA	2425
QY	2136	TTTAAACAATCAGGGCTTCAGAGAAATCCGCTCCCACTGATGATGATCACTCAGTTTT	2195
Db	2426	TTTAAACAATCAATGACTTCTGTGCAATCTGTCTCCCTGACATGATGATCACTCAGTTTT	2485
QY	2196	GAATAATGTTGCTCTTATTTGAATCATCAGTTGCAGAAAACCTGCTCATGCTTACACCTT	2255
Db	2486	GAATAATGTTGCTCTTATTTGAATCATCAGTTGCAGAAAACCTGCTCATGCTTACACCTT	2545
QY	2256	TGATGAGCTGCTCTTCTTCAAAAAGCTAGAGTGTGAGGGGGGTCTGCGAAGTGAATA	2315
Db	2546	TGATGAGCTGCTCTTCTTCAAAAAGCTAGAGTGTGAGGGGGGTCTGCGAAGTGAATA	2605
QY	2316	TGTT--GATTCGTGATTCCTTCAAGAAGAGGTTTCCATCTCTGAGAAAACCTTAAT	2372
Db	2606	TGTTGAAATTTCTGGATTCCTGACAGAAGAAATTTCCATCCTCGAAGAAACCTTCAT	2665
QY	2373	ACGCAATTTGGTATCTGAAAGATGTCGTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG	2432
Db	2666	AGTGGCTTTTGTATCTGAAAGATGTCGTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG	2725
QY	2433	GCTTGAAGAGATGAAGATTAATATGTTGCGCTATGTTTGTATTTCCAACCCCTTCTTCTGT	2492
Db	2726	GCTTGAAGAGATGAAGATTAATATGTTGCGCTATGTTTGTATTTCCAACCCCTTCTTCTGT	2785
QY	2493	CAAGAAATTTGGTATGTTAGTGGGAGCAAGTCAGATGCATATGCTTCACTTCATATCTAA	2552
Db	2786	CAAGAAATTTGAATTTGGGGGG--AGGAGAGAGCAGAGGTTTGGCTCCATATCTAA	2842
QY	2553	TCTCATGCTCTTACTTCCCTCCCAATTCGCTATPACAAAGAAAGAGTCTCAGTCCGAGA	2612
Db	2843	TCTCAGCACTTTACATCTCCCAAGATTTTTCAGTACCAACAGATGACTTCACTACGGA	2902
QY	2613	AGAGATTTCAAAAGCCTTGCAAACTCTCAATACTTGAATATCTCTTTTACTTCAATCT	2672
Db	2903	AGAGATTTCAAAAGCCTTGCAAACTCTCAATACTTGAATATCTCTTTTACTTGAATCT	2962
QY	2673	TAAAGAGTGTCTACAGGCTGTGCTATCTCANTGCTTGAACATCTGGAATTTGATAG	2732
Db	2963	CAGAAGTGTCTACAGGCTGTGCTATCTCANTGCTTGAACATTTGAATGCTGTGATTTGTGA	3022
QY	2733	TTGTTATGCACTAGAGATCTCCCCGAGGAAGGTGTGAAGGTTTAAATTTCACTCACACA	2792
Db	3023	TTGTTATGCACTAGAGATCTCCCCGAGGAAGGCTGTGAAGGTTTAAATTTCACTCACAGA	3082
QY	2793	GTTATCCATACATACCTGTGAATATGCTACATGTTTACCGGAGGATTTGCACACCTTAAC	2852
Db	3083	GTTATTTGTTGAACACCTGTACATGCTTAAATGTTTACCAAGAGGATTTGCACACCTTAAC	3142
QY	2853	AGCCTCACAAATTTATCAGTTGAGTTTGTCCAAACCTGGCCAAAGGGGTGAGAAAGGG	2912
Db	3143	AACCTCACAAATTTTAAATTTGGGGGATTTCCACATGATATTAACGGGTGTGAGAAAGGG	3202
QY	2913	AATAGGAAGACTGTACAAAATTTGCTCACATTCCTCGTGTATTATTTAT	2964
Db	3203	AATAGGAAGACTGTGACAAAATTTCTCACATTCCTTAATGTGAATATATAT	3254

AC ADF17764;
XX 12-FEB-2004 (first entry)
XX S_bulbocastanum RGc4-b1b coding DNA.
XX
XX gene; de; RGc4-b1b; Rpi-b1b gene cluster; growth regulant;
XX oomycete infection; introgression breeding; plant; late blight.
XX
XX Solanum bulbocastanum.
XX
XX Key Location/Qualifiers
XX CDS 1..3899
XX /tag= b
XX /product= "RGc4-b1b protein"
XX /note= "This sequence contains 3 introns and some
XX translation exceptions"
XX 1..433
XX /tag= a
XX /number= 1
XX /tag= C
XX /number= 1
XX /tag= 1
XX /tag= d
XX /number= 2
XX /tag= e
XX /number= 2
XX /tag= f
XX /number= 3
XX /tag= 3
XX /number= 3
XX /tag= h
XX /number= 4
XX
XX EPI334979-A1.
XX
XX 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Van Der Vossen BAG, Allefs JHM;
XX
XX WPI: 2003-714439/68.
XX P-PSDB; ADF17768.
XX
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX
XX Example 5; SEQ ID NO 40; 86pp; English.
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGc1-b1b, RGc3-b1b and RGc4-b1b, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.

CC This polynucleotide sequence is the Solanum bulbocastanum RGc4-b1b coding
CC DNA containing an intronic sequence in an exemplification of the
CC invention.
XX
XX Sequence 3899 BP; 1186 A; 678 C; 846 G; 1189 T; 0 U; 0 Other;
XX
XX Query Match 58.5%; Score 1736.2; DB 10; Length 3899;
XX Best Local Similarity 82.0%; Pred. No. 0;
XX Matches 2096; Conservative 0; Mismatches 428; Indels 33; Gaps 7;
XX
QY 426 AACGAGTTTGTGTTGATGACCAAGATTATGAGAGACAAAGAAAAGACGAGAT 485
DB 1361 AACAGGTTTGTGTTAAGTAACTGAAACCAAGATCTAGAGAGGACAAAGAGGATGAGAT 1420
QY 486 AGTAAATCTCGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
DB 1421 AGTAAATCTCGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1480
QY 546 TGTATGAGGAGGAGCTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
DB 1481 TGTATGAGGAGGAGCTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
QY 606 AATTGAGATTTTCATCCCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 665
DB 1541 AACTAGACATTTCAATCCCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1600
QY 666 GTTATAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
DB 1601 GTTATAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660
QY 726 TCCATTCCTCAAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 785
DB 1661 TTGATTTGAGAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720
QY 786 TGATGTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
DB 1721 TGATGTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780
QY 846 AGCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
DB 1781 AGCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1840
QY 906 AACATTCGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 965
DB 1841 AACGTTGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
QY 966 GCAACGTCATTTGGGACCAAGAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGA 1025
DB 1901 GCAACGTCATTTGGGACCAAGAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGA 1960
QY 1026 GATTGTGAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
DB 1961 GATTGTGAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2020
QY 1086 CTTTAAAGAGAGAAAG 1145
DB 2021 CTTTAAAG 2080
QY 1146 TCAGAGAGAAAGTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1205
DB 2081 TCAGAGAGAAAGTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2140
QY 1206 TTTGAGAGCAATGCTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1265
DB 2141 TTTGAGAGCAATGCTTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2200
QY 1266 AATATCATCTCTCTGATGAGCAATGCTTTCATATGATGATGATGATGATGATGATGATGAT 1325
DB 2201 AATATCATCTCTCTGATGAGCAATGCTTTCATATGATGATGATGATGATGATGATGATGAT 2260
QY 1326 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
DB 2261 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2320

QY 1386 TGAAGTTAATCTGCTCAAACTTATTTCAAGATGATGATCTCATGATCTGGCAAC 1445
 DB 2321 TGAAGTTAATCGGGTAATCTTATTTCAAGATGATGATCTCATGATGATGGCTAC 2380
 QY 1446 ATCTCTATTTTGGGCAAGACATCAAGACATATCCGAGAAATATTTGTAAGAAATTA 1505
 DB 2381 ATCTCTATTTTGGGCAAGACATCAAGACATATCCGAGAAATATTTGTAAGAAATTA 2440
 QY 1506 CATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
 DB 2441 TGAAGTTAATCTGCTCAAACTTATTTCAAGATGATGATGATCTCATGATCTGGCAAC 1625
 QY 1566 GCAGAAATTTGCTGCTGATGAGGCTTATTTCAAGATGATGATGATGATGATGATGATGAT 1625
 DB 2501 GAAAGATTTGCTGCTGATGAGGCTTATTTCAAGATGATGATGATGATGATGATGATGAT 2560
 QY 1626 GTCTTCATTTGGAATCTAGTACATTTAAGATGATGATGATGATGATGATGATGATGAT 1685
 DB 2561 GTCTTCATTTGGAATCTAGTACATTTAAGATGATGATGATGATGATGATGATGATGAT 2617
 QY 1686 TGTAGTCTTCCAAACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1745
 DB 2618 CCGTATGCTTCCAAACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2677
 QY 1746 CTGTCAATTCATTTGCTGCTGATGAGGCTTATTTCAAGATGATGATGATGATGATGATGAT 1805
 DB 2678 TGTAGTCTTCCAAACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2737
 QY 1806 TTTACTTGAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
 DB 2738 TGTAGTCTTCCAAACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2794
 QY 1866 CTTTAAAGCTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1925
 DB 2795 CTTTAAAGCTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2851
 QY 1926 ATTACGAAACCTGAATCTCTATGCTCAATGATGATGATGATGATGATGATGATGATGAT 1985
 DB 2852 ACTGAAACCTGAATCTCTATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2911
 QY 1986 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
 DB 2912 CGAT 2968
 QY 2046 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
 DB 2969 GAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3025
 QY 2106 AGCTCTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2165
 DB 3026 AGCTCTCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3085
 QY 2166 TCTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2225
 DB 3086 TTTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3145
 QY 2226 TTGCAAAACTGCTCATGCTTACCACTTGTGATGATGATGATGATGATGATGATGATGATGAT 2285
 DB 3146 CTGCAAAACTGCTCATGCTTACCACTTGTGATGATGATGATGATGATGATGATGATGATGAT 3205
 QY 2286 GTTGTGAGAGGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2330
 DB 3206 GTTGTGAGAGGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3265
 QY 2331 CCTCAAGAGAGAGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2390
 DB 3266 CTCCAGAGAGAGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3325
 QY 2391 GAAAGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2450
 DB 3326 GAAAGATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3385

QY 2451 TAAAGTTGCCATATGTTGTTATTTCCAAACCTTCTTCTGCTCAAGAAATTTGATGATGAT 2510
 DB 3386 TTTATATGCTCTGTTGTTGTTTCCAAACCTTCTTCTGCTCAAGAAATTTGATGATGAT 3445
 QY 2511 TGGGACAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2570
 DB 3446 CGG---CAAGCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3502
 QY 2571 CCTCAAAATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 2630
 DB 3503 CCTCCGATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 3562
 QY 2631 TGAATGCTCAAAATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 2690
 DB 3563 TGAATGCTCAAAATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 3622
 QY 2691 CTTGAGTCTCAATGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2750
 DB 3623 CTTGAGTCTCAATGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3682
 QY 2751 TCTCCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2810
 DB 3683 TTTCCCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3742
 QY 2811 TGAATGCTCAAAATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 2870
 DB 3743 TGAATGCTCAAAATTTGCTATTAACAAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTT 3802
 QY 2871 AGTTAGTTTGTCCAACTGCTGCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2930
 DB 3803 AGTTAGTTTGTCCAACTGCTGCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3862
 QY 2931 CAAATTTGCTCAATGCTGCTGCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2997
 DB 3863 CAAATTTGCTCAATGCTGCTGCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 3899

Search completed: April 16, 2005, 14:47:08
 Job time : 1458 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using BW model

Run on: April 16, 2005, 14:14:21 ; Search time 502 Seconds
(without alignments)
9670.982 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967
Sequence: 1 atgcgcgaagcttcctcctca.....ctcgctgttattattacag 2967

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTOS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	208.8	7.0	4465	US-08-930-996A-3	Sequence 3, Appli
2	202.6	6.8	4208	US-09-004-838-1	Sequence 1, Appli
3	201	6.8	4163	US-09-004-838-70	Sequence 70, Appli
4	200.8	6.8	1662	US-09-004-838-6	Sequence 6, Appli
5	196.6	6.6	2352	US-09-004-838-2	Sequence 2, Appli
6	177.8	6.0	4946	US-08-930-996A-1	Sequence 1, Appli
7	104	3.5	644	US-09-387-286-24	Sequence 24, Appli
8	93.6	3.2	1036	US-09-004-838-3	Sequence 3, Appli
9	88.4	3.0	3997	US-08-947-823-2	Sequence 2, Appli
10	88.4	3.0	51952	US-08-947-823-1	Sequence 1, Appli
11	88	3.0	946	US-09-004-838-4	Sequence 4, Appli
12	87.4	2.9	544	US-09-004-838-10	Sequence 10, Appli
13	87.4	2.9	544	US-09-004-838-137	Sequence 137, App
14	82.4	2.7	9870	US-09-245-928A-15	Sequence 15, Appli
15	80.8	2.7	3982	US-08-947-823-4	Sequence 4, Appli
16	77.8	2.6	499	US-09-004-838-9	Sequence 9, Appli
17	75	2.5	475	US-09-004-838-5	Sequence 5, Appli
18	73.6	2.5	475	US-09-004-838-8	Sequence 8, Appli
19	71.8	2.4	2718	US-09-360-186-4	Sequence 4, Appli
20	71.8	2.4	2718	US-09-864-680A-4	Sequence 4, Appli
21	71.8	2.4	3099	US-09-360-186-2	Sequence 2, Appli
22	71.8	2.4	3099	US-09-864-680A-2	Sequence 2, Appli
23	71.8	2.4	31491	US-09-360-186-1	Sequence 1, Appli
24	71.8	2.4	31491	US-09-864-680A-1	Sequence 1, Appli
25	70.8	2.4	7218	US-08-232-463-14	Sequence 14, Appli
26	69.8	2.4	384	US-09-004-838-7	Sequence 7, Appli
27	67.6	2.3	503	US-09-004-838-134	Sequence 134, App

28	59	2.0	3741	US-09-803-286A-1	Sequence 1, Appli
29	53.6	1.8	5475	US-08-680-327-1	Sequence 1, Appli
30	53.6	1.8	5475	US-09-228-246-3	Sequence 3, Appli
31	53.6	1.8	10968	US-08-680-327-2	Sequence 2, Appli
32	53.6	1.8	10968	US-09-228-246-1	Sequence 1, Appli
33	53	1.8	8190	US-09-949-016-17412	Sequence 17412, A
34	52.6	1.8	5113	US-09-336-946B-3	Sequence 3, Appli
35	52.6	1.8	5222	US-09-336-946B-68	Sequence 68, Appli
36	52.6	1.8	5222	US-09-993-170-57	Sequence 57, Appli
37	52.6	1.8	5696	US-09-993-170-60	Sequence 60, Appli
38	52.6	1.8	5757	US-09-336-946B-1	Sequence 1, Appli
39	52.6	1.8	5757	US-09-993-170-56	Sequence 56, Appli
40	52	1.8	1141	US-09-806-708B-22	Sequence 22, Appli
41	51.8	1.7	5134	US-08-310-912A-157	Sequence 157, App
42	51.8	1.7	5134	US-09-301-085-157	Sequence 157, App
43	51.8	1.7	5134	PCT-US95-04589-157	Sequence 157, App
44	46.6	1.6	1141	US-09-806-708B-22	Sequence 22, Appli
45	46.2	1.6	1238	US-08-414-938A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-3
; Sequence 3, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 PUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; NUMBER OF SEQUENCES: 12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 204..3923
; US-08-930-996A-3
; Query Match 7.0%; Score 208.8; DB 3; Length 4465;
; Best local Similarity 50.8%; Pred. No. 7e-50;
; Matches 675; Conservative 0; Mismatches 622; Indels 33; Gaps 6;

QY 91 TTGAAAAGCTTCAAGACGTTTACATCCAAAGCTGTGTAGAGATGCTCAAG 150
DB 330 TTAAAGAGCTGAAAATGACTTGGCTGTGATTCAGATTGTGTGTAAGTGAAGAAAT 389
QY 151 AGCAATTTAGAGACAAAGCAATAGAAAATTTGGTTCAGAAAATCAATCTGTGTGATAT 210
DB 390 AAGCAAGCATCAAAATCATCTGTGAGAGACTGCTTAATGAGCTTGAAGATGCTGTGCAC 449
QY 211 GAGGCTGATGACATCTTGACGAAATGTAATCACTGAGCAACAT-----T 255
DB 450 TCTGCTGAAAATTTAATAGAGAGTCAATTAAGAGCTTTGAGGCTTAAGGTGAAAGT 509
QY 256 AGACAGAGAGAGCAAAATATGAGTGTATTCATCCAAAGTTATCACTTTGTGCAAG 315
DB 510 CAGCATCAGAACTTTTCAAGAAACAGCAACAGCAAGTAAAGTAAATTTTCCCTAAC 569
QY 316 ATTGGAAAAAGATGAAAAAGATTATGAGAAATGATGATTAATGACGGAGCAAT 375
DB 570 ATAAAGGACAAAGTGGAGACACTATGAAACATTAAAGATTTGCAAGAGCAAAATGCT 629
QY 376 AAGTTTCATTT---GGATGAAGACATATAGAGACAAAGTGTGACACGCCAAACAGT 432
DB 630 CTCCTTGCTTAAAGAGATTTTGTATTCACAGAAATGAAACTAGAACACTTCAACT 689
QY 433 TTTGTTTGAATGAACCAACAGTTTATGAGAGACAAAGAAAGACAGATAGTGA 492
DB 690 TCTTGATTTGATGAACCAAGATATCTTTGGTGGACAGAGCAAAATGAGATTTGATGAC 749
QY 493 ATCCGATTAACAATGTTAGCAATGCCAAACATTCACAGTCTCCCAATCTGTGTATG 552
DB 750 CGTCAATGTCTGAAAGTGCAGAAATGAGAAATGACAGAGTGTCTTATGTTGGAATG 809
QY 553 GGGGACATAGAAAGACACTTGTCCCAATGATCTTCAATGATCAGAGATTAATGAG 612
DB 810 GGTGCTTGGGCAACCAACTTGTCTAAAGCCGATACATGATGAGAGTGTGAAGAC 869
QY 613 CATTTCCATCCAAATATGATTTGTGTCTGCGAAAGATTTTATGAAAGAGTTGATA 672
DB 870 CATTTGATTTGAAAGCTGTGTTTGTGTCTCGAGGCGTAAATGCTTTCAGAAATACA 929
QY 673 AAGAAATTTGAGATTTATGAAAGAAAGCACTGTGTGACATGAGCTTCCCACT 732
DB 930 AAAGGTTACTTCAAGAAATTTGCTCAATTTGATGATGACAACTTAATCACTGA 989
QY 733 CAAAAGAGCTTGGGACTTGTCTGATGAAAAAAATTTTGTCTGTCTTATGATGATG 792
DB 990 CAAGTCAATTTGAAGAGAAAGATTAAGAAAGAAAGTTCTTATCGTTCTGATGATG 1049
QY 793 TGSATGAAAGTCAAGATTAAGTGGCTAAGTTAAGCAAGTCTGAGAGTGTGAGCAAGT 852
DB 1050 TGAATGCAACTCAACAGATGGATGAATTTGAGAAATGTTTTGTAACAAGAGATATA 1109
QY 853 GGCCTTCTGTTTACCACTACTGTTCTTGAAGAGTGTGATCAATTAATGGAACAT 912
DB 1110 GGAAGTAAAGATCATTTGAGACAGACAGCAAGCAAGTGTGCTTGAATGGAAGAA 1169
QY 913 CAACCATATGATTTGTAATTTGTCTCAGAGAAATGTTGTTGTTCATGCAACGT 972
DB 1170 CA---AATTTAGCAATGGCAATTTGTCTAACCAAGCTTGTGTTTATTTCAAGACAT 1226
QY 973 GCATTTGGGACCAAGAGAAAT---AATTTATCTTGTGCTATCTGGAAGAGAAAT 1029
DB 1227 GCATTTGAAACATGATTCATTTGAGCAATTTGGAACCTTGAAGGTTTGAAGCAAAAT 1286
QY 1030 GTGAAAAAATGTGTGTGTGCTCTAGCAAGCTTAAATCTTTGAGAGTATTTTGGCTTT 1089
DB 1287 GCAGCTAAGTGAAGAGAGCTGCCCTTGAAGTGTGAGAGAGCTTGAAGTGAAGTCC 1346
QY 1090 AAGAGAGAGAGAGAGAGTGTGAGAACTGAGAGATGATGAGATTTGGAATTTGCTCAA 1149
DB 1347 AATTCAGAGGTTGAAGAGTGAATGTATTTCTGAGAGTGAATATTTGAGAGTGC----- 1401

QY 1150 GAAGAAATTTCTATTCCTGCTGCTGAGACTTATTAATCAATCACTTCCACTGATTTG 1209
DB 1402 -GAGCAATGACATATTAACAGCGTTAATGTTGAGTACAAATGATCTTCCGACATTTA 1460
QY 1210 AGACAACTCTTATTAATTTGTCAGATATTCCTCAAGAGTACCGAAATGGAAGAGAAAT 1269
DB 1461 AAGCATGCTTTCTTTTGTGCAATATTTCTTAAAGTTATTCATTTAGAGAAAGACAA 1520
QY 1270 CTATCTCTCTGTGAGTGCATGATGTTTATTTTATGAAAGAACTTGAAGCTAGAG 1329
DB 1521 GTTATTCATCTATGATGATTTGCCAATGCTGTGTACCTGTGAAAGATGAATTAATCAAG-- 1578
QY 1330 AATGATGATTAAGATGAGATGAAATTAATTAATTAATTAATTAATTAATTAATTA 1389
DB 1579 -ATTGAGCAACCAATTTCTTCTGAGTTGAGTTCAAGATCATTAATTTGAAGGCTCCA 1637
QY 1390 GTTAAATCTG 1399
DB 1638 AATCCTTCTG 1647

RESULT 2
US-09-004-838-1
; Sequence 1, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF INVENTION: Confering Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Binhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..4208
; OTHER INFORMATION: /note= "RLGIA"
; US-09-004-838-1

Query Match 6.8%; Score 202.6; DB 3; Length 4208;
Best Local Similarity 49.2%; Pred. No. 4.4e-48;

Matches 740; Conservative 10; Mismatches 704; Indels 51; Gaps 7;

QY 10 GCCTTCCTCAAGTCTGTAGACAACTGACTGTTTCATCCAGGGGAACTTGATG 69
DB 1120 GCTTCTTACAGTGTGTTTGAAGCTGSCATTTGAAGCTTGAAGAAATTTGTCG 1179
QY 70 ATCTCTGTTTAAAGATGAGTTCGAAAAGCTTCAAGACGTTTAACTAACATCAAGCT 129
DB 1180 TCCAAAAGAAATTAATCTAGCTTAAGAAATTAAGAGACATTAAGCAAAATCCAAAGAT 1239
QY 130 GTCCTAAGAGATGCTCAGAAAGCAATTAAGAGACAGGCAATTAAGAAATTTGTCAG 189
DB 1240 CTGCTTAAGAGATGCTTCCAGAAAGAAATTAAGAGCCGTTAAAGATGCTGAT 1299
QY 130 AAATCAATGCTGTCATATGAGGCTGATGACATCTTGAGCAATTAAGTAAATCTGAGCA 249
DB 1300 GATCTCCACATTTGGCTTATACATAGACGACTTATGATGATTTGCACTGAAGCT 1359
QY 250 CCAATTAGAAGAGAGAAAGAAATATAGG-----GTGTTATCATCCAAACGTTATC 300
DB 1360 GTTCAMCGTAGTTGACGAGAGAGGTTGAGGCTCTCCAGTATGTTAAGAAATCTAATC 1419
QY 301 ACTTTTCGTACAAAGATTGGGAAAGATGAAAAGATTATGAGAAATGATGATTAAT 360
DB 1420 CCAGATGTTGACAAAGTTTCTCAAAAGTAAATAGGATGCAAGCCAAAGTTATGATAT 1479
QY 361 GC-----AGCGAAGCAATTAAGTTTCATTTGGATGAAGAGAT 399
DB 1480 GGCACCAAGTTACAAAGAACTGTGTAAGAGCAAAATTAATCTTGTTTAAATGATTAACA 1539
QY 400 ATAGAGAGCAAGTTGCTACACGCCAAACAGGTTTGTGTTGATGAACCAACAGTTTAT 459
DB 1540 TATGAAAAGCCAAAATTAAGAAAGTATAGGCGTCTTTGATGATGAAGCGTACTGTC 1599
QY 460 GGAAGAGCAAAAGAAAGAGACAGATAGTGAATTCCTGAT-----AAACATGTTAGC 513
DB 1600 GGACCTGAAGATTAAGAAATTAATGCTGAGAAAGCTTTGGGAGATTAAGATCAATCA 1659
QY 514 AATGCCAAACACTCCAGTCTCCCAATTAATGTTGATGGGGGAGCTGGAAGAGCACT 573
DB 1660 GGGAGTCAAACTTCAAGATCTGCGCCAAATGTTGATGGGGGAGTTGTAACAACT 1719
QY 574 CTTGCCCAATGCTCTTCATGATCAGAGATTAATGAGCATTTCCATCCCAATATATG 633
DB 1720 CTAGCTAAGCTTTTGTATGATGAAGAAAGAGAGATCACTTGAAGCTCAGGCTTGG 1779
QY 634 ATTGTGCTCGAAGATTTTAATGAGAAAGGTTGATTAAGAAATTTGATCAAT 693
DB 1780 GTTGTGTTTCTGATGAGTTCAGTGTCCCAATATAGCAGATTAATTAATCAATCTGTG 1839
QY 694 GAAGAAAGTCACTTGTTGGCATGAGCTTGCTCCATTCAAAGAGCTTCCGAGACTTG 753
DB 1840 ACTGGGAAAGAGAGAGATTTGAAGACTTAACTGCTTCAAGAGCTTAAAGAAA 1899
QY 754 CTGAATGAAAAAATATTTGCTCGTTAGATGATGTTGATGAAGATCAAGATTAAG 813
DB 1900 CTTAGGAACACGACTTTTCTAATATTTTGAATGATGTTGCTGGAAGCATATGAT 1959
QY 814 TGGGCTTAAGTAAAGCAAGCTTGAAGTTGAGCAAGTGGCGCTTCTGTTTAACT 873
DB 1960 TGGGGAAGATTAAGTGGGCAATTCCTTGCGGGGCTCTCCGAAATGAAATATCATGCA 2019
QY 874 ACTGCTCTGAAAAGTTGATGATTAATGGAACATTTGCAACCATTAATGATGCAAT 933
DB 2020 ACTGGAAGAGCAATGCTCAGAAAGCTGGGCTTTTCTCAACAAAGCCCTCTGAGGCT 2079
QY 934 TTGCTCAAGAGATTTGTTGTTGTTCAAGCAAGCTTTGGGACCAAGAA--A 990
DB 2080 CTATCAAGAGATGATGCTTTGCTTTGTTGCTCAACAGCAATTTGGTGTAACAACTTT 2139
QY 991 GAAATTAATCTTAATCTTGCTGCTATCGAAAGAGATTTGAAAAATTTGGTGTTG 1050
DB 2140 GATTCACATCCAACTAAGGCCACATGGAAGCTGTTGTGAAGAAATGATGATGCTTA 2199

QY 1051 CCTTAGACGCTAAAACTCTTGAGGATTTTGGCTTTAAGAGAAAGAACAGTGG 1110
DB 2200 CCTTAGCTTTAAGAACACTTGAAGGTTATTAAGAACAAAACAGAGAAACAAATGG 2259
QY 1111 GAACATGAGAGATAGTGAATTTGGAATTTGCAAGTTCCTCAAGAAAGATTTATTCGCT 1170
DB 2260 AAGGAGCTGTTGATAGTGAATATGAGGTTAGAGAAAGACGA--TGAGATTTGTCG 2316
QY 1171 GCGCTGAGACTTAGTTATCATCACCTTCATTTGATTTGAGCAATGCTTAATATGTT 1230
DB 2317 GCTCTTAAGCTTAAGCTAAAGATTTTCTGCGCTTGAAGCTTTTGTTCATATGTC 2376
QY 1231 GCAGATTTCCCAAGATACCCGAATGGAAGAAAGAAATCTAATCTCTCTGATGCA 1290
DB 2377 TCTTGTGTTCCCAAGACTATGAGTTTGAAGAGAGATGATTTCTATTTGATGCA 2436
QY 1291 CATGGTTTAT--TTATGGAAGAAAGCTTGAGCTAGAGAAATGATGATGAAGTA 1347
DB 2437 GAAGGTTTTCACCAACCAACTATYAAACAACTCAAGCAACGKTGGCTTGGAATAT 2496
QY 1348 TGAATGATTAATCTGAGGCTTTCTTCCAGAGATGGAATTAATCTGTCAAAT 1407
DB 2497 TTTAAGATTTTGTCAAGTCTTTTTCGA-----CATGCTCTAATRRCAATCS 2550
QY 1408 TATTTCAAGATGATGATCTCATTCATGATCTGGCAACATCTTATTTTGGCAAGCA 1467
DB 2551 TTGTTTGAATGATGATGATTAATGATTTGGCTACATTTGTTGCTGGAATTTTTT 2610
QY 1468 TCAAG 1472
DB 2611 TCAAG 2615

RESULT 3
US-09-004-838-70
; Sequence 70, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmere, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Confering Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Binhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:

LENGTH: 4163 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY:
 LOCATION: 1..4163
 OTHER INFORMATION: /note="RLG1-E169"
 US-09-004-838-70

Query Match 6.8%; Score 201; DB 3; Length 4163;
 Best Local Similarity 49.1%; Pred. No. 1.3e-47;
 Matches 739; Conservative 10; Mismatches 705; Indels 51; Gaps 7;

10 GCTTCCCTCAAGTCTGTAGACAATCTGACTGTTTTCATCCAAAGGGAACCTTGAGT 69
 1120 GCCCTTCTTACAGAGTGTGTTTGAAGAGCTGGCAATGAAAGCTTGAAAGAAATTTGCGC 1179
 70 ATTCTGTGTTTAAAGATGATGTTCCAAAGCAAGTTCAAGCAAGTTTACTACATCCAGCT 129
 1180 TCCAAAAGATTAATCTGATCTGAGCTTAAGAAATTGAAGAGACATTTAGACCAAAATCCAGAT 1239
 130 GTGCTAGAAGATGCTCAGAAAGACAAATTGAAGACAAAGCAATGAAATTTGTTGAG 189
 1240 CTGCTTAACGATGCTCCAGAAAGAGTAACTAATGAAGCCGTTAAAGATGCGTAAT 1299
 190 AAATCAATGCTGCTGCAATGAGCTGATGACATCTTGAGCAATGTAATTAATCTGAGCA 249
 1300 GATCTTCAACATTTGGCTTATGACATGACGACTTACTGATGATGATTTGCAACTGAACT 1359
 250 CCAATTAGACAGAAAGAAACAATATG3-----GTGTTATCATCCAAAGCTTATC 300
 1360 GTTCAACGATGTTACGAGAGAGGTGAGGCTCTCCAGATGATGTAAGAAATTAATC 1419
 301 ACTTTTCTCACAAGATTTGGGAAAAGATGAAAGATTTAGAGAACTAGATTAAT 360
 1420 CCAGATTGTGCAAGATTTCTCAAAAGTATAGATGCAATGCAAGTTTATGATGATAT 1479
 361 GC-----ACGGAACGAATTTAATGTTTCAATTTGATGAAAGCACT 399
 1480 GCCACAGATTAACAAGAACTGCTAGAGGCAAAATTAATCTTGGTTTAAAGTGTAAACA 1539
 400 ATAGAGACAAAGTTCTACACGCCAAACAGTTTGTGTTGAATGAACAACAAGTTAT 459
 1540 TATGAAAGCCAAATTAATGAAGTATGAGGCTTTTGTGATGATGAAGGATGATCTC 1599
 460 GGAAGAGCAAAAGAAAGAGAGATAGTGAATCTGAT-----AAACATGTTAGC 513
 1600 GAGCGTGAAGATGATMAAGAAATTTGCTGGAAGAGCTGTGGGGATMAAGATGAATCA 1659
 514 AATGCCCAACACTTCCAGCTCCCAATACCTGGTATGGGGGAGCTAGAAAGACGACT 573
 1660 GGGAGTCAAACTTCAGATGCTGCCCTAGTTAGTTGGTGGAGTTGGTAAACAACCT 1719
 574 CTGCCCAATGCTTCTCAATGATCAGAGTAATGAGCAATTTCCATCCCAAAATATG 633
 1720 CTACTAGACTTTTGTATGATGAAGAAAGATGAAGATCACTTGAACCTCAGGCGTTGG 1779
 634 ATTGTGCTCGGAAGATTTAATGAGAAGAGTTGATGAAGAAATTTGATGATTAAT 693
 1780 GTTGTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1839
 694 GAAGAAAGTCACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 753
 1840 ACTGGGGAAGAAAGAGAGTTGAAGACTTAATCTGCTTCAAGAGCTCTTAAAGAGAA 1899
 754 CTGAATGAAAAAATTTGCTGCTTGAATGATGATGATGATGATGATGATGATGATGATG 813
 1900 CTTAGGAACGCTATTTCTAATGATTTTGGATGATGATGATGATGATGATGATGATGAT 1959
 814 TGGGCTAAGTTAAGACAGCTTGAAGTTGAGACAGTGGCGCTTCTGTTTCAACACT 873

Db 1960 TGGAGAAATTTAGTGGGCCCATTCCTTGGGGGCTCTCTGGAAGTATGATGACA 2019
 Qy 874 ACTGCTTTGAAAAGTTGATGATCAATTAATGGAACATTTGCAACCAATGATGCAAT 933
 Db 2020 ACTGGAAAGAGCAATCTCAGAAAGCTGGGCTTTTCTCATCAAGACCTCTGAGAGGT 2079
 Qy 934 TTGCTCAGAAAGATGTTGGTGTGTTGTATGATGACAGTGTGATTTGGGACCAAGA--A 990
 Db 2080 CTATCACAAGATGATGCTTGTGCTTGTGTTGCTCAACACGCAATTTGGTATCAAACTTT 2139
 Qy 991 GAAATTAATCTTAATCTTGTGGCTATGCGAAAGAGATTTGAAATAATGTTGGTGTG 1050
 Db 2140 GATTCACATCAACACTAGAGCCACATGAGAGACTGTTTGTGAGAAATGATGATGCTTA 2199
 Qy 1051 CCTTAGAGCTTAAACTCTTGAAGATTTTGGCTTTAAGAGAGAAAGACAGTGG 1110
 Db 2200 CCTTAGAGCTTAAAGACCTTGAAGATTTAAGACAAACAGACGAGAAACAATGG 2259
 Qy 1111 GAACATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1170
 Db 2260 AAGAGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2316
 Qy 1171 GCCCTGAGACTTATGATCAATCACTTCACTTGAATTTGAGACATGCTTTACATATGT 1230
 Db 2317 GCTCTTAGACTAAGCTACATGATCTTTCTGCGCTTGAAGCTRTTGTGATATG 2376
 Qy 1231 GCAATATTTCCAAAGATACCGAAATGAAAGGAAATTAATCTTCTCTGATGCA 1290
 Db 2377 TCTTGTGTTCCAAAGACTATGATGATGATGATGATGATGATGATGATGATG 2436
 Qy 1291 CATGTTTAT---TTATGAAAGAAACCTGGAGCTAGAGATGATGATGATGATG 1347
 Db 2437 GAAGGTTTTTGACCAACCAATTAATAAGATGAAAGAGAGAGAGAGAGAGAGAG 2496
 Qy 1348 TGGATTAATTAATCTGAGCTTTCTTCAAGATTTGAAGTTAATCTGATCAACT 1407
 Db 2497 TTTTAAAGATTTTGTCAAGATCTTTTCA-----CATGCTCTAATRCAATCS 2550
 Qy 1408 TATTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1467
 Db 2551 TTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2610
 Qy 1468 TCAAG 1472
 Db 2611 TCAAG 2615

RESULT 4
 US-09-004-838-6
 Sequence 6, Application US/0904838
 Patent No. 6350933
 GENERAL INFORMATION:
 APPLICANT: Michelmore, Richard W.
 APPLICANT: Shen, Kathy
 TITLE OF INVENTION: Procedures and Materials for
 TITLE OF INVENTION: Confering Pest Resistance in Plants
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/004,838
 FILING DATE: 09-JAN-1998

CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/781,734
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Einhorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 023070-07810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1662 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..1662
 OTHER INFORMATION: /note="RGLIF"
 US-09-004-838-6

Query Match 6.8%; Score 200.8; DB 3; Length 1662;
 Best Local Similarity 48.9%; Pred. No. 8.4e-48;
 Matches 720; Conservative 9; Mismatches 695; Indels 47; Gaps 6;

19 CAAGTCTGTTAGACATCTGATCTTTCATCCAAAGGGAACCTTGATGATTTCTGGT 78
 Db 59 CCAGATATCTTTGAAAGAGGCTTCTGAGCTTGAAGGCTTGAAGAGATCGCTGCTCATCG 118
 Qy 79 TTAAAGATGAGTTCGAAGAGCTTCAAGCAAGCTTACTACATCCAGCTGCTGTA 138
 Db 119 ATGATTTCTGAGCTCAAGAACTGAAGAGTCAATTAATCCAGATGATCTGTCTTAAT 178
 Qy 139 GATGCTCAGAAGAGCAATTTGAGAGCAAGGCAATAGAAATTTGGTTCAGAACTCAAT 198
 Db 179 GATGCTTCTGAGAGAGAAATAGTATGATGATCTGTTAAGAAATGCTGAATGCTTCCA 238
 Qy 199 GCTGCTGATATGAGGCTGATGACATCTTGAACGATGTAAACTGAGGCAACATTTGA 258
 Db 239 CATTTGCTTACGATAGACGACCTACTGATGATTTGGCAACGAAATCATGATCGT 298
 Qy 259 CAGAAAGAAACAAATATGGGTGTTA-----TCATC 289
 Db 299 GAGTTGACCCACGAGATCTGAGCCTCCACAGCTTGAAGAAAGTAATCCCACTGCTT 358
 Qy 290 CAAAGCTTATCACTTTTCTGCAAGATTTGGGAAAGATGAAAGATTTATGAGAAAC 349
 Db 359 GCACGATTTCTCACTAAGTATGATGATGCTTAACAGTTAGTATTAATTTACATCAAGT 418
 Qy 350 TAGATGTAATTCAGCGGACCAATTAAGTTTCAATTTGATGAAAGACTATAGAGAC 409
 Db 419 TACAAGAACTGTAGAGGAAAAAGATATCTTGGCTTAAGTGAAGAGTGAAGGCCAA 478
 Qy 410 AAGTTGCTACAGCCCAACAGGTTTGTGTTGA--ATGAACCAACAGTTTATGGAAG 466
 Db 479 AACCTACCAACAGAGATTTACAGACCTTTTGTAGATGATCTAGCATTTATGGTCTG 538
 Qy 467 ACAAGAAAGAGAGAGATGATGAAATCTGATTAACATGTTAGCAATGCCCAACAC 526
 Db 539 AAGGTGATAGAGATCTTCTCCATAGCTGCTGAGAGATGAACCAAGTATGAAACT 598
 Qy 527 TTCCAGTCTCCCAATCTTGTGATGAGGAGGACTAGAAAGACGACTTTGCCCAATG 586
 Db 599 TTAGCATGCTCAATATGTTGTATGAGGTGAGTGAAGACGACTTACATGACTT 658
 Qy 587 TCTTCAATGATCAAGAGATTAATGAGCAATTTCCATCCCAAAATATGATTTGTCTCG 646
 Db 659 TGTATGACGAGATGCAAGAGATCACTTCAAGCTCAAGCGGTGTTGTGTCTG 718
 Qy 647 AAGATTTTATGAGAGAGTTGATTAAGAAATTTGATTAATCTATTAAGAAAGTCAAC 706

Db 719 ATGATTTGATATCTCAATTAAGCAAGTATCTTCAATCATAGTGTGAGAAC 778
 Qy 707 TTGGTGGATGATGATTTGGCTCCACTTCAAAAAGCTTGGGACTTGTGTAATGGA 766
 Db 779 AAGATTTTAAAGACTTAAATCTCTCAAGTACGTGAAGAAAGATTTCAAGAAAC 838
 Qy 767 AATATTTGCTGCTTATGATGATGTTGGAATGAAGATCAAGATAGTGGCTAAGTTA 826
 Db 839 GATTTCTTTTGTCTGATGATATTTTGAAGTGAAGCTATACGAATGGAATTTCTG 898
 Qy 827 GACAAAGCTTGAAGGTTGAGCAAGTGGCGCTTGTCTTCAACCACTACCTGCTTGA 886
 Db 899 CACGTCAATTTCTGACAGGGGCAACAGAGTAAATATATATATATATATATATATAT 958
 Qy 887 AGTTGATCAATTAATGGAACATTTGCAACCATATGATTAATGTCAAATTTGTCTA 946
 Db 959 CGTTGCTAACCAACTGGTTACAAATCAACCTTCAACCTTTCGTTTGTACATGATA 1018
 Qy 947 ATTTGGTGTGTTGTCATGCAAGTGCATTTGGGCAACAGA--AGAAATTAATCTTA 1003
 Db 1019 ATGCTTGTCTTATTTCTGTCAGATGATGATGATGATGATGATGATGATGATGAT 1078
 Qy 1004 ATCTTGTGCTATGGAAGAGATTTGGAATAATGTTGTGTGCTTACCACTA 1063
 Db 1079 CACTTAACCAACAGAGTGAAGATTTGTAATAATGATGACGGTTTACATTTGCTTT 1138
 Qy 1064 AAATCTTGAAGATTTTGTGCTTGAAGAGAAAGAAACAGTGGGAAATGTGAG 1123
 Db 1139 TTGCACTTGGAGATTTGTGARGAACAAACAGATGAGAAAGATGAAAGATGTTGA 1198
 Qy 1124 ATATGAGATTTGGAATTTGCTCAGAGAAAGATTTCAATTTCTGCTGCTGAGACTTA 1183
 Db 1199 ATATGAAATATG--GGGTCAAGAAAGAGATGATGATTTGCTTCACTTA 1255
 Qy 1184 GTTACCATCACTTCACTGATTTGAGACATGCTTACATATTTGTCAGATTTCCAA 1243
 Db 1256 GCTACATGATCTCTGCTCTTGAAGAGTTGTTGATGATGCTCTGTTTCCAA 1315
 Qy 1244 AGATACCGAAATGGAAGAGAAATCTATCTCTCTGATGAGCAATGTTTAT-- 1301
 Db 1316 AAGATATGTTGCTGATAGAGAGATGATTTGTTGTGATGAGCAAGAGGTTTTC 1375
 Qy 1302 -TTATGAAAGAGAACTTGGAGTAGAGATGATGATGATGATGATGATGATGAT 1360
 Db 1376 ACCAATCAACACAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1435
 Qy 1421 ATGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1451
 Db 1490 ATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1520

RESULT 5
 US-09-004-838-2
 Sequence 2, Application US/09004838

GENERAL INFORMATION:
 Patent No. 6350933
 APPLICANT: Michellmore, Richard W.
 APPLICANT: Meyers, Blake
 TITLE OF INVENTION: Procedures and Materials for
 CONFERRING PEST RESISTANCE IN PLANTS
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townend and Townend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JUN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..2353
OTHER INFORMATION: /note= "RLG1B"
US-09-004-838-2

Query Match 6.6%; Score 196.6; DB 3; Length 2353;
Best Local Similarity 48.8%; Pred. No. 1.7e-46;
Matches 767; Conservative 1; Mismatches 754; Indels 51; Gaps 7;

QY 10 GCTTCTCTCAAGTCTGTTAGACATCTGCTTCTTCATCCAGGGAATCTTGATTG 69
DB 298 GCGTCTTTGGGGTCTTTGAAAGCTGCTTGAAGCTTGAAGAGGCTTGCTTGC 357
QY 70 ATTCTGTTTAAAGAGAGTTCGAAAGCTTCAAGCAGTTTACTACATCCAGCT 129
DB 358 TCCAAAGTAATTCAGAGAGCTCGAGAAATGTAATGCTCATGATCAATTAAGCT 417
QY 130 GTGCTAGAAAGTCTCAGAGAGCAATTCAGAGCAAGGCAATTAAGAAATGGTGGAG 189
DB 418 CTGCTCAATGATGCTTCTCAGAGAGAAATTAAGTAAGAGCTTTAAAGAAATGGTGA 477
QY 190 AAATCTCAATGCTGCTCATATGAGGCTGATGACATCTTGAAGAATGTAAATCGAGCA 249
DB 478 GCTCTTCAACATTTGCTTACGACATAGATGATCTTGGCGATTGGCAACCAAGCT 537
QY 250 CCAATTCAGAGAGAGAAACAATATGAGGTGTATCATCCAAACGTTATCACTTTTCT 309
DB 538 ATCCATGCTAATGTTCTCTGAGGAATACGGGCCACCATCAACCAAGTAACGAAGTTAAT 597
QY 310 CAC-----AAGATTGGGAAAGAGTAAAGATTATG 342
DB 598 CCAATCTGTTTCTCTAGTTTGTCAAGTACTAAGATGGCAACAGATACATTAATTTACC 657
QY 343 GAGAAATCTAGATGTAATTCAGCGCAAGCAATTAAGTTTCAATTTGATGAAGACATATA 402
DB 658 AGCAAGTTTACAAAGACTATTAAGAGAGAAATATCTTGATATATGTGAATTTGGTGA 717
QY 403 GAGAGCAAGTTGCTACACGCCCAACAGCTTTTGTTTGATGAACAACAAGTTTATGA 462
DB 718 AGCCGAAATCTTGAATATGAATAATCAGAGACCTCTGTGCTAGATCCATCTAGATTTGTT 777
QY 463 AGAGCAAAAGAAAGAGAGAGATAGTGAATAATCTGATTAACAATGTTAGCAATGCCCA 522
DB 778 GGAGCGACAGATATGAAGAGAGCGTGTCTTCAAGCTATA---TGAACATGTGATAGA 834

QY 523 AACCTTCAGTCTCTCCCAATCTTGATATGGGGGAGCTAGAGAAAGACCTCTTGCCCA 582
DB 835 AACTTTAGCATCTTCCCAATAGTTGTATGGGTGGTTAGTAAGACCACTTAAGTAGTA 894
QY 583 ATGGCTTCAATGATCAGAGATTAATGAGACTTTTCATCCCAATATATGATTTGTGTC 642
DB 895 CTTTGTATGATTAATAATGCAAGTGAAGATCACTTCGAACCTCAAGGGCTGGTTTGTCT 954
QY 643 TCGAAGATTTTAATGAGAGAGGTTGATTAAGAAATGTGATATCTATTAAGAAAG 702
DB 955 TCTGATGAGTTGATATCTTCTGATATAGCAAAACCAATTTTCAATGATATAGAGGGGGA 1014
QY 703 TCACCTGGTGCATGAGCTTGAGCTCACTTCAAAAGAGCTGGGGCACTTGATATGA 762
DB 1015 AACCAAGTTTAAAGATTAATTAATCTGCTTCAGGTGCTTTAAAGGAAATCTCAAG 1074
QY 763 AAAAAATATTTGCTCGTCTTATGATGATGTTTGAATGATCAAGATTAAGTGGCTAG 822
DB 1075 AAACGATTTTCTGTTGTTCTGATGATGATATGAGCGAGCTATACTGATTTGGAAAT 1134
QY 823 TTAAGACAAGCTTGAAGGTTGAGCAAGGCGCTTCTGTTCAACCACTACTCTGCTT 882
DB 1135 CTAGAACGTCATTTCTAGAGAGGACACAGAAAGTAAGTAATCATCACACCCGCAAG 1194
QY 883 GAAAGGTTGATCAATTAATGAGGAACATTCGAACCATATGAAATTTGCAATTTGTC 942
DB 1195 TTGCTGTTGCTTAACCAATTTGGGTCATGATCAACCATATTTGCTGATTTGTCA 1254
QY 943 GAAGATTTGTTGTTGTTGTTTCAATGCAACGTGCAATTTGGGACCAAGAA---GAATTAAT 999
DB 1255 GACATGCTCTATCTTAATTTTGTCAACGCAATTTGGTGAATATGCTTGAATCAAT 1314
QY 1000 CTTAATCTTGCTGCTATCGGAAAGAGATGTGAAAATATGATGATGCTCTAGCA 1059
DB 1315 CCGATCTTAAACCACTGATGAGGTAAGGTAATTTGAAAATATGATGATGCTTGGCT 1374
QY 1060 GCTAAATCTGTAAGGTAATTTGCGCTTAAAGAGAAAGAAAGAGAGCAATGTG 1119
DB 1375 TTGATTCGACTTGGAGGTTATTTAGAGCAAAAAGATGAGAAAGATGAAAGAACTA 1434
QY 1120 AGAGATATGAGATTTGAAATTTGCTCAAGAAAGATTTATTTCTGCTGCTGCTGAG 1179
DB 1435 TTGAATATGAGATGATGAGAGTTAGAAAGAGAGA---TGAGATTTATTCGGGCTTGA 1491
QY 1180 CTTAGTTACCATCATCTTCACCTTGAATTTGAGCAATGCTTATCATATGTCAGATTC 1239
DB 1492 CTAGCTATATATATCTTCTGCTCTTGAAGCAAGTGTTCATATATGCTCTTGTTC 1551
QY 1240 CCAAGGATACCGAAATGAGAAAGGAAATCTAATCTCTCTGATGACACATGTTTT 1299
DB 1552 CCCAAAGACTATGTTTCAACAGAGAGAGTTGATTTTATATGATGCAAGAGGTTT 1611
QY 1300 ATTTTATCGAAAG---AACTTGAAGCTAGAGATGTAAGATGATGAATGA 1356
DB 1612 TTGCACAATGAAATACAAACAAAGCAATGGAACGCTTGAATTTGAATTTTGAAGCA 1671
QY 1357 TTATCTTGAAGCTTCTTCTTCAAGAGATTTGAATTAATCTGTCATTAATTTCAAG 1416
DB 1672 TTGTGTCAAGGTCATTTTTCACATGCACTGATGACA-----AATGTTGTTTGTG 1725
QY 1417 ATGCATGATCTCATTCATGATCTGGCAACATCTCT-----ATTTTGGCAAGACATCA 1470
DB 1726 GTGCAAGACCTCATGATGATGATCTGGCCATCTGTGTGAGATTAATTTTAAGATTA 1785
QY 1471 AGAGCAATATCCGAAATATATGAGAAATTTACATCATATGATGTCATTTGTTTC 1530
DB 1786 GACATTTGAATGAAAAAGAGAGCTTTGAAAAATACGACATATGATGATTTTGTGTAG 1845
QY 1531 ACTAAAGTGAT 1543
DB 1846 AGTTACATGTTTT 1858

RESULT 6
US-08-930-996A-1; Sequence 1, Application US/08930996A
; Patent No. 6100449

GENERAL INFORMATION:

APPLICANT: FUHR, Robert
 APPLICANT: ESHED, Yuval
 APPLICANT: ORI, Naomi
 APPLICANT: PARAN, Ilan
 APPLICANT: ZAMIR, Daniel
 TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
 TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/930,996A
 FILING DATE: 09-DEC-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05272
 FILING DATE: 15-APR-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: IL 113,373
 FILING DATE: 13-APR-1995

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4946 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 299...3958

US-08-930-996A-1

Query Match 6.0%; Score 177.8; DB 3; Length 4946;
 Best Local Similarity 50.4%; Pred. No. 8.4e-41;

Matches 641; Conservative 0; Mismatches 567; Indels 63; Gaps 6;

91 TTCGAAAGCTTCAAGACGCTTACTCAATCCAGCTGCTGTAAGAAAGCTCAGAG 150
 425 TTTGGAAGCTGGGGGACATTTGCTTCTTCAATTGCTTAAGTGAAGAGAT 484
 151 AAGCAATTGAAGAGACAGCAATAGAAATTGGTTCAGAACTCAATGCTGCATAT 210
 485 AAGAAAGCATGATCAATTTGTGAGCCAGTGTTCATTAAGCTTCAAGTCTGTGAC 544
 211 GAGGCTGATGATCTTGAAGA-----ATGTAAACTGAGCACAATTAGACAGA 262
 545 GCTGTGAAAGCTTGAAGCAAGTCAATATGAAGCTTGAAGCTTAAAGTGAAGCA 604
 263 AGAAGAACAAATATGGGTATATCATCCAAAGCT---TATCATTTTGTGTCAAGATT 318
 605 AGCAACCGACAGATGAGACCTCAACTGTGCTGAGTGAATGATTTCTTTTAAACTA 664
 319 GGGAAAGAGATGAAGAAAGTTATGAGAACTGATGTATATGACGGAAAGCAATTAG 378
 665 AAGAGAAAGTTGAAGACACATTTTAAAGAACTGAGGTGTGAGAAAGCAATTGCTGC 724
 379 TTTCAATTGATGAAGAGCATATAGAG---ACAAGTTGCTACAGCCAAACAGGTTT 435

725 CTGGCTTAAAGAGCATTTTATTTCCAGCAACAAAGAACTAGAACCTTCAACTTCT 784
 436 GTTTTGAATGACCAAGTTTATGAGAAAGACAAAGAAAGAGCGATATGAAATC 495
 785 TTGGTGTATGATTTTGGATCTTTGGAAGAGATGAAATAGAAATTTGGTGGCCGT 844
 496 CTGATTAACAAATGTTAGCATGCCAAACACTTCCAGTCTTCCAAATCTTGTATGGG 555
 845 TTGTTGCTATGATACAAAGCCGAAATCTGGCTGATGTTCTTAATTTGTGGAATGGC 904
 556 GGAATAGAAAGAGACTCTTGGCCAAATGCTCTTCAATGATGAGAGTATGAGAT 615
 905 GGCATGGGTAAAGACACCTTGTCTTAAAGCGTTTACATGATGAGAGTGCAGAAACAT 964
 616 TTCCATCCCAAAATATGATGATTTGTCTCGAAGATTTTATGAGAAAGGTTGATTAAG 675
 965 TTGGTGTGACAGTTGGTTTGTGTGTTTGTGAGGATATGATGCTTCAAGAAATCCAAA 1024
 676 GAAATTTGATATCTATTG----- 694
 1025 GATTACTTCAAGAAATTTGATCAACTGACTTGAAGCTGATGACAAATCTTAATCAGCTA 1084
 695 -AAGAAAGTCACTTGGTGGATGAGACTTGGCTCCACTTCAAAAGAGCTTGGGACTG 753
 1085 CAAGTCAAAATTTGAAGCTGATGACAAATCTTAATGAGCTACAAATGGAAGGAAAG 1144
 754 CTGAATGGAAGAAATATTTGCTGCTCTAGATGATGTTGGAATGAGATCAAGATTAAG 813
 1145 CTGAATGGAAGAAAGTTTCTTGTGCTCTTGTATGATGATGAGATGATTAATCTCGAG 1204
 814 TGGGCTAAGTTAAGACAACTTTGAAGTTGAGCAAGTGGCGCTTGTCTTAACACT 873
 1205 TGGATGACTTGAAGAAATCTTTTTCAGAGGATATGAGAAATGATCATTTGTAACG 1264
 874 ACTGCTCTGAAAAGTTGGATCAATTAATGAGAACTTGCACCAATATGATTTGCAAT 933
 1265 ACAAGTAAAGAGATGTTGCTTGTATGATGATGATGATGATGATGATGATGATGAT 1321
 934 TTGCTCAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 993
 1322 CTGCTAGTGAAGCTCTTGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1381
 994 AT--AAATCTTAATCTTGTGCTATGCGAAGAGAAATGTAAGAAATGATGATGATG 1050
 1382 AAGAAATCCAGAAATTTGAAGAGATTTGAAGAAACAAATTTGAGACAAATGGAAGG 1441
 1051 CCTTACAGCTAAATCTTGTGAGATTTTGGCTTTTAAAGAGAAAGACAGTGG 1110
 1442 CCTTACCTCTTAAAGACCTTGTGATGTTTAAAGAGCAATATGAGAGATGATGATG 1501
 1111 GAATATGAGATATGAGATTTGGAATTTGCTCAAGAAAGATTTGATTTGCTGCT 1170
 1502 AGAAACATTTTACAGAAATGAAATGAGAGCTTCAAGTTGTTGAATGATATTTACA 1561
 1171 GCCCTGAGACTTATGATCAATCACTTCACTTGAATTTGAGACAAATCTTATATTTGT 1230
 1562 GCGCTAATGTTGAGCTCAATGATCTCCCTGCAATTTAAAGCAATTTGGCTTATTTGT 1621
 1231 GCAGTATTTCCAAAGATACCGAAATGAGAAAGGAAATCTATCTCTCTGATGCA 1290
 1622 GCAATATATCCCAAGATATCAATTTGCAAGAGCAAGTATATCACTGTGATGATGCT 1681
 1291 CATGCTTTTAT 1301
 1682 AATGCTCTGT 1692

RESULT 7
US-09-387-286-24

; Sequence 24, Application US/09387286
 ; Patent No. 6544733

GENERAL INFORMATION:

; APPLICANT: Rommens, Caius M T

APPLICANT: Zhang, Bei
APPLICANT: Swords, Kathy M
APPLICANT: Yan, Hua
TITLE OF INVENTION: A new method of identifying non-host plant disease
FILE REFERENCE: r gene patent
CURRENT APPLICATION NUMBER: US/09/387,286
EARLIER APPLICATION NUMBER: 60/098,402
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 24
LENGTH: 644
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-387-286-24

Query Match 3.5%; Score 104; DB 4; Length 644;
Best Local Similarity 54.2%; Pred. No. 8,6e-20;
Matches 281; Conservative 0; Mismatches 225; Indels 12; Gaps 3;

547 GGTATCGGGGAGCTAGGAAGACACTCTGCGCAATGCTTCAATGATAGAGAGTA 606
|||
76 GGCATGCGGGGAGTGGCAAGACACCTTGTAAAGCCGTTTACAAATGATAGAGGGTG 135
607 ATTGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAATGAGAAGAG 666
|||
136 AAGAAACATTTTGTGTTGAAGCTTGTTTGTCTGAGGACATGATGCTTTGCA 195
667 TTGATTAAGAAATTTGTAATCTATTGA-----GAAAGTCACTTGTGGCATGAGC 720
196 ATAAACAAAGGATCTTCMAAAATTTGAAATTTGACTCAAGAGATGTCACAAACAT 255
721 TTGGCTCCACTTCAAAAGAGCTTGGGACTTGTAATGAAAAAATTTGCTGCTC 780
256 CTTATACGCTTCAAGTCAAAATTTGAAGAAAGCTTGAAGGAAAGATTCCTATTGTT 315
781 TTGATGATGTTTGAATGAAGATCAAGATTAAGTGGGCTTAAGTTAAGCAAGTCTTGAAG 840
316 TTGATGATGTTTGAATGAAGATCAAGATTAAGTGGGCTTAAGTTAAGCAAGTCTTGAAG 840
841 GTTGAAGCAAGTGGGCTTGTCTTAACTACTACTGCTTGAAGAGTTGATCAATT 900
316 CAAGGAGATTAAGAGATTAAGATCAATTAAGACACCTTAAGATGATGCTTGAAG 435
901 ATGGGAATTTGCAACATTAATGATTAATTTGCAAAATTTGCTCAAGAAAGATTTGTTGTTG 960
436 ATGGTTTGGGGCAATCTAGC---TGGGAATCTGTCTAGTGAAGACTCTTGGGCTTTA 492
961 TTCTATGCAAGTGTATTTGGGCAACAGAA--AGAAATTAATCTTAATCTTGTGGCTATC 1017
493 TTCAACGACATTTCACTGAAAAATAGGATCTGAGAAACATTCAGATTTGAAGAGTT 552
1018 GGAAGAGGATTTGAAAAAATGTTGTTGCTGCTC 1055
553 GGAAGAGGATTTGAAAAAATGTTGTTGCTGCTC 1055

RESULT 8
US-09-004-838-3
Sequence 3-3, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1036
OTHER INFORMATION: /note= "RLGIC"
US-09-004-838-3

Query Match 3.2%; Score 93.6; DB 3; Length 1036;
Best Local Similarity 48.2%; Pred. No. 1.3e-16;
Matches 375; Conservative 0; Mismatches 376; Indels 27; Gaps 3;

308 GTCAAGATTTGGAAAAAGATGAAAAATTTGAGAAATCTAGATGATTCAGCGG 367
254 GTATAGAGATGATGACAGGTTATGATGATTTGCCCTAAGTAAAGAACTGGTGAAG 313
368 AAGAAATTAATCTTGGTTTGAATGAAGACCTATAGAGACAAAGTTGCTACAGCCAA 427
314 CGAAATTAATCTTGGTTTGAATGAAGACCTATAGAGACAAAGTTGCTACAGCCAA 427
428 CAGGTTTGTGTTGAATGAAGACCAAGTTTGAAGAGACAAAGAAAGACGAGATAG 487
374 AGCGTNTTTGTTGATGATGCAAGGTATCATTTGACGTGAAGATGATTAAGAAAAATTCG 433
488 TGAATTCCTGAT-----AAACAATGTTAGCAATGCCCAACACTTCCAGTCTCCCA 541
434 TTCAAGAGCTGTTGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 493
542 TACTTGTTATGGGGGACTAGGAAGACGACTCTTGGCCCAATGCTTCAATGATCAGA 601
494 TACTTGTTATGGGGGACTAGGAAGACGACTCTTGGCCCAATGCTTCAATGATCAGA 601
602 GAGTAATTAAGCAATTTCCATCCCAAAATTAATGATTTGTCTCGAAGATTTTAATGAGA 661
554 AAGTGAAGATCACTTGAAGATCAAGGTTTGGGTTTGTCTGATGATGATGATGATGATGAT 613
662 AGAGTTGATTAAGAGAAATTTGATGATCAATTAATTAATTAATTAATTAATTAATTAAT 721
614 CCAATTAAGAGAGATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 673
722 TGGCTTCACTTCAAAAGAACTTGGGACTTGTGATGATGATGATGATGATGATGATGATGAT 781
674 TAAATCTGCTCAAGAAAGCTTAAAGAAAGCTTCAAGAAAGCTTCAAGAAAGCTTCAAGAA 733
782 TGAATGATTTTGAATGAAGATCAAGATTAAGTGGGCTTAAGTTAAGACAAAGCTTGAAG 841

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Blinhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..946
OTHER INFORMATION: /note="RLGID"
US-09-004-838-4

Query Match 3.0%; Score 88; DB 3; Length 946;

Best Local Similarity 48.1%; Pred. No. 5.1e-15;

Matches 277; Conservative 0; Mismatches 294; Indels 5; Gaps 1;

308 GTCAAGATTGGGAAAAGATGAAAAGATTATGAGAAAATGATGTAATTCAGCGG 367
245 GTTAGAGATGATCCAGTAAAGTAGATGATTCAGCAGGTTACAAAGATCGTAGAGG 304
368 AACGAATTAACTTATTTGATGTAAGAGATATGAGAGACAGTCTTACAGCCAA 427
305 CAAAAAATATCTTGTTAAGTGTGATTAACATATGAAAAGCCAAATTAAGAGTGTG 364
428 CAGTTTGTGTTGAATGAACACAAATTTATGAGAGACAAAGAAAGGACGATAG 487
365 AGGATCTTTGTGATGACAAAGTGTATTTTGGCGTTAGATGATGAAAATTTGA 424
488 TGAATCTGATTAACAATGTTAGCAATGCC-----CAACACTTCAGTCTCCCAAT 542
425 TGGAGAGCTGTGAGAGATTAAGATGATCCGAGTCMAAATTCACAGATCTGCCAT 484
543 ACTTGATGAGGAGGAGTGAAGAGACAGCTCTTCCCAATGCTTCAATGATCAGAG 602
485 AATTGATGAGGAGTGAAGTGAAGCAACTTACTGACTCTTGTGATGAAAAGAC 544
603 AGTATGAGATTTCCATCCCAAAATATGATTTGTGCTCGAAGATTTTAATGAGAA 662
545 AGTGAAGATCACTTGAATCTGAGGCTTGAGTTGTGTTCTGATGATTCAGATTTCT 604
663 GAGGTGTAAGAGAAATTTGATGATCTATTTGAAGAAAGTCACTTGTGCGATGACT 722
605 CAACATAGCAAAAGTATCTATCAATCTGTGACCGGAGAAAAGAGTTGAAGACTT 664
723 GGTCTCACTTCAAAAGAGCTTGGGACTTGTGATGAGAAAATTAATTTGCTGCTT 782
665 AAATCTGCTTCAAGAGCTTGTAGAGGAAATCAAAAACAACTATTTCTAATAGTTT 724
783 AGATGATGTTGAATGAAGATCAAGATAGAGGCTAAGTTAAGCAAGTCTGAAGGT 842
725 GATATGATGATGAGGAGAGTATGATGATTTGGAGAAATTAATGAGGCAATTTCTAT 784
843 TGGAGCAAGTGGCGCTTCTGTTCTAACCATACTCG 878

Db 785 TGGAGCTTGTGAAGATGAATATCATGACTACTCG 820

RESULT 12

US-09-004-838-10

/ Sequence 10, Application US/09004838
Patent No. 6350933

GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.

APPLICANT: Shen, Kathy

APPLICANT: Meyers, Blake

TITLE OF INVENTION: Procedures and Materials for
Conferring Pest Resistance in Plants

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998

CLASSIFICATION: 800
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Blinhorn, Gregory P.

REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: -

LOCATION: 1..544
OTHER INFORMATION: /note="RLGID"

US-09-004-838-10

Query Match 2.9%; Score 87.4; DB 3; Length 544;

Best Local Similarity 49.5%; Pred. No. 5.5e-15;

Matches 251; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

556 GGAATGAGAAAGAGCTTGGCCAAATGCTCTTCAATGATCAGAGATTAATGAGCAT 615
18 GGTCTGTGTAAGAGAGCTTGAAGATCTTGTATGAGAAATGCAAGGAGAGATCAC 77
616 TTCATCCCAAAATATGATTTGTGCTCGGAAATTTTAATGAGAAAGGTGATAAG 675
78 TTCGAATCTTAAGGCGGTGATGTTCTTGTATGATGATTTCTCAATATTAAGCAA 137
676 GAAATTTGATATCTATTTGAAGAAAGTCACTTGTGAGATGAGCTTGGCTCACTCAA 735
138 ATATCTTACATGATGATGAGGAGTGAAGAAACAAAGATTTACGACTTAACCTGCTTGA 197
736 AAGAGCTTGGGAGCTTGTGATGAGAAATTAATTTGCTGCTTGAATGATGATTTGG 795
198 GTACCTTTAAAGAGAGATCTCAAGAAAGATTTCTTGTGTTGATGATGATTTGG 257

QY 796 AATGAGATCAAGATAGTGGCTAAGTTAAGACAAGTCTTGAAGGTTGAGCAAGTGCC 855
DB 258 AGTGAACCTATACCGATTGGGAATTTTGAACCCCATTTCTTGCAAGGGGCACTTGA 317
QY 856 GCTTCTGTTCTAACCACTACTGCTTGAAGAGGTTGATCAATTATGGAACATTGCA 915
DB 318 AGTAGATTTATATATACCAACCGGAAGCTGATCTTTAAACAACTCGTTACATCAA 377
QY 916 CCATATGATTTGTCATATTTGCTCAAGAAATTTGTTGTTGTTGTCATGCAAGTTCG 975
DB 378 CCTTCAACCTTTGCGTTTTCACATGAGAAATGCTTTTATTTCTGTACATGCA 437
QY 976 TTGGGCAACCAAGA--AGAAATTAATCTTAATCTTGCGCTATGCGAAGAGATTTG 1032
DB 438 TTGGGTGAAGATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTA 497
QY 1033 AAAAAATGT 1059
DB 498 GAAAAATGT 524

RESULT 13

US-09-004-838-137
; Sequence 137, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmere, Richard W.
; APPLICANT: Shen, Kathy
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eibhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..544
; OTHER INFORMATION: /note= "RLG1B - Diana"
US-09-004-838-137

Query Match 2.9%; Score 87.4; DB 3; Length 544;
Best Local Similarity 49.5%; Pred. No. 5.5e-15;

Matches 251; Conservative 0; Mismatches 253; Indels 3; Gaps 1;
QY 556 GGACTAGAAAAGAGACTCTTGGCCAAATGGTCTTCAATGATCGAAGATTAATGAGCAT 615
DB 18 GGTGTGTGTGAAGAGACTCTTGAAGACTTTTGTATGAGAAATGCAAGGGAAGATCAC 77
QY 616 TTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAAAGAGATTGAAG 675
DB 78 TTCCAACTTAAAGGGGTGGTATGTGTTTGTATGAGATTTATATCTTAATATAGCAA 137
QY 676 GAAATTTGAATTAATTAATTAAGAAAGTCACTTGTGGCATGACTTGTCCACTTCAA 735
DB 138 ATTAATCTTAATGATGATGAGGATGAGAAACCAAGAAATTTTACGACTTAACTGCTTGA 197
QY 736 AAGAACTTGGGACTTGTCTGAATGAAATAAATTTGCTCGCTAGATGATGTTGG 795
DB 198 GTACCTTTAAAGGAAGATCTCAAGAAAGATTTCTTGTCTTGAATGATGTTGG 257
QY 796 AATGAGATCAAGATAGTGGCTAAGTTAAGACAAGTCTTGAAGGTTGAGCAAGTGCC 855
DB 258 AGTGAACCTATACCGATTGGGAATTTTGAACCCCATTTCTTGCAAGGGGCACTTGA 317
QY 856 GCTTCTGTTCTAACCACTACTGCTTGAAGAGGTTGATCAATTATGGAACATTGCA 915
DB 318 AGTAGATTTATATATACCAACCGGAAGCTGATCTTTAAACAACTCGTTACATCAA 377
QY 916 CCATATGATTTGTCATATTTGCTCAAGAAATTTGTTGTTGTTGTCATGCAAGTTCG 975
DB 378 CCTTCAACCTTTGCGTTTTCACATGAGAAATGCTTTTATTTCTGTACATGCA 437
QY 976 TTGGGCAACCAAGA--AGAAATTAATCTTAATCTTGCGCTATGCGAAGAGATTTG 1032
DB 438 TTGGGTGAAGATTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTA 497
QY 1033 AAAAAATGT 1059
DB 498 GAAAAATGT 524

RESULT 14

US-09-245-928A-15
; Sequence 15, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245,928A
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Mi resistance gene
US-09-245-928A-15

Query Match 2.8%; Score 82.4; DB 4; Length 9870;

Best Local Similarity 45.0%; Pred. No. 9e-13;

Matches 434; Conservative 0; Mismatches 521; Indels 9; Gaps 3;

QY 476 AGGACGATGATGAATCTGATTAACATGTTGACATGCCCAACACTTCCAGTCC 535
DB 4914 AGGAGGAGCAAACTTGTATCTTAAGAAAGTCAACGATGAGACCGGAGATTGATGTC 4973
QY 536 TCCCATATCTGTGTATGGGGGACTGAGAAAGCACTTGGCCCAATGCTTCAATG 595

Db 4974 TTTCATGACCGGATGCGGGTTCAGGTAACTATTGGCATACAAAGTATACAAATG 5033
Qy ATCAGAGATATATGAGCATTTTCATCCCAAAATATGATTTGTCTCGAAGATTTTA 655
Db 5034 ATAGTCAGTTTCTAGACATTTTTCATCTCGCATGTGACGCTCATCAGATATG 5093
Qy 656 ATGAGAGAGGTTGATTAAGAAATTTGATATCTATTGAAAGAAAGTCACTTGTGCA 715
Db 5094 ACGACAGAGAGTTGTGATACAAATTTTCAGTCAAGTATAGTGTCTCAGATTCAAATTTGA 5153
Qy 716 TGGACTTGCTTCACCTTCAAAAAGCTTCGGGACTTGTGTAATGAAAAATATTTTGC 775
Db 5154 GTGAGATATTTGATGTCTGTCTGTAATTTGCGGAAACAATGTTTGAAGAGTCTTA 5213
Qy 776 TCGCTTATGATGATTTTGAATGAAATCAAGATTAAGGGGCTAAGTTAAGACAGTCT 835
Db 5214 TTGCTTATGATGATGTGTGGATCTACTAC--TTGATGATGTTGACAAAGACCTTTTC 5270
Qy 836 TGAAGTTGAGACAGTGGCGCTTCTGTTCTAACCACTACTGCTTGAAGAGTTGGAT 895
Db 5271 CTGAAGCTAAGAAAGAGTATGATATTTTGAACAACCTCGAAGAAAGAGTGGCTTGC 5330
Qy 896 CAATTATGGAACATTCACACCAATGATGTAATTTGTCTCAAGAAAGTGTGCT 955
Db 5331 ATGGAAGCTGAACATGATCTCTTGAACCTTGAACCTGAAGACAGATGAAGTTGG 5390
Qy 956 TGTGTTATGCAAGTGCATTTTGGGCAACCAAGAAATTAATTTATCTTGTGCTA 1015
Db 5391 AACTTTTGAAGAAAGACATTTG--TAATGAAGTTCCTGATTAACATTAATGATG 5447
Qy 1016 TCGGAAGAGATTTGTGAAGAAATGTGTGTGCTCTTACAGACATA--AACTCTTG 1072
Db 5448 TCGGAAGAAATATGCGAAATTTTAAAGGCTTCTTGTGTGCTATCTGATTTGCTG 5507
Qy 1073 GAGTATTTTGGCTTAAAGAGAGAAAGACAGTGGAAACATGTGAGATGATGAGA 1132
Db 5508 GAGTCATTTGCTGGAGGAGAAAGAAAGAGTGTGCTGAAAGTCAAGATGATTTGA 5567
Qy 1133 TTGGAAATGCTCTCAAGAAAGTCTAATTTCTGCTGCTGCTGAGCTTGAATGATC 1192
Db 5568 GTTCTTTATTTTGAACAGTGAAGTGAAGTGAATTAATTAATTAATTAATTAATG 5627
Qy 1193 AACTTCACTGATTTTGAAGACATGCTTATTAATTTTGAAGTATTTCCAAAGATACG 1252
Db 5628 ATTTACCAATCACTCAAGCATGCTTCTTCACTTTTGAAGTGTGCGGAGACATCTC 5687
Qy 1253 AAATGAAAGAGGAATCTAATCTCTCTGTGATGCAATGCTTTATTTATGAAAG 1312
Db 5688 CTTTGACATCTAATTTGTTGACTGTTTATTTGGGTGCTGAAGATTTTGAAGACGG 5747
Qy 1313 GAACTTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1372
Db 5748 AGATGAAGGATTAAGAAAGTGAAGATTTATATGATTAATTTTCCAGTACT 5807
Qy 1373 TCTTCAAGAGATTTGAAGTAAATCTGTCAAACTTTTCAAGATGATCTCATTTG 1432
Db 5808 TGTGATTTTGTTCATATGATAGTATGATATGATTTTCAATTTATGATCTTGTGC 5867
Qy 1433 ATGA 1436
Db 5868 ATGA 5871

RESULT 15
US-08-947-823-4
Sequence 4, Application US/08947823

GENERAL INFORMATION:

APPLICANT: Williamson, Valerie M.
APPLICANT: Kailashan, Irgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen

TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..3860
OTHER INFORMATION: /note="Copy 2 cDNA for M1 nematode
OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-4
Query Match 2.7%; Score 80.8; DB 3; Length 3982;
Best Local Similarity 44.9%; Pred. No. 1.5e-12;
Matches 433; Conservative 0; Mismatches 522; Indels 9; Gaps 3;
Qy 476 AGGACGATAGTGAATAATCTGATTAACAATGTTAGCAATGCCCAACACTTCAGTCC 535
Db 1663 AGGAGGAGACAACTGATTAACAAAGCTCACACAGTGACCCGCAATTAATGATCA 1722
Qy 536 TCCCAATCTGATGAGGGGAGCTAGAGAAAGACACTTGGCCAAATGCTTTCAATG 595
Db 1723 TTGATACACCGGATGCTCCGGGTTCAAGTAAATCTATTTGCAATTAATATGATG 1782
Qy 596 ATCAGAGATTAATGACATTTTCATCCCAAAATATGATGATTTGTCTCGAAGATTTTA 655
Db 1783 ATAGTCAGTTTCTAGACATTTTGAACCTTGTGATGATGATGATGATGATGATG 1842
Qy 656 ATGAGAGAGTGAATTAAGAAATTTGATGATCTATTTGAAGAAAGTCACTTGTGCA 715
Db 1843 ACGACAGAGAGTTGTGATACAAATTTTCAAGTATGATGATGATGATGATGATGATG 1902
Qy 716 TGGACTTGCTTCACCTTCAAAAAGCTTCGGGACTTGTGTAATGAAAAATATTTTGC 775
Db 1903 CTGAAGATTTGATGATGATGATTAATTTGCGGAAACAACATGTTTGAAGAGATCTTA 1962
Qy 776 TCGCTTATGATGATTTTGAATGAAATCAAGATTAAGGGGCTAAGTTAAGACAGTCT 835
Db 1963 TTGCTTATGATGATGTGTGGATCTACTACA--TTGATGATGATGACAAAGACCTTTTC 2019

QY 836 TGAAGTTGAGCAAGTGGCGCTTCGTTCTAACAACCTACTGCTCTTGAAAGTTTGAT 895
 Db 2020 CTGAAGCTTAAGAAAGAGATAGATTATTTGACAACTGAGAAAAGAGTGGCTTGC 2079
 QY 896 CAATTATGGGAACATTGCAACCATATGAATGTCAAATTTGTCTCAGAAGATTGTGGT 955
 Db 2080 ATGAAAGCTGAACATGATCTCTTGACCTTCGATTTGCTAAGACCAAGTGAAGTTGGG 2139
 QY 956 TGTGTTCATGCAAGTGTGATTTGGGACCAAGAAATAATCTTAATCTTGTGGCTA 1015
 Db 2140 AACTTTAGATTAAGAAAGACATTGG--TAATGAGATTGCCCTGATGAACTATTAGATG 2196
 QY 1016 TCGAAAGGAGATTGTGAAAATATGTGTGTGCTCTAGCACTAA--AACTCTTG 1072
 Db 2197 TCGTAAGGAATATACCGAAATTTGTAAGGGCTTCTTTGGTGGCTGATCTGATTTGCTG 2256
 QY 1073 GAGTATTTTGGCTTTAAGAGAGAAAGACAGTGGGAACATGTGAGAGATAGTGA 1132
 Db 2257 GAGTCATTGCTGGGAGGAAAGAAAGAGAGTGTGGCTTGAAAGTTCAAAGTAGTTGA 2316
 QY 1133 TTGGAATTTGCTCAAGAAAGTTCTATTCGCTGCTGCCCTGAGACTTATGATCCATC 1192
 Db 2317 GTTCTTTATTTTGAACAGTGAAGTGAAGTGAATTAAGATTAAATTAAGAC 2376
 QY 1193 ACCTTCACTTGATTTGAGACATGCTTTACATATTGTGACATTTCCCAAAGATACCG 1252
 Db 2377 ATTACCACTCACTCAAGCATGCTTGTCTTCACTTGGCAAGTTGGCGAAAGACATC 2436
 QY 1253 AAATGAAAAGGAAATCTAATCTCTCTGTGATGGCAATGTTTATTTATCGAAAG 1312
 Db 2437 CTTTGACATCTAATTTTCTGTTTACTGTTTATTTGGGTGCTGAAGGATTTGTGAAAAGACG 2496
 QY 1313 GAAACTTGAAGTGAAGATGATGATGAATGAATGATGATGAATGAATTAATTAAGGTCTT 1372
 Db 2497 AGATGAAGGATATGAGAAAGTGTGAAGATTATATGATGATTAATTTCCAGTAGCT 2556
 QY 1373 TCTTCCAAGAGATTGAATTAATCTGTCAAACTTATTTCAAGATGATGATCTCATTC 1432
 Db 2557 TGGTAATTTGTTCAATGATGATGATGATGATGATGATTTCCAAATTCATGATCTGTGTC 2616
 QY 1433 ATGA 1436
 Db 2617 ATGA 2620

Search completed: April 16, 2005, 20:42:22
 Job time : 508 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2005, 18:12:22 ; Search time 1570 Seconds
(without alignments)
11464.925 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967
Sequence: 1 atgcgtgaagcttcctcca.....ctcgtgtcttattatag 2967

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/BCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/ECTOS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09B_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2967	100.0	US-10-647-268-1	Sequence 1, Appli
2	2541.8	85.7	US-10-647-268-3	Sequence 3, Appli
3	2541.8	85.7	US-10-647-268-9	Sequence 9, Appli
4	2309	77.8	US-10-647-268-5	Sequence 5, Appli
5	2077.2	70.0	US-10-360-522-48	Sequence 48, Appli
6	1880.8	63.4	US-10-360-522-52	Sequence 52, Appli
7	1805.8	60.9	US-10-360-522-49	Sequence 49, Appli
8	1805.8	60.9	US-10-360-522-50	Sequence 50, Appli
9	1771.6	59.7	US-10-360-522-51	Sequence 51, Appli
10	1736.2	58.5	US-10-360-522-53	Sequence 53, Appli
11	1599.2	53.9	US-10-647-268-7	Sequence 7, Appli

12	274.4	9.2	2409	18	US-10-437-963-67879	Sequence 67879, A
13	269	9.1	3333	18	US-10-437-963-79971	Sequence 79971, A
14	268.6	9.1	3615	18	US-10-437-963-33626	Sequence 33626, A
15	268.6	9.1	3852	18	US-10-437-963-33659	Sequence 33659, A
16	265.6	9.0	2565	18	US-10-437-963-56879	Sequence 56879, A
17	257.8	8.7	2597	18	US-10-437-963-50413	Sequence 50413, A
18	255.2	8.6	3366	18	US-10-437-963-57476	Sequence 57476, A
19	242.4	8.2	6779	18	US-10-437-963-29812	Sequence 29812, A
20	236.6	8.0	3669	18	US-10-437-963-51007	Sequence 51007, A
21	236.2	8.0	2883	18	US-10-437-963-65578	Sequence 26579, A
22	234.2	7.9	4206	18	US-10-437-963-96637	Sequence 96697, A
23	232.4	7.8	5498	18	US-10-437-963-29817	Sequence 29817, A
24	217.6	7.3	2415	18	US-10-437-963-24753	Sequence 24753, A
25	212.2	7.2	3858	18	US-10-437-963-57795	Sequence 57795, A
26	211.4	7.1	3759	17	US-10-425-114-29667	Sequence 29667, A
27	201.8	6.8	2603	18	US-10-437-963-40346	Sequence 40346, A
28	201.8	6.8	3369	18	US-10-437-963-40347	Sequence 40347, A
29	192.6	6.5	2949	18	US-10-437-963-79939	Sequence 79939, A
30	192.6	6.5	4372	18	US-10-437-963-87934	Sequence 87934, A
31	184	6.2	2481	18	US-10-437-963-92298	Sequence 92298, A
32	183.6	6.2	2982	18	US-10-437-963-94718	Sequence 94718, A
33	182.6	6.2	3172	18	US-10-437-963-10860	Sequence 10860, A
34	181.4	6.1	3497	17	US-10-424-599-24653	Sequence 24663, A
35	181	6.1	2709	18	US-10-437-963-15352	Sequence 15352, A
36	180.8	6.1	3633	18	US-10-437-963-92921	Sequence 92921, A
37	180.4	6.1	3276	18	US-10-437-963-92169	Sequence 92169, A
38	177.6	6.0	2985	18	US-10-437-963-26581	Sequence 26581, A
39	177	6.0	1226	18	US-10-437-963-57477	Sequence 57477, A
40	174.6	5.9	708	17	US-10-424-599-25254	Sequence 25254, A
41	174.2	5.9	2229	18	US-10-437-963-6807	Sequence 6807, Ap
42	173	5.8	1158	17	US-10-424-599-97562	Sequence 97562, A
43	170	5.7	3822	18	US-10-437-963-100477	Sequence 100477, A
44	169	5.7	2067	18	US-10-437-963-100511	Sequence 100511, A
45	168.8	5.7	3447	18	US-10-437-963-17974	Sequence 17974, A

ALIGNMENTS

RESULT 1
US-10-647-268-1 Application US/10647268
; Sequence 1, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647.268
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 3193
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(3018)
US-10-647-268-1

Query Match 100.0%; Score 2967; DB 18; Length 3193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTGAAGCTTCTTCAAGTCTGTGACATCTGCTTTTCATCCAAAGGGA 60
DB	52	ATGCTGAAGCTTCTTCAAGTCTGTGACATCTGCTTTTCATCCAAAGGGA 111
QY	61	CTTGATGATTTCTTGTGTTTAAAGATGATGAAAAGCTTCAAGCAGCTTACTACA 120
DB	112	CTTGATGATTTCTTGTGTTTAAAGATGATGAAAAGCTTCAAGCAGCTTACTACA 171

Qy	121	ATCCAAAGCTGTCTAGAAAGATGCTCAGAAAGCAATTTGAAGACAAGGCAATAGAAAT	187
Db	172	ATCCAACTGTGCTTAGAAGATGCTCAGAAAGCAATTTGAAGACAAGGCAATAGAAAT	233
Qy	181	TGGTTGAGAAACCTCANTGCTGCTGCATATGAGGCTGATGACATCTTGGACGAACTGTA	240
Db	232	TGGTTGAGAAACCTCAATGCTGCTGCATATGAGGCTGATGACATCTTGGACGAACTGTA	291
Qy	241	ACTGAGCAACCAATTTAGACAGAAAGAAACAATAATGAGTGTTATCATCCAAAGTTATC	300
Db	292	ACTGAGCAACCAATTTAGACAGAAAGAAACAATAATGAGTGTTATCATCCAAAGTTATC	351
Qy	301	ACTTTTGTCAACAAGATTGGGAAAAAGATGAAAAGATTTAGAGAAACTAGATGTAATT	360
Db	352	ACTTTTGTCAACAAGATTGGGAAAAAGATGAAAAGATTTAGAGAAACTAGATGTAATT	411
Qy	361	GCAGCGGAACGAATTTAAGTTTCATTTGGATGAAAGGCTATATGAGAGACAAGTTGCTACA	420
Db	412	GCAGCGGAACGAATTTAAGTTTCATTTGGATGAAAGGCTATATGAGAGACAAGTTGCTACA	471
Qy	421	CGCCAAACAGGTTTGTGTTTGAATGAAACAACAAGTTATGGAAGAGACAAGAAAAAGAC	480
Db	472	CGCCAAACAGGTTTGTGTTTGAATGAAACAACAAGTTATGGAAGAGACAAGAAAAAGAC	531
Qy	481	GAGATAGTGAATTCCTGATTAACATATGTTAGCAATGCCCAACACTTCCAGTCTCCCA	540
Db	532	GAGATAGTGAATTCCTGATTAACATATGTTAGCAATGCCCAACACTTCCAGTCTCCCA	591
Qy	541	ATACTTGGTATGAGGGGAGCTAGGAAAGACGACTCTGCCCAATGCTCTTCAATGATCAG	600
Db	592	ATACTTGGTATGAGGGGAGCTAGGAAAGACGACTCTGCCCAATGCTCTTCAATGATCAG	651
Qy	601	AAGATTAATGAGATTTCCATCCCAAAATATGAGATTGTGCTCGGAAATTTAATGAG	660
Db	652	AAGATTAATGAGATTTCCATCCCAAAATATGAGATTGTGCTCGGAAATTTAATGAG	711
Qy	661	AAGAGCTTATAAAGAAATTTGAGAACTAATGAAAGAAAGCACTTGTGGCAATGAGC	720
Db	712	AAGAGCTTATAAAGAAATTTGAGAACTAATGAAAGAAAGCACTTGTGGCAATGAGC	771
Qy	721	TTGGCTCCACTTCAAAAGAGCTTGGGACTTGCCTGAATGAGAAAAAATATTTGCTCGTC	780
Db	772	TTGGCTCCACTTCAAAAGAGCTTGGGACTTGCCTGAATGAGAAAAAATATTTGCTCGTC	831
Qy	781	TTAGATGATGTTTGAATTAAGATCAAGATAGCTGGGCTAAGTTAAGACAAGCTTTGAAG	840
Db	832	TTAGATGATGTTTGAATTAAGATCAAGATAGCTGGGCTAAGTTAAGACAAGCTTTGAAG	891
Qy	841	GTTGAGCAAGTGGGCGCTTCTGTTTAAACACTACCTCGCTTGAAGAAAGGTGATCAATT	900
Db	892	GTTGAGCAAGTGGGCGCTTCTGTTTAAACACTACCTCGCTTGAAGAAAGGTGATCAATT	951
Qy	901	ATGGGAACATTGCCAACATATGAAATTTGTCAAATTTGTCTCAAGAAAGATTTGTTGTG	960
Db	952	ATGGGAACATTGCCAACATATGAAATTTGTCAAATTTGTCTCAAGAAAGATTTGTTGTG	1011
Qy	961	TTCAATGCAACGTCATTTGGGACCAACAAGAAATTAATCTTAATCTGTGGCTATCGGA	1020
Db	1012	TTCAATGCAACGTCATTTGGGACCAACAAGAAATTAATCTTAATCTGTGGCTATCGGA	1071
Qy	1021	AAGAGATTTGTGAAAAAATGTGTGTGTGCTCTTACGACGCTAAACAATCTTGAAGTAT	1088
Db	1072	AAGAGATTTGTGAAAAAATGTGTGTGTGCTCTTACGACGCTAAACAATCTTGAAGTAT	1131
Qy	1081	TTGGGCTTTAAGAGAGAAAGACAGTGGGAACAATGTGAGAGATAGTGAATTTGAAA	1140
Db	1132	TTGGGCTTTAAGAGAGAAAGACAGTGGGAACAATGTGAGAGATAGTGAATTTGAAA	1191
Qy	1141	TTGGCTCAAGAGAAAGTATTATTTCTGCTGCCGCGAGAACTTAGTTCACATCACTTCCA	1200
Db	1192	TTGGCTCAAGAGAAAGTATTATTTCTGCTGCCGCGAGAACTTAGTTCACATCACTTCCA	1251

Qy	1201	CTTGATTTGGACAACAAAGCTTTTACATATTTGTGCGAGTATTCCCAAAGGATACCGAATGSA	126
Db	1252	CTTGATTTTGGACAAAGCTTTTACATATTTGTGCGAGTATTCCCAAAGGATACCGAATGSA	131
Qy	1261	AAGGAAATCTAATCTCTCTCGAGAGGCAACAGTGTATTTATTTATTCGAAAGAAACCTTG	132
Db	1312	AAGGAAATCTAATCTCTCTCGAGAGGCAACAGTGTATTTATTTATTCGAAAGAAACCTTG	137
Qy	1321	GAGCTAGAGATGTAGGTATAGAAAGTAGAAATTAATTAAGTGTGAGTCTTTCTTCCAA	138
Db	1372	GAGCTAGAGATGTAGGTATAGAAAGTAGAAATTAATTAAGTGTGAGTCTTTCTTCCAA	143
Qy	1381	GAGATTAAGATTAATCTGCTCAAACTTTATTTCCAGAGCAAGATCTCAATGATGATCTG	144
Db	1432	GAGATTAAGATTAATCTGCTCAAACTTTATTTCCAGAGCAAGATCTCAATGATGATCTG	149
Qy	1441	GCAACATCTCTATTTTTCGCAAGCAATCAAGCAGCAATATCCGAAATAATTTAGAA	150
Db	1492	GCAACATCTCTATTTTTCGCAAGCAATCAAGCAGCAATATCCGAAATAATTTAGAA	155
Qy	1501	AATTACATCATATGATGATGCCATTTGGTTTCACTAAAGTGATCTTTCTTACTCTTTC	156
Db	1552	AATTACATCATATGATGATGCCATTTGGTTTCACTAAAGTGATCTTTCTTACTCTTTC	161
Qy	1561	CACCTGCAAGATTTGTCTCGTTGAGGAGCTAATCTAAGGACATATAAATTAAAGAG	162
Db	1612	CACCTGCAAGATTTGTCTCGTTGAGGAGCTAATCTAAGGACATATAAATTAAAGAG	167
Qy	1621	TTACCGTCTTCCATTGGAGATCTAGTACATTTAAGATACCTTAACTTGTCTGGCAATCT	168
Db	1672	TTACCGTCTTCCATTGGAGATCTAGTACATTTAAGATACCTTAACTTGTCTGGCAATCT	173
Qy	1681	AGTATTTCCGATCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTCGAGACTCTGATCTA	174
Db	1732	AGTATTTCCGATCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTCGAGACTCTGATCTA	179
Qy	1741	CATGCGTCTCATTCACTTTGTGTGTGCAAAAGAAACAAAGCAAACTTGTAGTCTTGA	180
Db	1792	CATGCGTCTCATTCACTTTGTGTGTGCAAAAGAAACAAAGCAAACTTGTAGTCTTGA	185
Qy	1801	AATCTTTTACCTGATGATGTTGCTATAGAGATGACCTTGATGCAACCAAGATAGATCTTTG	186
Db	1852	AATCTTTTACTGATGATGTTGCTATAGAGATGACCTTGATGCAACCAAGATAGATCTTTG	191
Qy	1861	ACATGCCCTTAAAGACTCTAAGTAGATTTTGTGTGGGAATTCAGAAAGAAAGTTGCACTT	192
Db	1912	ACATGCCCTTAAAGACTCTAAGTAGATTTTGTGTGGGAATTCAGAAAGAAAGTTGCACTT	197
Qy	1921	GGTGAATTTACGAAACCTGAATCTCTATGAGCTCAATTGAAATCACGCATCTTGGAGAGTG	198
Db	1972	GGTGAATTTACGAAACCTGAATCTCTATGAGCTCAATTGAAATCACGCATCTTGGAGAGTG	203
Qy	1981	AAGAATGATATGATGTGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCATTTCTTA	204
Db	2032	AAGAATGATATGATGTGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCATTTCTTA	209
Qy	2041	AGCATGAAATGGATGACGATGAACGTCCACGTATATATGAATCAAGAAAAGTTGAAGTG	210
Db	2092	AGCATGAAATGGATGACGATGAACGTCCACGTATATATGAATCAAGAAAAGTTGAAGTG	215
Qy	2101	CTTGAAGCTCTCAAAACGACACTCCAAATCTGATCTTATTAACATCAGGGGCTTCAAGGA	216
Db	2152	CTTGAAGCTCTCAAAACGACACTCCAAATCTGATCTTATTAACATCAGGGGCTTCAAGGA	221
Qy	2161	ATCCGTCTCCCAAGCTGAGATGAATCACTCAGTTTGTGAAAATGTGTTCTCTATTTGAATC	222
Db	2212	ATCCGTCTCCCAAGCTGAGATGAATCACTCAGTTTGTGAAAATGTGTTCTCTATTTGAATC	227
Qy	2221	ATCAGTTGCAAAAACGTGCTCATGCTTACACACCTTTGTGAGAGCTGCTTGTCTTAAAGT	228
Db	2272	ATCAGTTGCAAAAACGTGCTCATGCTTACACACCTTTGTGAGAGCTGCTTGTCTTAAAGT	233
Qy	2281	CTAGAGTTGTGGAAGGGGATCTGCGGAAGTGGAGATATGTTGATCTTGGATTTCCCTACAA	234

```
Db 2332 CTGAGATTGTCGAGGGGCTGCGGAGTGGAGTATGTTGATTCGAGATCCCTACAGA 2391
Qy 2341 AGAAGGTTTCATCTCTGAGAAAACCTTAATATAGCCAAATTTGGTAATCTGAAGAGATG 2400
Db 2392 AGAAGGTTTCATCTCTGAGAAAACCTTAATATAGCCAAATTTGGTAATCTGAAGAGATG 2451
Qy 2401 CTGAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 2452 CTGAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2511
Qy 2461 CTAATGTTGTTTATTCACAAACCTTTCTTCTGTCAGAAATTTGGTAGTGGGAGACAG 2520
Db 2512 CTAATGTTGTTTATTCACAAACCTTTCTTCTGTCAGAAATTTGGTAGTGGGAGACAG 2571
Qy 2521 TCAGATGCAATAGGTTTCAGTTCCATCTAATCTCATGAGCTTTACTTCCCTCCCAATT 2580
Db 2572 TCAGATGCAATAGGTTTCAGTTCCATCTAATCTCATGAGCTTTACTTCCCTCCCAATT 2631
Qy 2581 CGCTATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
Db 2632 CGCTATTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
Qy 2641 AATACTGTAATATCTCTTTTACTTCAATCTTAAGAGCTGCTACAGCCTGGCTAGT 2700
Db 2692 AATACTGTAATATCTCTTTTACTTCAATCTTAAGAGCTGCTACAGCCTGGCTAGT 2751
Qy 2701 CTCAATGCTTTGAGAGCATCTGAGAAATCATAGTTGTTATGCACTAGAGAGTCTCCCGAG 2760
Db 2752 CTCAATGCTTTGAGAGCATCTGAGAAATCATAGTTGTTATGCACTAGAGAGTCTCCCGAG 2811
Qy 2761 GAAGGTGGAAGGTTTAATTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2820
Db 2812 GAAGGTGGAAGGTTTAATTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2871
Qy 2821 CAATGTTTACCGAGAGAGATTCAGACACCTTAACAGCCCTCACAAATTTATCAGTTGAGTTT 2880
Db 2872 CAATGTTTACCGAGAGAGATTCAGACACCTTAACAGCCCTCACAAATTTATCAGTTGAGTTT 2931
Qy 2881 TGTCCAACTCTGGCCAGAGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
Db 2932 TGTCCAACTCTGGCCAGAGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2991
Qy 2941 CACATTCCTGCTGTTGTTATTTAG 2967
Db 2992 CACATTCCTGCTGTTGTTATTTAG 3018
```

RESULT 2

```
US-10-647-268-3
; Sequence 3, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155 02
; CURRENT APPLICATION NUMBER: US/10/647,268
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3595
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(487)
; OTHER INFORMATION: Spu11 protein
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (488)..(899)
```

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: (900)..(13432)
US-10-647-268-3
```

```
Query Match 85.7%; Score 2541.8; DB 18; Length 3595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 428 CAGGTTTGTGTTGAATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAGAGAGAGAGAGAG 487
Db 896 CAGGTTTGTGTTGAATGAACCAACAGTTTATGGAAGAGACAAAGAAAGAGAGAGAGAGAGAG 955
Qy 488 TGAATATCTGATTAACAATGTTAGCAATGCCCAACATTCAGCTCTCCCAATACCTG 547
Db 956 TGAATATCTGATTAACAATGTTAGCAATGCCCAACATTCAGCTCTCCCAATACCTG 1015
Qy 548 GTATGGGGGAGCTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
Db 1016 GTATGGGGGAGCTAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1075
Qy 608 TTGAGCAATTCATCCCAAAATATGAGATTGTCCTGGAGAGATTTTAATGAGAGAGGT 667
Db 1076 TTGAGCAATTCATCCCAAAATATGAGATTGTCCTGGAGAGATTTTAATGAGAGAGGT 1135
Qy 668 TGATTAAGAGAAATTTGATGAATCTATTGAAGAAAGTCACTTGTCGATGAGACTTGCTC 727
Db 1136 TGATTAAGAGAAATTTGATGAATCTATTGAAGAAAGTCACTTGTCGATGAGACTTGCTC 1195
Qy 728 CACTTCAAAAGAGCTTGGAGACTTGCTGTAATGAGAAAGAAATTTTGTGCTCTTAATG 787
Db 1196 CACTTCAAAAGAGCTTGGAGACTTGCTGTAATGAGAAAGAAATTTTGTGCTCTTAATG 1255
Qy 788 ATGTTTGAATGAAGATCAAGATAGTGGGCTAATGTAAGCAAGTCTTGAAGGTGAG 847
Db 1256 ATGTTTGAATGAAGATCAAGATAGTGGGCTAATGTAAGCAAGTCTTGAAGGTGAG 1315
Qy 848 CAACTGGCGCTTCTGTTCTAACACTACTCGTCTTGAAGAGTTGATCAATTAAGGAA 907
Db 1316 CAACTGGCGCTTCTGTTCTAACACTACTCGTCTTGAAGAGTTGATCAATTAAGGAA 1375
Qy 908 CATTGCAACCATATGATTTGCAATTTGTTCTCAAGAGATTTGTTGTTGTTGCTCAGC 967
Db 1376 CATTGCAACCATATGATTTGTTCTCAAGAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1435
Qy 968 AACGTGATTTGGGACCAAGAGAAATTAATCTTAATCTTGGGCTATCGGAAAGAGAG 1027
Db 1436 AACGTGATTTGGGACCAAGAGAAATTAATCTTGGGCTATCGGAAAGAGAG 1495
Qy 1028 TTGTGAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1087
Db 1496 TTGTGAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1555
Qy 1088 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
Db 1556 TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Qy 1148 AAGAGAGAGAGTTCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207
Db 1616 AAGAGAGAGAGTTCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1675
Qy 1208 TGAGACATGCTTTACATATTTGTCAGATTTCCAAAGAGATACGAAATGAGAAAGGAA 1267
Db 1676 TGAGACATGCTTTACATATTTGTCAGATTTCCAAAGAGATACGAAATGAGAAAGGAA 1735
Qy 1268 ATCTAATCTCTCTGATGAGCAATGTTTATTTATGCAAGAGAACTTTGAGCTAG 1327
Db 1736 ATCTAATCTCTCTGATGAGCAATGTTTATTTATGCAAGAGAACTTTGAGCTAG 1795
Qy 1328 AGAATGTAAGTAATGAAGTATGAAATGAAATTAATCTTGAAGGCTTCTTCCAGAGATG 1387
Db 1796 AGAATGTAAGTAATGAAGTATGAAATTAATCTTGAAGGCTTCTTCCAGAGATG 1855
```

QY 1388 AAGTTAAATCTGTCACAACTTATTTCAAGATGATGATCTCATTCATGATGTCGCAACAT 1447
DB 1856 AAGTTAAATCTGTCACAACTTATTTCAAGATGATGATCTCATTCATGATGTCGCAACAT 1915
QY 1448 CTGATATTTGGGAGAGACATCAAGACGCAATATCCGAGAAATATTTAGAAAATTACA 1507
DB 1916 CTGATATTTGGGAGAGACATCAAGACGCAATATCCGAGAAATATTTAGAAAATTACA 1975
QY 1508 TACATATGATGTCATGTCGTCCTTAAGTGTATCTTCTTACTCTCTTCCCATTCG 1567
DB 1976 TACATATGATGTCATGTCGTCCTTAAGTGTATCTTCTTACTCTCTTCCCATTCG 2035
QY 1568 AGAAGTTGTCTGTCGTCGTCCTTAAGTGTATCTTCTTACTCTCTTCCCATTCG 1627
DB 2036 AGAAGTTGTCTGTCGTCGTCCTTAAGTGTATCTTCTTACTCTCTTCCCATTCG 2095
QY 1628 CTTCATGAGATCTAGTATGATTAAGATACCTAACTGTCTGTCGCAATCTAGTATTC 1687
DB 2096 CTTCATGAGATCTAGTATGATTAAGATACCTAACTGTCTGTCGCAATCTAGTATTC 2155
QY 1688 GTAGTCTTCCAAACAGTATGCAAGCTTCAAAATCTGACAGCTTTGATCTACATGGCT 1747
DB 2156 GTAGTCTTCCAAACAGTATGCAAGCTTCAAAATCTGACAGCTTTGATCTACATGGCT 2215
QY 1748 GTCATTCACCTTGTGTCGCAAAAGAAAGCAAGCACTTGATCTTCAATCTTT 1807
DB 2216 GTCATTCACCTTGTGTCGCAAAAGAAAGCAAGCACTTGATCTTCAATCTTT 2275
QY 1808 TACTTGTATGTCATGATGATGATCTGTATGCCAAGATAGATCTTTGACATGCC 1867
DB 2276 TACTTGTATGTCATGATGATGATCTGTATGCCAAGATAGATCTTTGACATGCC 2335
QY 1868 TTAAGACTCTAGATGATGATGTCGTCGCAAAAGAAAGTTCACCTTGAT 1927
DB 2336 TTAAGACTCTAGATGATGATGTCGTCGCAAAAGAAAGTTCACCTTGAT 2395
QY 1928 TACGAAACCTGATCTCTATGATCTCAATGAAATCAAGCATCTTGAGAGATGAAATG 1987
DB 2396 TACGAAACCTGATCTCTATGATCTCAATGAAATCAAGCATCTTGAGAGATGAAATG 2455
QY 1988 ATATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGATCTTTAAGCATGA 2047
DB 2456 ATATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGATCTTTAAGCATGA 2515
QY 2048 AATGGATGACGATGAAAGCTCAGATATATGATGATGCAAAAGAAAGTGAAGTCTGAG 2107
DB 2516 AATGGATGACGATGAAAGCTCAGATATATGATGATGCAAAAGAAAGTGAAGTCTGAG 2575
QY 2108 CTCTCAAAACACATCTCAATCTGATCTTTAACAATCAGAGGGCTTCAGAGAAATCCGTC 2167
DB 2576 CTCTCAAAACACATCTCAATCTGATCTTTAACAATCAGAGGGCTTCAGAGAAATCCGTC 2635
QY 2168 TCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2227
DB 2636 TCCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2695
QY 2228 GCAAAAACGTCATGTCCTTACACCCCTTGGTGAAGCTGCTTGTCTTAAAAAGCTAGAGT 2287
DB 2696 GCAAAAACGTCATGTCCTTACACCCCTTGGTGAAGCTGCTTGTCTTAAAAAGCTAGAGT 2755
QY 2288 TGTGAGAGGGGCTCTGCGAAGTGAAGTATGTTGATCTGATTCCTTACAGAGAAAGT 2347
DB 2756 TATGAGAGGGGCTCTGCGAAGTGAAGTATGTTGATCTGATTCCTTACAGAGAAAGT 2815
QY 2348 TTCCATCTCTGAGAAAACTTATATACGCGAATTTGATCTGAAAGAGATGCTGAAAA 2407
DB 2816 TTCCATCTCTGAGAAAACTTATATACGCGAATTTGATCTGAAAGAGATGCTGAAAA 2875
QY 2408 AGGAG 2467
DB 2876 AGGAG 2935
-QY 2468 TTGTTATTCACACCTTCTTCTGTCAGAAATGATGATGAGGGAGACAAAGTCAGATG 2527

DB 2936 TTGTTATTCACACCTTCTTCTGTCAGAAATGATGATGATGAGGGAGACAGTCAGATG 2995
QY 2528 CAATAGGTTTCAGTTCATATCTATATCTCATGCTCTTACTTCCCTCAAAATTCGCTATA 2587
DB 2996 CAATAGGTTTCAGTTCATATCTATATCTCATGCTCTTACTTCCCTCAAAATTCGCTATA 3055
QY 2588 ACAAG 2647
DB 3056 ACAAG 3115
QY 2648 TGAATATCTCTTCTTACTTCAATCTTAAAGAGCTCTTACCAAGCTGCTAGTCTCAATG 2707
DB 3116 TGAATATCTCTTCTTACTTCAATCTTAAAGAGCTCTTACCAAGCTGCTAGTCTCAATG 3175
QY 2708 CTTTGAAGCATCTGGAATTCATATGTTGATGATGATGATGATGATGATGATGATG 2767
DB 3176 CTTTGAAGCATCTGGAATTCATATGTTGATGATGATGATGATGATGATGATGATG 3235
QY 2768 TGAAGGTTTAAATTCATCTACAGATATTCATACATACATCTGGAATGCTACATGTT 2827
DB 3236 TGAAGGTTTAAATTCATCTACAGATATTCATACATACATCTGGAATGCTACATGTT 3295
QY 2828 TACCGAGAGATGTCAGACCTTACACAGCCCTTCACAAAATTTATCAGTTGATCTCAA 2887
DB 3296 TACCGAGAGATGTCAGACCTTACACAGCCCTTCACAAAATTTATCAGTTGATCTCAA 3355
QY 2888 CACTGGCCAAAGCGGTGGAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2947
DB 3356 CACTGGCCAAAGCGGTGGAAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3415
QY 2948 CTGCTGTTTATTTATTTAG 2967
DB 3416 CTGCTGTTTATTTATTTAG 3435

RESULT 3
US-10-647-268-9
Sequence 9, Application US/10647268
Publication No. US20040237137A1
GENERAL INFORMATION:
APPLICANT: Oosumi et al., Teruko
TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
FILE REFERENCE: 0155.02
CURRENT APPLICATION NUMBER: US/10/647,268
PRIOR FILING DATE: 60/407,100
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 5028
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURES:
NAME/KEY: promoter
LOCATION: (1) ..(953)
OTHER INFORMATION: Potato Ub13 promoter
FEATURE:
NAME/KEY: gene
LOCATION: (973) ..(4566)
OTHER INFORMATION: Solanum bulbocastanum genomic Shu11
FEATURE:
NAME/KEY: CDS
LOCATION: (1029) ..(1459)
FEATURE:
NAME/KEY: Intron
LOCATION: (1460) ..(1871)
FEATURE:
NAME/KEY: CDS
LOCATION: (1872) ..(4404)
US-10-647-268-9

Query Match 85.7%; Score 2541.8; DB 18; Length 5028;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 428 CAGGTTTGGTTTGAATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 487
Db 1868 CAGGTTTGGTTTGAATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 1927
Qy 488 TGAATATCTGATTAACATGTTAGCAATGCCCAACCTTCCAGTCTCCCAATCTTG 547
Db 1328 TGAATATCTGATTAACATGTTAGCAATGCCCAACCTTCCAGTCTCCCAATCTTG 1987
Qy 548 GTATGGGGGGAAGTGAAGAAAGAGCTTGGCCCAATGCTTCAATGATCAGAGATTA 607
Db 1988 GTATGGGGGGAAGTGAAGAAAGAGCTTGGCCCAATGCTTCAATGATCAGAGATTA 2047
Qy 608 TTGAGCATTTTCATCCCAAAATATGAGATTTGTCTCGAAAGATTTTATGGAAGAGT 667
Db 2048 TTGAGCATTTTCATCCCAAAATATGAGATTTGTCTCGAAAGATTTTATGGAAGAGT 2107
Qy 668 TGATTAAGGAATTTGATGATCTATTTGAAGAAAGTCACTTGGGCAATGACCTTGGCTC 727
Db 2108 TGATTAAGGAATTTGATGATCTATTTGAAGAAAGTCACTTGGGCAATGACCTTGGCTC 2167
Qy 728 CACTTCAAAAGAGCTTCGGGACTTGTCTGAATGGAAGAAATATTTGCTCGCTTAGATG 787
Db 2168 CACTTCAAAAGAGCTTCGGGACTTGTCTGAATGGAAGAAATATTTGCTCGCTTAGATG 2227
Qy 788 ATGTTTGGATGAAGATCAAGATTAAGTGGCTAAGTAAAGCAAGCTTTGAAGGTTGAG 847
Db 2228 ATGTTTGGATGAAGATCAAGATTAAGTGGCTAAGTAAAGCAAGCTTTGAAGGTTGAG 2287
Qy 848 CAAAGGGGCTTCTGTTCTAACAACACTGCTTGAAGAGTTGATCAATTAATGGGAA 907
Db 2288 CAAAGGGGCTTCTGTTCTAACAACACTGCTTGAAGAGTTGATCAATTAATGGGAA 2347
Qy 908 CATTGCAACCATATGATTTGTCAATTTGTCTCAAGAGATTTGTTGTTGTTTCATGC 967
Db 2348 CATTGCAACCATATGATTTGTCAATTTGTCTCAAGAGATTTGTTGTTGTTTCATGC 2407
Qy 968 AACGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGAGA 1027
Db 2408 AACGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGAGA 2467
Qy 1028 TTGTAAGAAAAATGAGTGGTGGCTCTAGAGACCTAATCTTGAAGGTTATTTGGCTC 1087
Db 2468 TTGTAAGAAAAATGAGTGGTGGCTCTAGAGACCTAATCTTGAAGGTTATTTGGCTC 2527
Qy 1088 TTAAGAGAGAAAGACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGGCTC 1147
Db 2528 TTAAGAGAGAAAGACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGGCTC 2587
Qy 1148 AAGAGAAAGTTCTAATCTGCTGGCTCGCTGAGACTTAAGTACATCACTTGCACCTGAT 1207
Db 2588 AAGAGAAAGTTCTAATCTGCTGGCTCGCTGAGACTTAAGTACATCACTTGCACCTGAT 2647
Qy 1208 TGAACAATGCTTTACATATGTCAGATATCCCAAGAGATACCGAAATGGAAGAAAGGAA 1267
Db 2648 TGAACAATGCTTTACATATGTCAGATATCCCAAGAGATACCGAAATGGAAGAAAGGAA 2707
Qy 1268 ATCTAATCTCTCTGATGAGCAATGTTTATTTATTCGAAAGAAACTTTGAGCTAG 1327
Db 2708 ATCTAATCTCTCTGATGAGCAATGTTTATTTATTCGAAAGAAACTTTGAGCTAG 2767
Qy 1328 AGAATGATGATTAAGATGATGAATTAATCTTGAAGGCTTTTCTTCCAGAGATG 1387
Db 2768 AGAATGATGATTAAGATGATGAATTAATCTTGAAGGCTTTTCTTCCAGAGATG 2827
Qy 1388 AAGTAAATCTGATCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAT 1447
Db 2828 AAGTAAATCTGATCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAT 2887
Qy 1448 CTCTATTTTCGGCAAGCAGATCAAGCAGCATATCCGAAATATATGTAAGAAATTAACA 1507

Db 2888 CTCTATTTTCGGCAAGCAGATCAAGCAGCATATCCGAAATATATGTAAGAAATTAACA 2947
Qy 1508 TACATATGATGTCATGTTGTTTCACTAAGGATGTCCTTACTCTTCCCATGTC 1567
Db 2948 TACATATGATGTCATGTTGTTTCACTAAGGATGTCCTTACTCTTCCCATGTC 3007
Qy 1568 AGAATTTGTCCTGTAAGGGTGTCTTAATCTAATGACATTAATACTTAAGCAGTTACCGT 1627
Db 3008 AGAATTTGTCCTGTAAGGGTGTCTTAATCTAATGACATTAATACTTAAGCAGTTACCGT 3067
Qy 1628 CTTCATTTGAGATCTAGTACATTTAAGATCCTTAACCTTGTCTGGCAATCTAGATTC 1687
Db 3068 CTTCATTTGAGATCTAGTACATTTAAGATCCTTAACCTTGTCTGGCAATCTAGATTC 3127
Qy 1688 GTAGTCTTCCAAACAGTATTAAGAGCTTCAAAATCTGCAAGACCTTGAATCAATGCTC 1747
Db 3128 GTAGTCTTCCAAACAGTATTAAGAGCTTCAAAATCTGCAAGACCTTGAATCAATGCTC 3187
Qy 1748 GTCATTCACCTTGTGTTGGCAAAAGCAACCAACCTTGTAGTCTTGAATCTTT 1807
Db 3188 GTCATTCACCTTGTGTTGGCAAAAGCAACCAACCTTGTAGTCTTGAATCTTT 3247
Qy 3248 TACTTGAATGTTGCTATGATTAAGCTTGTATGCCAACCAAGATAGATCTTTGACATGCC 3307
Db 1808 TACTTGAATGTTGCTATGATTAAGCTTGTATGCCAACCAAGATAGATCTTTGACATGCC 1867
Qy 1868 TTAAGACTCTAAGATTAATTTGTGTGGGAAATTCGAAAGAAAGTTGCAATTTGAT 1927
Db 3308 TTAAGACTCTAAGATTAATTTGTGTGGGAAATTCGAAAGAAAGTTGCAATTTGAT 3367
Qy 1928 TACGAAACCTGAATCTCTAATGCTCAATGAAATCAAGCATCTTGAAGAGTGAAGATG 1987
Db 3368 TACGAAACCTGAATCTCTAATGCTCAATGAAATCAAGCATCTTGAAGAGTGAAGATG 3427
Qy 1988 ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGCATGA 2047
Db 3428 ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGCATGA 3487
Qy 2048 AATGAGATGACATGAAACCTCCACGTATATATGAAATCAAGAAAGTTGAATGCTTGAAG 2107
Db 3488 AATGAGATGACATGAAACCTCCACGTATATATGAAATCAAGAAAGTTGAATGCTTGAAG 3547
Qy 2108 CTCTCAACCAACATCTCAATCTGACTTGTTAACATCAAGGGGCTTCAGAGAAATCCGTC 2167
Db 3548 CTCTCAACCAACATCTCAATCTGACTTGTTAACATCAAGGGGCTTCAGAGAAATCCGTC 3607
Qy 2168 TCCGAGCTGATGATCACTCAAGTTTGAAGAAATGTTGCTCTAATGAATCATCACTT 2227
Db 3608 TCCGAGCTGATGATCACTCAAGTTTGAAGAAATGTTGCTCTAATGAATCATCACTT 3667
Qy 2228 GCAGAAACCTGCTACCTTACACCTTTGTTGAGCTGCTTGTCTAATAAAGTCTAAGT 2287
Db 3668 GCAGAAACCTGCTACCTTGTACACCTTTGTTGAGCTGCTTGTCTAATAAAGTCTAAGT 3727
Qy 2288 TGTGAGGGGGGCTGCGGAAAGTGAAGTATGTTGATCTCGAATTCCTTCAAGAAAGAGT 2347
Db 3728 TGTGAGGGGGGCTGCGGAAAGTGAAGTATGTTGATCTCGAATTCCTTCAAGAAAGAGT 3787
Qy 2348 TTCCATCTCTGAGAAACCTTAATATACGCGAATTTGTAATCTGAAAGATTTGCTGAAA 2407
Db 3788 TTCCATCTCTGAGAAACCTTAATATACGCGAATTTGTAATCTGAAAGATTTGCTGAAA 3847
Qy 2408 AGAAGAGAGAGAGCAATGCCCTGTGCTTGAAGATGAGATTAATGTTGCCCTATGT 2467
Db 3848 AGAAGAGAGAGAGCAATGCCCTGTGCTTGAAGATGAGATTAATGTTGCCCTATGT 3907
Qy 2468 TTGTTATTTCAACCTTTCTTCTGTCAAGAAATTTGATGAGGGGCAAGTCAAGT 2527
Db 3908 TTGTTATTTCAACCTTTCTTCTGTCAAGAAATTTGATGAGGGGCAAGTCAAGT 3967
Qy 2528 CAATAGTTTCAGTTCCATATCTAATCTCATGCTCTTAATCTTCCCTCAAAATTCCTATA 2587

Dp	1257	ACTGCGTCTTGAAGAAAGGTGGATGCATATATGCAAACTTTGGACAACCATATGATGTGCAAC	13116
Oy	934	TTGTCTCAAGAAAGATTGTTGGTTGTGTTCAATGCACAGTCGATTTGGGCACCAAGAAAGA	993
Dp	1317	TTGTGTCAAGAAAGATTGCTGGTGTGTGTTCTATGCAACCTGCAATTTGGGCACCAAGAAAGA	1376
Oy	994	ATTAATCTTAATCTTGTCGTATCGGAAGAGATGTGAAAAAATGTGGGTGTGCT	1053
Dp	1377	ATTAATCTTAATCTTGTCGTATCGGAAGAGATGTGAAAAAATGTGGGTGTGCT	1436
Oy	1054	CTAGACGTAAAACTCTTGGAGGTATTTTGGCTTTAAGAGAGAAAGAACAGTGGAA	1113
Dp	1437	CTAGACGTAAAACTCTTGGAGGTATTTTGGCATTAAGAGACAAAGAAAGCAATGGGAA	1496
Oy	1114	CATGTGAGAGATAGTGAGATTTGGAAATTTGCTCAGAGAAAGTTCTATTCTGCTGCC	1173
Dp	1497	CATGTGAGAGATAGTGAGATTTGGAAATTTGCTCAGAGAAAGTTCTATTCTGCTGCC	1556
Oy	1174	CTGAGACTTAATTCACATCACCTTCCATCTGATTTTGAGCAAAATGCTTACATATGTGCA	1233
Dp	1557	CTGAACTTAATTCACATCACCTTCCATCTGATTTTGAGCAAAATGCTTACATATGTGCA	1616
Oy	1234	GTATTTCCAAAGATACCGGAATGGAAAGGAAATCTAATCTGCTCTGATGGCACAT	1293
Dp	1617	GTATTTCCAAAGATACCGGAATGGAAAGGAAATCTAATCTGCTCTGATGGCACAT	1676
Oy	1294	GGTTTATATTTATCGAAGAGAACTTGGAGCTAGAGATGTAGTAAATGAATGGAAT	1353
Dp	1677	GGTTTATATTTATCGAAGAGAACTTGGAGCTAGAGATGTAGTAAATGAATGGAAT	1736
Oy	1354	GAATTTATCTTGAGGTCTTTCTTCCAGAGATTTGAAGTTAAATCTGGTCAAACTTATTTCC	1413
Dp	1737	GAATTTATCTTGAGGTCTTTCTTCCAGAGATTTGAAGTTAAATCTGGTCAAACTTATTTCC	1796
Oy	1414	AAGATGCATGATCTCATTCATGATCTGGCAACATCTCTAATTTTGGGCAAGCACATCAAGC	1473
Dp	1797	AAGATGCATGATCTCATTCATGATCTGGCAACATCTCTAATTTTGGGCAAGCACATCAAGC	1856
Oy	1474	AGCAATATCCGAGAAATTAATGTAGAAATTAACATACATATGATGTCCATTTGGTTCACT	1533
Dp	1857	AACATATATCCGAGAAATTAATGTAGAAATTAACCAATATGATGTCCATTTGGTTGCA	1916
Oy	1534	AAAGTGTGATCTTCTTACTCTCTTTCCACTTGCAGAAAGTTGTCTGTTAGGGTGTCTT	1593
Dp	1917	AAAGTGTGTCTTTTACTCTCTGTTCTCACTTCAMAAAGTTGTCTGTTAGGGTGTCTT	1976
Oy	1594	AATCTAAGTGCATTAACCTTAAGCAGTTAACCGTCTTCCATTTGGAGATCTATGACATTTA	1653
Dp	1977	AATCTAAGTGCATTAAGCCTCAGCAGAGTTACCAATCTTCAATTTGGAGATCTATGACATTTA	2036
Oy	1654	AGATATCTTAACCTTGTCTGCGCAATACTGTATTTGTGTAGTCTTCCAAAACAGTTATGCAAG	1713
Dp	2037	AGATATCTTAACCTTGTCTGCGCAATATATGTATTTGTGTAGTCTTCCAAAACAGTTATGCAAG	2096
Oy	1714	CTTCAAAATCTGCAGACTCTTGATCTACATGCTGTCACTTCACTTGTGTGTTGCCAAA	1773
Dp	2097	CTTCAAAATCTGCAGACTCTTGATCTACATGCTGTGTGCTACAGACTTCTGTGTTGCCAAA	2156
Oy	1774	GAAACCAAGCAACTTGTGTAGTCTTGGAAATCTTTTACCTGATGTGTGCTAATGATATGACT	1833
Dp	2157	GAAACCAAGCAACTTGTGTAGTCTTGGAAATCTTTTACCTGATGTGTGCTAATGATATGACT	2216
Oy	1834	TGTATGCAACCAAGGATAGGATCTTTGACATGCTTAAGACCTTAAGTAGATTTGTGGTGTG	1893
Dp	2217	TGTATGCAACCAAGGATAGGATCTATGACATGCTTAAGACCTTAAGATCGTTTGTGCATG	2276
Oy	1894	GGAATTCAGAGAAAGTTGTCAACTTGTGTGAATTTACGAAACTGGAATCTCTATGTGCTCA	1953
Dp	2277	GGAATTCAGAGAAAGTTGTCAACTTGTGTGAATTTACGAAACTGGAATCTCTATGTGCTCA	2333
Oy	1954	ATTGGAATCAAGCATTTGAGAGAGTGAAGATGATATGAGATGCAAAAAGAACCAATTTA	2013
Dp	2334	ATTGGAATCAAGCATTTGAGAGAGTGAAGATGATATGAGATGCAAAAAGAACCAATTTA	2393

OY	201	TCGCAAAAGAAATCTGCATTCCTTTAAGCATGAAAGGATGACATGAAAGCTGCACGT	2073
Db	2294	TCCTCAAAAGAAATCTGCATTCCTTTAAGCATGAAAGGATGACATGAAAGCTGCACAT	2453
OY	2074	ATATATGAAATCAGAAAAAGTTGAAGCTCTGAAGCTCTCAACCACTCCAAATCTGACT	2133
Db	2454	AGATATGAAATCAGAAAGATGTTGAAGCTCTGAAGCCTCTCAACCACTCCAAATCTGACT	2513
OY	2134	TGTTTAAACATCAGGGGCTTCAGAGGAATCCCTCTCCCAAGCTGGATGAATCACTCAGTT	2193
Db	2514	TGTTTAACAATTAATGAGCTTCAGAGGAATCCCTCTCCCAAGCTGGATGAATCACTCAGTT	2573
OY	2194	TTGAAAAATGTTGCTCTCATATTGAAATCATCAGTTGCAGAAAATGCTCATGCTTACACACC	2253
Db	2574	TTGAAAAATGTTGCTCTCTCTTGAAATCATGCAAGATTGCAGAAAATGCTCATGCTTACACACC	2633
OY	2254	TTTGTGAGCTGCCTTGTCTAAAAAGTCTAGAGTTGTGAGGGGGTCTGCGGAAGTGGAG	2313
Db	2634	TTTGTGAACTGCCTTGTCTAAAAATGCTACAGTTATGAGTGGGGTCTGCGGAAGTGGAG	2693
OY	2314	TATGTGATTTCTGGATTCCTCTCAAGAAAGAGTTTCCATCTCTGAGAAAACTTAATATA	2373
Db	2694	TATATTAATTTCTGGATTCCTCTCAAGAAAGAGTTTCCATCTCTGAGAAAACTTAATATA	2753
OY	2374	CGCGAATTTGGTAACTCGAAAGAGTTGCTGAAAAAGAGAGAGCAATGCGCTGTG	2433
Db	2754	GCGCAATTTGTATATCTGAAAGAGATTGTTGAAAAAGAGAGAGCAATTCCTCTGTG	2813
OY	2434	CTTGAAAGAGATGAGATTAATATGTTGCCATATGTTTGTATATTCCAACCTTTTCTGTCTG	2493
Db	2814	CTTGAAAGAGATGAGATTAATCTGGTGCCCTATGTTTGTATATTCGCAACCTTTTCTGTCTG	2873
OY	2494	AAGAAATTTGTATATGTTAGTGGGACAACTCGAATGCCAATAGTTTCACTCAATCTAAT	2553
Db	2874	AACCAATTTGATGATTAATGAGGAGAAAGTACAGATGCAATAGGCTTCACTCAATCTAAT	2933
OY	2554	CTCATGCTCTTACCTTCCCTCCAAATTCGGCTATPACAAAGAGTCTTCACTCCAGAA	2613
Db	2934	CTCAGGCTCTTACTTCTCTCAATTAAGCTATPACTGAGCTACTTCACTCCAGAA	2993
OY	2614	GAGATGTTCAAAAGCCTTGCAATCTCAATAATCTTGAAATATCTCTTTTACTTCAATCTT	2673
Db	2994	GAGATGTTCAAAAGCCTTGCAAAATCTPAAATATCTGAAATATCTTAATCTTCAAGAAATCTC	3053
OY	2674	AAAAGTGCTCTACACCTGGCTGAGTCTCAATGCTTTGAAGCATCTGAAATTCATAGT	2733
Db	3054	AAAAGTGCTCTACCAACTGGCTGAGTCTTAAATGCTTTGAAGCATCTGAAATTCATAGT	3113
OY	2734	TGTTATGACCTAGAGATCTCCCGAGAGAGGTGTGAAAGGTTTAATTTCACTCACACAG	2793
Db	3114	TGTTATGACCTAGAGATCTCTCCCGAGAGAGGTGTGAAAGGTTTAATTTCACTCACAA	3173
OY	2794	TTATTCATTAACATCTGTGAATGCTACAAATGTTTACCGAGGGATTCGACACCTTACA	2853
Db	3174	TTATTCATTAACATCTACTGCAAGATGCTACAAATGTTTACGAGGGATTCGACACCTTACA	3233
OY	2854	GCCTTCACAAATTTATCAGTTGAGTTTGTCCAAACATCTGGCCAAAGCGGTGTGAAAGGA	2913
Db	3234	GCCTTCACAAATTTATCAGTTGAGATTGTTCACACATCTGGCCAAAGCATGTGAAAGGA	3293
OY	2914	ATAGAGAGAGCTGGTACAAATTTGCTCACATTCCTGTTGTTTATTTATTA	2966
Db	3294	ATAGAGAGAGCTGGTACAAAAATTTGCTCACATTCCTGATGTTTATCCGTTA	3346
RESULT 5			
US-10-360-522-48			
; Sequence 48, Application US/10360522			
; Publication No. US20030221215A1			
; GENERAL INFORMATION:			
; APPLICANT: Allele, Josephus J.H.M.			
; APPLICANT: Vossen v.d., Edwin A.G.			

RESULT 5
US-10-360-522-48
; Sequence 48, Application US/10360522
; Publication No. US2003022125A1
; GENERAL INFORMATION:
; APPLICANT: Alieff, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360,522
PRIORITY FILING DATE: 2003-02-07
PRIORITY APPLICATION NUMBER: EP 02075565.8
PRIORITY FILING DATE: 2002-02-08
PRIORITY APPLICATION NUMBER: PCT/NL03/00091
PRIORITY FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 2913
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(2913)
OTHER INFORMATION: /note="Rpi-d1b"
US-10-360-522-48

Query Match 70.0%; Score 2077.2; DB 17; Length 2913;
Best Local Similarity 83.5%; Pred. No. 0;

Matches 2495; Conservative 0; Mismatches 388; Indels 105; Gaps 8;

QY 1 ATGGCTGAAGCTTCTTCAAGTCTGTTAGACAATCTGACCTGTTTCATCCAGGGGAA 60
DB 1 ATGGCTGAAGCTTCTTCAAGTCTGTTAGACAATCTGACCTGTTTCATCCAGGGGAA 60
QY 61 CTGGATTTGATTTCTTGGTTTAAAGATGAGTTCGAAAGCTTCAAGGACGTTTACTACA 120
DB 61 CTGGATTTGATTTCTTGGTTTAAAGATGAGTTCGAAAGCTTCAAGGACGTTTACTACA 120
QY 121 ATCCAGCTGCTGTAAGATGCTCAGAAAGCAATGGAAGACAGGCAATGAAAT 180
DB 121 ATCCAGCTGCTGTAAGATGCTCAGAAAGCAATGGAAGACAGGCAATGAAAT 180
QY 121 ATTGAAGCCGCTCTTGAAGATCTCAGAGAGCAACCAACACCTCTGAAAT 180
DB 121 ATTGAAGCCGCTCTTGAAGATCTCAGAGAGCAACCAACACCTCTGAAAT 180
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATCATCTTGGAGCAATGTAA 240
DB 181 TGGTTGCAAGAACTCAATGCTGCTGATATGAGGCTGATCATCTTGGAGCAATGTAA 240
QY 241 ACTGAGCAACCAATTTAGACAGAAAGCAAAATATGGGTATTCATCCAAAGTTATC 300
DB 241 ACTGAGCAACCAATTTAGACAGAAAGCAAAATATGGGTATTCATCCAAAGTTATC 300
QY 241 ACCAAGGCGACA--AGATCTCCCAATCTGAATATGGCGTTATCATCCAAAGTTATC 297
DB 241 ACCAAGGCGACA--AGATCTCCCAATCTGAATATGGCGTTATCATCCAAAGTTATC 297
QY 301 ACTTTTGTCAAGATTTGGGAAAAAGATGAAAAAGATTATGGAAAATCTGATTAAT 360
DB 301 ACTTTTGTCAAGATTTGGGAAAAAGATGAAAAAGATTATGGAAAATCTGATTAAT 360
QY 298 CTTTTCGCTCAAGAGTTCGGGAAAAAGATGCAAGTGAATGAAAACTTAAAGCAATT 357
DB 298 CTTTTCGCTCAAGAGTTCGGGAAAAAGATGCAAGTGAATGAAAACTTAAAGCAATT 357
QY 361 GCAGCGGAAAGCAATTAAGTTTCAATTTGGATGAAGAGCAATATGAGAGCAAGTTGCTACA 420
DB 361 GCAGCGGAAAGCAATTAAGTTTCAATTTGGATGAAGAGCAATATGAGAGCAAGTTGCTACA 420
QY 421 CGCCAAACAGGTTTGTGTTTGAATGAACCAACAGTTTATGGAAGAGCAAAAGAAAGAC 480
DB 421 CGCCAAACAGGTTTGTGTTTGAATGAACCAACAGTTTATGGAAGAGCAAAAGAAAGAC 480
QY 418 CGGAAAACAGGTTCTGATTTAACCGAACCGCAGGTTTATGGAAGAGCAAAAGAAAGAT 477
DB 418 CGGAAAACAGGTTCTGATTTAACCGAACCGCAGGTTTATGGAAGAGCAAAAGAAAGAT 477
QY 481 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTCTCCA 540
DB 481 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTCTCCA 540
QY 478 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTCTCCA 537
DB 478 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTCTCCA 537
QY 541 ATACTTGTATGGGAGGACTAGAAAGCACTCTTGCCCAATGATGTTCAATGATCAG 600
DB 541 ATACTTGTATGGGAGGACTAGAAAGCACTCTTGCCCAATGATGTTCAATGATCAG 600
QY 538 ATACTTGTATGGGAGGACTAGAAAGCACTCTTGCCCAATGATGTTCAATGATCAG 597
DB 538 ATACTTGTATGGGAGGACTAGAAAGCACTCTTGCCCAATGATGTTCAATGATCAG 597
QY 601 AGAGTAAATGAGATTTCCATCCAAAATATGATTTGTCTCGGAAGATTTTATGAG 660
DB 601 AGAGTAAATGAGATTTCCATCCAAAATATGATTTGTCTCGGAAGATTTTATGAG 660
QY 598 AGAGTAAATGAGATTTCCATCCAAAATATGATTTGTCTCGGAAGATTTTATGAG 657
DB 598 AGAGTAAATGAGATTTCCATCCAAAATATGATTTGTCTCGGAAGATTTTATGAG 657
QY 661 AAGAGTTGATTAAGAAATTTGATCTATTTGAAGAAAGTCT--ACTTGTGGCATG 717
DB 661 AAGAGTTGATTAAGAAATTTGATCTATTTGAAGAAAGTCT--ACTTGTGGCATG 717
QY 658 AAGAGTTGATTAAGAAATTTGATCTATTTGAAGAAAGTCTATTTGTGTGATG 717
DB 658 AAGAGTTGATTAAGAAATTTGATCTATTTGAAGAAAGTCTATTTGTGTGATG 717

QY 718 GACTTGGCTCCATTCAAAAGAAAGCTTCGGGACTTGTGATGAGAAAAATATTGCTC 777
DB 718 GACTTGGCTCCATTCAAAAGAAAGCTTCAGGAGTTGCTGATGAGAAAAATATTGCTC 777
QY 778 GTCTTAAGATGATTTTGAATGAAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
DB 778 GTCTTAAGATGATTTTGAATGAAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
QY 838 AAGTTGAGCAATTCGCTGCTTCTTAACCACTCTGCTTGAAGAGTTGATCA 897
DB 838 AAGTTGAGCAATTCGCTGCTTCTTAACCACTCTGCTTGAAGAGTTGATCA 897
QY 838 AAGTTGAGCAATTCGCTGCTTCTTAACCACTCTGCTTGAAGAGTTGATCA 897
DB 838 AAGTTGAGCAATTCGCTGCTTCTTAACCACTCTGCTTGAAGAGTTGATCA 897
QY 898 ATTATGGAACATTTGCAACCAATATGAATTTGCAATTTGCTCAAGAGATTTGTTG 957
DB 898 ATTATGGAACATTTGCAACCAATATGAATTTGCAATTTGCTCAAGAGATTTGTTG 957
QY 958 TTGTTCAATGCAACGTCATTTGGGACCAAGAAATTAATCTTTATCTTGGCTATC 1017
DB 958 TTGTTCAATGCAACGTCATTTGGGACCAAGAAATTAATCTTTATCTTGGCTATC 1017
QY 1018 GGAAGAGATTTGGAAGAAATGTTGTTGCTTGAAGCTTAAGCTTGGAGGT 1077
DB 1018 GGAAGAGATTTGGAAGAAATGTTGTTGCTTGAAGCTTAAGCTTGGAGGT 1077
QY 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAACATGTAGAGATGATGATTTGG 1137
DB 1078 ATTTTGGCTTTAAGAGAGAAAGACAGTGGGAACATGTAGAGATGATGATTTGG 1137
QY 1138 AAATTTGCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTTATGATCATCCTT 1197
DB 1138 AAATTTGCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTTATGATCATCCTT 1197
QY 1138 AAATTTGCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTTATGATCATCCTT 1197
DB 1138 AAATTTGCTTCAAGAGAAAGTTCTATTTCTGCTGCTGAGACTTATGATCATCCTT 1197
QY 1198 CCACTTATTTGAGACATGCTTATCATATTTGTCAGATTTCCAAAGATACCGAATG 1257
DB 1198 CCACTTATTTGAGACATGCTTATCATATTTGTCAGATTTCCAAAGATACCGAATG 1257
QY 1258 GAAAAAGAAATCTAATCTCTCTCTGATGAGCAATGTTTATTTATGAAAGAAAC 1317
DB 1258 GAAAAAGAAATCTAATCTCTCTCTGATGAGCAATGTTTATTTATGAAAGAAAC 1317
QY 1318 TTGGAGCTAAGAAATGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1377
DB 1318 TTGGAGCTAAGAAATGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1377
QY 1318 ATGAGGCTAAGAGATGAGGAGATGAAGATTAAGAAATTAAGATTAAGATTAAG 1377
DB 1318 ATGAGGCTAAGAGATGAGGAGATGAAGATTAAGAAATTAAGATTAAGATTAAG 1377
QY 1378 CAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1437
DB 1378 CAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1437
QY 1438 CTGGCAACATCTATTTTGGGCAAGACATCAAGCAAGCAATTCGGAATTAATGTA 1497
DB 1438 CTGGCAACATCTATTTTGGGCAAGACATCAAGCAAGCAATTCGGAATTAATGTA 1497
QY 1498 GAAATTAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1498 GAAATTAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
QY 1498 CACAGTTACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
DB 1498 CACAGTTACACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
QY 1558 TCCACTTGAAGAAATTTGCTGCTGAGGAGGCTTATGATGATGATGATGATGATGAT 1617
DB 1558 TCCACTTGAAGAAATTTGCTGCTGAGGAGGCTTATGATGATGATGATGATGATGAT 1617
QY 1618 CAGTTACCGTCTTCAATTTGAGATCTAATTAAGATTAAGATTAAGATTAAGATTA 1677
DB 1618 CAGTTACCGTCTTCAATTTGAGATCTAATTAAGATTAAGATTAAGATTAAGATTA 1677
QY 1618 AAGTTACCATCTTCAATTTGAGATCTAATTAAGATTAAGATTAAGATTAAGATTA 1674
DB 1618 AAGTTACCATCTTCAATTTGAGATCTAATTAAGATTAAGATTAAGATTAAGATTA 1674
QY 1678 ACTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737
DB 1678 ACTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737
QY 1675 AGTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1734
DB 1675 AGTGGCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1734
QY 1738 CTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797
DB 1738 CTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797
QY 1735 CTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
DB 1735 CTACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
QY 1798 GAAATCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857
DB 1798 GAAATCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857

Db 1934 AACATGCAACCATATGAAATTGTCAAAATCTGTCTCCAGAGATTGTGTTTTTGTTCAT 1993
Qy 966 GCAACGTGCAATTTGGGCAACCAAGAAAGAAATTAATCTTATCTTGTGGCTATCGAAAGGA 1025
Db 1994 GCACCGTGCAATTTGGGCAACCAAGAAAGAAATTAATCTTATCTTGTGGCTATCGAAAGGA 2053
Qy 1026 GATTGTGAAAAAATGTGGTGTGTGCTCTGACAGCTAAAACTCTGGAGGATTTTTGGCG 1085
Db 2054 GATTGTGAAAAAATGTGGTGTGTGCTCTGACAGCTAAAACTCTGGAGGATTTTTGGCG 2113
Qy 1086 CTTTAAAGAGAGAAAGAAAGAGATGGGAAACATGTGAGAGATGAGATTTGAAATTTGCC 1145
Db 2114 CTTCAAGAGAGAAAGAAAGAGATGGGAAACATGTGAGAGACAGTCCGATTTTGAATTTGCC 2173
Qy 1146 TCAGAGAGAAAGTTCTATCTGCTGCTGCTGAGACTTATGTTACATCACTTCCACTTGA 1205
Db 2174 TCAGAGAGAAAGTTCTATCTGCTGCTGCTGAGCTTATGATCAATCTTCCACTTGA 2233
Qy 1206 TTTGAGACAATGCTTTACATATTGTGACATATTCCTCAAGATACCGAAATGAGAAAGGG 1265
Db 2234 TTTGAGACAATGCTTTGTGTATTTGTGCGGTATTTCCAAAGACACCAAAATGGCAAGGA 2293
Qy 1266 AAATCTAATCTCTCTGTGATGAGACATGTTTTATTTATCGAAAGGAACTTGGAGCT 1325
Db 2294 AAATCTAATCTCTCTGTGATGAGACATGTTTTATTTATCGAAAGGAACTTGGAGCT 2353
Qy 1326 AGAGAAAGTGTATGAAAGTAAAGTAAATGAAATTAATCTTGAAGTCTTCTTCCAGAGAT 1385
Db 2354 AGAGAAAGTGTATGAAAGTAAAGTAAATGAAATTAATCTTGAAGTCTTCTTCCAGAGAT 2413
Qy 1386 TGAAGTTAAATCTGTGCAAACTTATTTCAAGATCAATGATCTCAATGATCTGGCAAC 1445
Db 2414 TGAAGTTAAATCTGTGCAAACTTATTTCAAGATCAATGATCTCAATGATTTGGCTAC 2473
Qy 1446 ATCTCTAATTTTGGCAAGACATCAAGACAAATATCGAGAAATTAATTTGAGAAATTA 1505
Db 2474 ATCTCTGTTTTCAAGCAAAACATCAAGACAAATATCGAGAAATTAATTTGAGAAATTA 2533
Qy 1506 CATCATATGATGTCATGTTGGTTTCACTAAAGTGTATCTTCAATCTCTTCCCACTT 1565
Db 2534 TGGATATATGATGTCATGTTGGTTTCACTAAAGTGTATCTTCAATCTCTTCCCACTT 2593
Qy 1566 GCAGAAAGTTTGTCTGTTGAGGGTCTTAAATCTAAGTGCATTAACCTTAAAGCAGTTAAC 1625
Db 2594 GCAGAAAGTTTGTCTGTTGAGGGTCTTAAATCTAAGTGCATTAACCTTAAAGCAGTTAAC 2653
Qy 1626 GTCTTCAATGAGATCTAATGACATTTTAAGTACTTAACTTGTCTGCAATACTAATAT 1685
Db 2654 ATCTTCAATGAGATCTAATGACATTTTAAGTACTTAACTTGTCTGCAATACTAATAT 2713
Qy 1686 TCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGACAGCTCTGATCTACATTA 1745
Db 2714 TCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGACAGCTCTTGAATCTACATTA 2773
Qy 1746 CTGTCAATCACTTGTGTGTTGCCAAAAAGAAACAGCAAACTTGTAGTCTTGGAAATCT 1805
Db 2774 TTGGGACCTCTCTTCTTGTGTTGCCAAAAAGAAACAGCAAACTTGTAGTCTTGGAAATCT 2833
Qy 1806 TTTTACTGATGATGTTGCTATGATGACTTGTATGCCCAAGAGATAGATCTTTGACATG 1865
Db 2834 TTTTACTGATG--GCTGTTCATTTAGCTCAACGCCCAAGAGATAGATTTGTTGACATG 2890
Qy 1866 CCTTAAGACTCTAAGTATTTGTGTGGGAATTCAGAGAAAGTTGTCAACTTGGTGA 1925
Db 2891 CCTTAAGCTCTAAGTATTTGTGTGGGAATTCAGAGAAAGTTGTCAACTTGGTGA 2947
Qy 1926 ATTACGAACCTGAATCTATGCTCATGCTCAATGGAATCAGCATCTTGAAGAGTGAAGAA 1985
Db 2948 ACTAAAAAACTTAATCTATGCTCAATTTCAATCACAAAACTTGAAGAGTGAAGAA 3007
Qy 1986 TGTATGATGAGCAAAAGCAATTTATCTGCAAAAGAAATTTGCATTTTAAGCAT 2045
Db 3008 AGATAGGATGAGCAAAAGCAATTTATCTGCTAAAGCAAAATCTGCACTTTATGCTT 3067

Qy 2046 GAAATGGGATGACGATGAAAGCTCCAGTATATATGAAATCAGAAAAAGTTGAAGTCTTGA 2105
Db 3068 GAGTTGGACCTTGTAGAAA--ACATAGATATGATTTCA-----GAAAGTCTTGA 3115
Qy 2106 AGCTCTCAAAACCAACCTCCAACTGACTGTTTAAATCAATGAGGGCTTCAAGAGAAATCCG 2165
Db 3116 AGCCCTCAAAACCAACCTCCAACTGAAATATTTGAATATCAATGAGCTTGGAGAAATCCG 3175
Qy 2166 TCTCCAGACTGATGATCACTCAAGTTTGAAGAAATGTTGTCTCTATTTGAATCATCAG 2225
Db 3176 TCTCCAGATTTGATGATCAATCAGTTTGAAGAAATGTTGTCTCTATTTGAATTTAGAG 3235
Qy 2226 TTGCAAAACCTGCTCAATGCTTACCACTTGTGAGCTGCTGCTGCTTCAAAAGTCTAGA 2285
Db 3236 TTGCAAAACCTGCTCAATGCTTACCACTTGTGAGCTGCTGCTGCTTCAAAAGTCTAGA 3295
Qy 2286 GTTGTGAGGGGGGTCTGCGAAGTGAATGTTGATTTCTGATTTCCCTACMAAGAAAG 2345
Db 3296 GTTACACACCGGGTCAACGATGTGAGTATGTTGAAGATTAATGTCATCCTG--GAG 3352
Qy 2346 GTTTCCATCTCTGAGAAACTTAATATACCGAATTTGTTATCTGAAAGATTTGCTGA 2405
Db 3353 GTTTCATCTCTGAGAAACTTGTATATGAGACTTTAGTATCTTAAAGATTTGCTGA 3412
Qy 2406 AAAGAGAGAGAGAGCAATGCCCTGCTTGAAGATGAGATTAATGTTGCCCTAT 2465
Db 3413 AAAGAGAGAGAGAGCAATGCCCTGCTTGAAGATGAGATTAATGTTGCCCTAT 3472
Qy 2466 GTTGTATTTCCAACTCTTCTCTGTCAGAAATTTGTAATGTTAGTGGGACAAAGTCA 2525
Db 3473 GTTGTATTTCCAACTCTTCTCTGTCAGAACTTGAAGATTAATGTTAGTGGGACAAAGTCA 3526
Qy 2526 TGCATATGTTTCAATTTCCATATCTATCTGATGCTCTTACTTCCCTCCAAATTTGCTA 2585
Db 3527 TGCATATGTTTCAATTTCCATATCTATCTGATGCTCTTACTTCCCTCCAAATTTGCTA 3586
Qy 2586 TTAACAAAGAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGAATCTCAATTA 2645
Db 3587 TTAACAAAGAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGAATCTCAATTA 3646
Qy 2646 CTGGAATATCTCTTTTACTTAATCTTAAGAGCTGCTTCAACAGCTGCTGATGCTCA 2705
Db 3647 CTGGAATATCTCTTTTACTTAATCTTAAGAGCTGCTTCAACAGCTGCTGATGCTCA 3706
Qy 2706 TGCCTTGAAGCTGGAATGATATGTTGTATGCACTGAGAGTCTCCCGAGAGAG 2765
Db 3707 TGCCTTGAAGCTGGAATGATATGTTGTATGCACTGAGAGTCTCCCGAGAGAG 3766
Qy 2766 TGTGAAAGTTTAAATTTCACTCAACAGTTATCTAATCAATCTGTAAGATGCTACATG 2825
Db 3767 GTTGAAGAGTTTAAATTTCACTCAACAGTTATCTAATCAATCTGTAAGATGCTACATG 3826
Qy 2826 TTTACCGAGAGATTTGACAGCACTTAACAGCTTCAAAATTTATCACTGATGTTGTCC 2885
Db 3827 TTTACCGAGAGATTTGACAGCACTTAACAGCTTCAAAATTTATCACTGATGTTGTCC 3886
Qy 2886 AAGACTGGCCAGCGGTGAGAGAGGATAGAGAGAGCTGATACAAATTTGTCACAT 2945
Db 3887 AAGACTGGCCAGCGGTGAGAGAGGATAGAGAGAGCTGATACAAATTTGTCACAT 3946
Qy 2946 TCCCTGTTGTTTATTTATTTAG 2967
Db 3947 TCCATATTTGACTCTATATAG 3968

RESULT 7
US-10-360-522-49
; Sequence 49, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vosseen v.d., Edwin A.G.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360,522
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02075565.8
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 3592
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(3591)
OTHER INFORMATION: /note="Rpi-b1b including intron sequence (position
US-10-360-522-49

Query Match 60.9%; Score 1805.8; DB 17; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
426 AACAGTTTGTGTAATGAACCAAGTTTATGGAAGAGCAAGAAAGAGAGAT 485
1102 ACCAGGTTCTGTATTAACCGAACCGAGTTTATGGAAGAGCAAGAAAGAGAT 1161
486 AGTGAATTCGTATTAACCAATGTAGCAATGCCCAACCTTCAGTCTCCCAACT 545
1162 AGTGAATTCGTATTAACCAATGTAGCAATGCCCAACCTTCAGTCTCCCAACT 1221
546 TGTATGAGGGGAGTGAAGAAAGAGCTCTTGGCCCAATGTCTTCATGATCAGAGT 605
1222 TGTATGAGGGGAGTGAAGAAAGAGCTCTTGGCCCAATGTCTTCATGATCAGAGT 1281
606 AATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAAAG 665
1282 TACTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAAAG 1341
666 GTTGATTAAGAAATTTGATGATCTATTGAAGAAAGTCTTACTGTCGATGACTT 722
1342 GTTATTAAGAAATTTGATGATCTATTGAAGAAAGTCTTACTGTCGATGACTT 1401
723 GGTCTCACTTCAAAAGAGCTTCGGGACTTGTGATGAGAAATTTTGTCTGCTT 782
1402 GGTCTCACTTCAAAAGAGCTTCGGGACTTGTGATGAGAAATTTTGTCTGCTT 1461
783 AGATGATTTTGAATGAAGATCAAGATTAAGTGGCTTAAGTTAAGCAAGTCTGAAGT 842
1462 AGATGATTTTGAATGAAGATCAAGATTAAGTGGCTTAAGTTAAGCAAGTCTGAAGT 1521
843 TGGAGCAAGTGGCGCTTCTGTTCTTAACCACTACTGCTTGAAGAAAGTGTGATCAATTAT 902
1522 TGGAGCAAGTGGCGCTTCTGTTCTTAACCACTACTGCTTGAAGAAAGTGTGATCAATTAT 1581
903 GGAACATTTGCAACCATATGATGATTTGTCTCAGAGAAATGTTGTTGTTGTT 962
1582 GGAACATTTGCAACCATATGATGATTTGTCTCAGAGAAATGTTGTTGTTGTT 1641
963 CATGCAACGTGATTTGGGCAACCAAGAAATTAATTTTATCTTTGCTGCTATGGA 1022
1642 CATGCAACGTGATTTGGGCAACCAAGAAATTAATTTTATCTTTGCTGCTATGGA 1701
1023 GGAATTTGGAAGAAATGTTGTTGCTCTAGACATTAATCTTTGGAATTTT 1082
1702 GGAATTTGGAAGAAATGTTGTTGCTCTAGACATTAATCTTTGGAATTTT 1761
1083 GCGCTTTAAGAGAAAGACAGTGGAAATCATGTGAGATGATGATTTGGAATTT 1142
1762 GCGCTTTAAGAGAAAGACAGTGGAAATCATGTGAGATGATGATTTGGAATTT 1821

1143 GCTCAAGAGAAAGTTCTATTTCTGCTGCTGCTGAGACTTATGATCACTTCACT 1202
1822 GCTCAAGAGAAAGTTCTATTTCTGCTGCTGCTGAGACTTATGATCACTTCACT 1881
1203 TGAATTTGAGCAATGCTTTTACATATTTGTCAGATTTCCCAAGAAATGGAATG 1262
1882 TGAATTTGAGCAATGCTTTTACATATTTGTCAGATTTCCCAAGAAATGGAATG 1941
1263 GGAATTTGAGCAATGCTTTTACATATTTGTCAGATTTCCCAAGAAATGGAATG 1322
1942 GGAATTTGAGCAATGCTTTTACATATTTGTCAGATTTCCCAAGAAATGGAATG 2001
1323 GCTGAGATTTGAGTATGAGATGAGATGAGATTTATCTTGAAGTCTTTTCCAGA 1382
2002 GCTGAGATTTGAGTATGAGATGAGATGAGATTTATCTTGAAGTCTTTTCCAGA 2061
1383 GATTGAAGTTAATCTGTCGCAACTTATTTCAAGATGATGATCTTCAATGATCTGGC 1442
2062 GATTGAAGTTAATCTGTCGCAACTTATTTCAAGATGATGATCTTCAATGATCTGGC 2121
1443 AACATCTCTATTTTCCGCAACATCAAGCAATTCGAGAAATTAATTTAGAAA 1502
2122 AACATCTCTATTTTCCGCAACATCAAGCAATTCGAGAAATTAATTTAGAAA 2181
1503 TTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
2182 TTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2241
1563 CTTCAGAAAGTTTGTCTGTTGAGGAGTCTTATCTTAAGTACATTAATTAAGCACTT 1622
2242 CTTCAGAAAGTTTGTCTGTTGAGGAGTCTTATCTTAAGTACATTAATTAAGCACTT 2301
1623 ACCGTTCTTCCATTTGAGATCTATGATCTTATTAAGTACATTAATTAAGCACTT 1682
2302 ACCGTTCTTCCATTTGAGATCTATGATCTTATTAAGTACATTAATTAAGCACTT 2358
1683 TATTCGTAGTCTTCCAAACGATTAAGTATGATGATGATGATGATGATGATGATGAT 1742
2359 CATGCTAGTCTTCCAAACGATTAAGTATGATGATGATGATGATGATGATGATGAT 2418
1743 TGGCTGATCTTCACTTGTGTTGTTGCCAAAGAAAGCAAGCACTTGTAGCTTGGAA 1802
2419 ATATTTGACCAAGCTTGTGTTGTTGCCAAAGAAAGCAAGCACTTGTAGCTTGGAA 2478
1803 TCTTTTACTTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1862
2479 TCTTTTACTTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2538
1863 ATGCTTTAAGCTCTTAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1922
2539 ATGCTTTAAGCTCTTAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2595
1923 TGAATTTAAGAACTGATCTTATGCTCAATTTGAATTCACGATCTTGAAGAGTGA 1982
2596 TGAATTTAAGAACTGATCTTATGCTCAATTTGAATTCACGATCTTGAAGAGTGA 2655
1983 GAATGATTTGAGTGAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTTAA 2042
2656 GAATGATTTGAGTGAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTTAA 2715
2043 CATGAATTTGAGTGAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTTAA 2102
2716 CATGAATTTGAGTGAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTTAA 2772
2103 TGAAGCTCTCAACACACATCTCAATCTGATCTTGAATTCAGAGGCTTCAAGAAAT 2162
2773 TGAAGCTCTCAACACACATCTCAATCTGATCTTGAATTCAGAGGCTTCAAGAAAT 2832
2163 CCGTCTCCAGACGTGATGATCACTCAGTTTGAAGAAATGTTGTTCTTATTTGAATCAT 2222
2833 CCGTCTCCAGACGTGATGATCACTCAGTTTGAAGAAATGTTGTTCTTATTTGAATCAT 2892

QY	2222	CAGTTGGCAAAACGCTCATGCTTACACACCCCTTGGTAGGCTGCTGTCTAAAAAAGCT	2282
Db	2893	CAACTTCAGAAACTGCTCATGCTTACACACCCCTTGGTAGGCTGCTGTCTAAGAAAGCT	2952
QY	2283	AGAGTTGTGGAGGGGGGCTCTGGCGAAGTGGAGTATGTTG-----A	2321
Db	2953	AGAGTTACACCTGGGGGGCTCTGGCGAAGTGGAGTATGTTGAGTATGTAATGATTCA	3012
QY	2222	TTCTGGATTCCTCTACAGAGAGGTTTCCATCTCTGAGAAAATTATATATACCGGAAT	2381
Db	3013	TTCTGGATTCCTCCACAGAGATATGATTTCATCTCTTGGAGAACTGTATATATGGGACT	3072
QY	2382	TGTTATCTGAAAAGGATGTCTGAAAAGAGAAAGAAAGAGCAATGCCCTGTGCTTGAAGA	2441
Db	3073	TGTTATCTGAAAAGGATGTCTGAAAAGAGAAAGAGAGCAATTCCTGTGCTTGAAGA	3122
QY	2442	GATAGAGATTAAATGTTGGCCCTATGTTGTTATTCCAACCCCTTCTCTGTCAAGAAATT	2501
Db	3133	GATAGATTATTCACAGAGTCC-----TCTTCTGACCCCTTCT-----	3168
QY	2502	GGTAGTTATGTGGGACAAAGTCAGATGCATATGATTTCAAGTTCCATATCTCATATGC	2561
Db	3170	-----TCTAATCTTAAAGGC	3183
QY	2562	TCTTACTTCCCTCCAAATTCGTATTAACAAAGAGATGCTTCACTCCAGAGAGATGT	2621
Db	3184	TCTTACTTCCCTCAGAAATTTGCTATTAATTAAGTACACTCTCATTTCCAGAGAGATGT	3243
QY	2622	CAAAAGCCTTGCAAAATCTCAAAATCTTGAAATATCTCTTTTAACTTCAATCTTAAAGACT	2681
Db	3244	CAAAAGCCTTGCAAAATCTCAAAATCTTGAAATATCTCTGGTGCAATATCTCAAAAGACT	3303
QY	2682	GCTTACCAAGCCTGGCTAGTCTCATGCTTTTGAGAGACTTGGAAATTCATAGTTGTATGC	2741
Db	3304	GCTTACCAAGCTGGCTAGTCTGAAAGCTTTGAAAGCTTAAAAATTCATATGTGTGTGCG	3363
QY	2742	ACTGAGAGGCTCCCCCGAGGAAAGGTGTAAGGTTAATTTCACTCACACAGTTATCCAT	2801
Db	3364	ACTGAGAGGCTCCCTCGAGGAAAGGCTGTAAGGTTAATTTCACTCACAGGTTATTTGT	3422
QY	2802	AACATCTAGTGAATGTCTACATGTTTACCGGAGGATTTGACGACCTTAAGCCCTCAC	2861
Db	3424	TGAACACGTGAACATGCTTAATATGTTTACAGAGGATTTGACGACCTTAACACCTCAC	3483
Db	3484	AAAGTTAAAAATTCGGGGATGTCACAACTGATCAAGCGGTGTGAGAGGGAATGAGAGA	3543
QY	2922	AGACTGTGACAAAATTGCTCACATTCCTCGTGTGTTATTTAT	2964
Db	3544	AGACTGTGACAAAATTCTCACATTCCTTAATGTGAATATATAT	3586
RESULT 8			
US-10-360-522-50			
; Sequence 50, Application US/10360522			
; Publication No. US20030221215A1			
; GENERAL INFORMATION:			
; APPLICANT: Vossen v.d., Edwin A.G.			
; APPLICANT: Vossen v.d., Edwin A.G.			
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS			
; FILE REFERENCE: U 014413-9			
; CURRENT APPLICATION NUMBER: US/10/360,522			
; CURRENT FILING DATE: 2003-02-07			
; PRIOR APPLICATION NUMBER: EP 02015565.8			
; PRIOR FILING DATE: 2002-02-08			
; PRIOR APPLICATION NUMBER: PCT/NL03/00091			
; PRIOR FILING DATE: 2003-02-07			
; NUMBER OF SEQ ID NOS: 63			
; SOFTWARE: PatentIn Ver. 2.1.			
; SEQ ID NO 50			
; LENGTH: 5191			

```

: TYPE: DNA
: ORGANISM: Artificial Sequence
FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: sequence of
: OTHER INFORMATION: 5.2 kb Sca I genomic DNA fragment of S.
: OTHER INFORMATION: bulbocastaneum BAC SPB 4 present in pBGC2-blb
US-10-360-522-50

```

Query Match	60.9%;	Score 1805.8;	DB 17;	Length 5191;
Best Local Similarity	84.2%;	Pred. No. 0;		
Matches 2159;	Conservative	0;	Mismatches 302;	Indels 102;
			Gaps	7.

QY	426	AACGAGTTTGTGTTGATGAAACCAAGATTTATGAAAGAGACAAAGAAAAGCCAGAT	485
Db	2292	ACCAAGTTCGTGATTAACCGAACCCGAGGTTTATGAAAGAGACAAAGAAAAGATGAGAT	2351
QY	486	AGTGAATAATCCGTATAAACAATGTTAGCAATGCCCAACACTTCCAGTCCCTCCAAATCT	545
Db	2352	AGTGAATAATCCGTATAAACAATGTTAGTATGCCCAACACTTCCAGTCCCTCCAAATCT	2411
QY	546	TGCTATAGGGGGGACATAGAAAGACGACTCTTGCCCAATGAGTCTTCAATGATCAGAGAT	605
Db	2412	TGCTATAGGGGGGATAGGAAAAGACACTTGGCCCAATGAGTCTTCAATGATCAGAGAT	2471
QY	606	AATTGACACTTTCATCCCAAAATATGATATTTGTCTCGGAAGATTTTAATGAAGAG	665
Db	2472	TACTGACACTTTCATCCCAAAATATGATATTTGTCTCGGAAGATTTTAATGAAGAG	2531
QY	666	GTTGATATAAGAAATTTGATATCTTATGAAAGAAAGTC--ACTTGTCATGAGACTT	722
Db	2532	GTTATATAAGGCAATTTGATATCTTATGAAAGAAAGCCACTAATGTTGATGAGACTT	2591
QY	723	GGCTCCACTTCAAAAGAGCTGGGAGCTTGCTGTAATGGAAGAAAATAATTTGCTGCTT	782
Db	2592	GGCTCCACTTCAAAAGAGCTTCAGAGTTGCTGTAATGGAAGAAAAGATATCTTGCTT	2651
QY	783	AGATGATGTTTGGAAATGAAAGATCAAGATTAAGTGGCTAAGTTAAGACAAGCTTGAAGT	842
Db	2652	AGATGATGTTTGGAAATGAAAGATCAAGAGTGGGCTAATTTAAGACAAGCTTGAAGT	2711
QY	843	TGAGCAAGTGGCGCTTCTGTCTTAACAACACTACTCGTCTTGAAGAAAGTTGATCAATAT	902
Db	2712	TGAGCAAGTGGTCTTCTGTCTTAACACACTACTCGTCTTGAAGAAAGTTGATCAATAT	2771
QY	903	GGGAAACATTGCAACCATATGAAATTTGTCTCAAGAAAGTTGGTGGTGGTT	962
Db	2772	GGGAAACATTGCAACCATATGAACTGTCAAACTGTCTCAAGAAATTTGGTGGTGGTT	2831
QY	963	CATGCAACGTGCAATTTGGGCGACCAAGAAAGAAATTAATCTTAATCTTGCTATCGGAA	1022
Db	2832	CATGCAACGTGCAATTTGGACACCAAGAAAGAAATTAATCTTAATCTTGCTATCGGAA	2891
QY	1023	GGAGATTTGTGAAAAAATGTGTGTGTGCTCTAGACAGCTAATAAATCTTGAGAGTATTTT	1082
Db	2892	GGAGATTTGTGAAAAAATGTGTGTGTGCTCTAGACAGCCAAAATCTTGAGAGGATATTTT	2951
QY	1083	GGCGTTTAAGGAAAGAAAGACAGGTGGAAACATGTAGAGATGTGAGATTTGGAATTT	1142
Db	2952	GTGCTTCAAGGAAAGAAAGAGCATGTGGAAACATGTAGAGACAGTCCGATTTGGAATTT	3011
QY	1143	GGCTCAAGAAAGAAAGTTCTATTTGCGCTGACCTGAGACTTAAGTTACCATCACTTCACAT	1202
Db	3012	GGCTCAAGATTAAGTTCTATTTGCGCTGACCTGAGGCTTAAGTTACCATCAACTTCACAT	3071
QY	1203	TGATTTGAGCAATGCTTTACATATTTGTGAGATTTCCCAAGAGATACCGAATGGAATA	1262
Db	3072	TGATTTGAAACAAATGCTTTGCGTATTTGTCGAGTGTCCCAAGAGATGCAAAAATGGAATA	3131
QY	1263	GGGAAATTAATCTCTCTCTGAGATGGCAATGTTTTATTTATCGAAGGAACCTTGGAA	1322
Db	3132	AGAAAGCTAATCTCTCTCTGAGATGGGCAATGTTTTCTTTATCAAAAGGAACATGGA	3191
QY	1323	GCTAGAGATGTAGGTATGAAAGTATGGAATGATATTAATCTTGAGAGTCTTCTTCAAGA	1382

Db 704 AGCAGTGTGTTGTTTAACTGAGCCAAAAGTTATGAAAGGAAAAAGAGAGATGAGAT 763
Qy 486 AGTGAATAATCCGTGAATAAATAATGTAAGCAATGCCAAACACTTCCAGTCCCTCCCAATCT 545
Db 764 AGTGAATAATCTGATTAACAAATGTTAGTTATTCAGAAAGATTCAGATACCTCCCAATCT 823
Qy 546 TGTATGAGGGGGAGCTAGGAAAGACGACTCTTGCCCAATGTCCTTCAATGATCAGAGAGT 605
Db 824 TGTATGAGGGGGAGCTAGGAAAGACGACTCTAGCCCAATGTCCTTCAATGATCAGAGAGT 883
Qy 606 AATTGAGCATTTCCATCCCAAAATATGATTTGTGTCTGCGAAGATTTTAATGAGAAG 665
Db 884 TACTGAGCATTTCAATCTAAAGATATGGGTTGTGTCTCAGATGATTTTGTATGAMAAG 943
Qy 666 GTTGATTAAGGAAATTTGATGATCTAATTGAAAGAAAGTCACTGGTGGCATGAGACTTGGC 725
Db 944 GTTGATTAAGGCAATTTGATGATCTAATTGAAAGAAAGTCACTGGTGGCATGAGACTTGGC 1003
Qy 726 TCCACTTCAAAAAGAACTTCGGGACTGTGCTGATGAAAAAAATATTTGCTGCTTGA 785
Db 1004 TCCCTCCAGAAAAGCTTCAGAGAGTTGTGATGAAAAAAAGATCTTTGTTTGA 1063
Qy 786 TGAATGTTGGAATGAAGATCAAGATTAAGTGGCTTAAGTAAACAAGTCTTGAAAGTTGG 845
Db 1064 TGAATGTTGGAATGAAGATCAAGAAAGTGGATTAATCTTAGAGCAGATTTGAAGATTTGG 1123
Qy 846 AGCAGTGGGCTCTGTTCTTACCACTACTGCTTGAAGAAAGTTGGATCAATTATGG 905
Db 1124 AGCTATGATGCTTCAATTTCTAATTTACTACTGCTTGAAGAAATTTGATCAATTTATGG 1183
Qy 906 AACATTTGCAACCATATGAAATTTGTCAAAATTTGTCTCAAGAAAGTTGGTGTGTTGAT 965
Db 1184 AACTTTGCAACCATATGAAATTTGTCAAAATTTGTCTCAAGAAAGTTGGTGTGTTGAT 1243
Qy 966 GCAACGTGCATTTGGGCAACCAAGAAATAAATTTTATCTTGAGCTATCGGAAAGGA 1025
Db 1244 GCAACGTGCATTTGGGCAACCAAGAAATAAATTTTATCTTGAGCTATCGGAAAGGA 1303
Qy 1026 GATTGTGAAAAAATGTTGTTGCTGCTCTAGCAGCTAAACTCTTGAGAGTATTTTGGC 1085
Db 1304 GATTGTGAAAAAATGTTGTTGCTGCTCTAGCAGCTAAACTCTTGAGAGCTTTTACG 1363
Qy 1086 CTTTAAAGAGAAAGAAAGACGTGGAAACATGTGAGATGATGAGATTTGAAATTTGCC 1145
Db 1364 CTTTAAAGAGAAAGAAAGTGAATGGAAACATGTGAGATGATGAGATTTGAAATTTTACC 1423
Qy 1146 TCAGAAGAAAGTCTATTTCTGCGCTGCGCTGAGACTTAGTACATCACTTCCACTTGA 1205
Db 1424 TCAGAAGAAAGTCTATTTCTGCGCTGCGCTGAGACTTAGTACATCACTTCCACTTGA 1483
Qy 1206 TTTGAGACAATGCTTTACATATTTGTGACATTTCCCAAGAGATCCGAATGAAAAAGG 1265
Db 1484 TTTGAGACAATGTTTGTGATTTGGAGATTTCCCAAGAGACACCAAAATATGAAAAAGGA 1543
Qy 1266 AAATCTAATCTCTCTCTGAGATGCAATGGTTTATTTATCGAAGAGAACTTTGAGCT 1325
Db 1544 ATATCTAATCTCTCTCTGAGATGCAACAGTTTCTTTTATCAAAAGGAAACATGAGAGCT 1603
Qy 1326 AGAGAATGATGATGATGAAATGAAATGAAATTAATCTGAGGCTTTCTTCCAGAGAT 1385
Db 1604 AGAGAATGATGATGAAATGAAATGAAATTAATCTGAGGCTTTCTTCCAGAGAT 1663
Qy 1386 TGAAGTTAAATCTGTCACAACTTATTTCAAGATCAGATCTCAATGATCTGGAAC 1445
Db 1664 TGAAGTTAAATCTGTCACAACTTATTTCAAGATCAGATCTCAATGATCTGGAAC 1723
Qy 1446 ATCTCTATTTTTCGCAAGACATCAAGACCAATATCCGAGAAATTA----- 1491
Db 1724 ATCTATGTTTTCGCAAGACGATCAAGACCAATATCCGCAAAATATGTAAGATGA 1783
Qy 1492 -----ATTGTAAGAAATTTACATATGATGATGTCATTTGGTCTTCACTAA 1535
Db 1784 TGAAGATATGATGTTCACTTTGTAACAAATTTATTAAGATATGATGTCATTTGGTCTTCCGA 1843

Qy 1536 AGTGTATCTCTTACTCTCTTCCACTTGCAGAAAGTTGTCTGTTAGGGTGTCTAA 1595
Db 1844 AGTGTATCTCTTACTCTCTTCCACTTGCAGAAAGTTGTCTGTTAGGGTGTCTAA 1903
Qy 1596 TCTAAGTACATAAACTTAAAGCATTAACGCTCTTCCATTTGAGATCTAGTACATTTAAG 1655
Db 1904 TCTAAGTACATAAACTTAAAGCATTAACGCTCTTCCGTTGAGATCTAGTACATTTAAG 1963
Qy 1656 ATACTTAACCTTGTCTGGCAATACTAGTATTCGATGCTTCCAAACCAAGTATGCAAGCT 1715
Db 1964 ATACTTGAACCTGTCTGGTATTAATA-----ATTGTAGTCTTCCAAAGAGTGTGCAAGCT 2020
Qy 1716 TCAAAATCTGAGACTCTGATCTACATGAGCTGATTCATCTTGTGTTGCCAAAAGA 1775
Db 2021 TCAAAATCTGAGACTCTTATCTATTAATATGACAGTCACTTCTTGTGCCAAAAGA 2080
Qy 1776 AACAAAGCAAACTTGATGCTTGAATACTTTATCTTGATGTTGCTATGAGATTTGACTTG 1835
Db 2081 AACAAAGTAAAGCTTTGATGCTCCGAAATCTTGACTTGA-----TCAGTCCATGACTTTC 2137
Qy 1836 TATGCCAACAAAGATTAAGATCTTGAATGCTTAAGACTCTAGTATTTGTGTGGG 1895
Db 2138 TATGCCAACAAAGATTAAGATTTGATGATGCTTTAAGACACTAGCTTACTTGTGTAGG 2197
Qy 1896 AATTCAAGAAAGAAAGTTGTCNACTTGGTGAATTAAGAAACCTGAATCTATGCTCAAT 1955
Db 2198 ---CGAAGAGAAAGTTATCACTTGGTGAACCTAGCAAAATTTAACCCTCGGTGTGCAT 2254
Qy 1956 TGAATCAACGATCTTGAAGAGTGAAGAAATGATATGATGCAAAAGACCAATTTATC 2015
Db 2255 TTTCAATCAACATCTTGAAGAGTGAAGAAATGATATGATGCAAAAGACCAATTTATC 2314
Qy 2016 TGCAAAAGAAATGTGATCTTTAAGCATGAATGAGATGAGATGAGTCCAGCTAT 2075
Db 2315 TGCAAAAGCAATTTACATCTTTAAGCATGAGTGGATTA-----GACCAAAACG 2365
Qy 2076 ATATGAATCAAGAAAGAAAGTTGAAGTCTTGAAGCTTCAAAACCACTCAATCTGACTTG 2135
Db 2366 ATATGAATCAAGAAAGAAAGTTGAAGTCTTGAAGCTTCAAAACCACTCAATCTGAAATA 2425
Qy 2136 TTTTAAACATCAGGGGCTTCAAGAGATCCGCTTCCGACATCTGATGATTAATCACTAGTTT 2195
Db 2426 TTTTAAAGATCAATGACCTTGTGATGATCTGTCTCCGACATGATGATCACTCAGTTT 2485
Qy 2196 GAAAAATGTTGTCTATTAATAATCATCAGTTGCAAAAACGTGCTCATGCTTACCAACCTT 2255
Db 2486 GAAAAATGTTGTCTATTTCTAATTTAGCGGTTGTGAAAACTGCTCGTGTACCACTT 2545
Qy 2256 TGTGAGCTGCTTGTCTAATAAAGTCTAAGATTTGTGAGGGGGTCTGCGAAGTGAAGTA 2315
Db 2546 TGTGAGCTGCTTGTCTAATAAAGTCTAAGATTTGTGAGGGGGTCTGCGAAGTGAAGTA 2605
Qy 2316 TGTGTT---GATTCTGATTTCCCTACAGAAAGAGTTTCCATCTCTGAGAAACTTAATAT 2372
Db 2606 TGTGTTGAGATTTCTGATTTCTGTACAGAAAGAGATTTCCATCTCTGAGAAACTTAATAT 2665
Qy 2373 ACGGAAATTTGATTAATCTGAAGAGATTTGTAAGAAAGAGAGAGAAAGAGCAATGCTGT 2432
Db 2666 AGGTGGCTTTTGTATTTGTAAGAGATTTGCAAGATTTGCAAGAGAGAGAGCAATTTCCCGT 2725
Qy 2433 GCTTGAAGAGATTAAGATTAATGTTGCTGCTATGTTTGTATTTCAACCTTTCTTCTGT 2492
Db 2726 GCTTGAAGAGATTAAGATTTGCAAGATTTGCAAGATTTGTTTGTGTTTCCGACCTTTCTTCTGT 2785
Qy 2493 CAAGAAATTTGATGATTAAGTGGGAGCAAGTGAATGCAATAGTGTTCAGTTCCATATCTTA 2552
Db 2786 CAAGAAATTTGAATTTGGGGGG---AGGCAAGATGCAAGGGGTTTGTGCTCCATATCTTA 2842
Qy 2553 TCTCATGCTCTTACTTCCCTCCAAATGCTTAATTAACAAAGAGATGCTTCACTCCAGA 2612
Db 2843 TCTCATGCTCTTACTTCCCTCCAAAGATTTTCAAGATTTTCAAGTACACAGTGACTTCACTCGGA 2902

Qy	2613	AGAAATGTTCAAAAGCCCTTGGAAATTCGAATCTACTGAAATATCTCTTTTACTCAATCT	2672
Db	2903	AGAAATGTTCAAAACCTTGA AAAATCTCATATCTTGAGTCTCTTCTTTGAGAAATCT	2962
Qy	2673	TAAAGAGCTGCCTACAGCCTGGCTAGTCTCAATGCTTTGAAGCATCGAAATTCATAG	2732
Db	2963	CAAAAGCTGCTTACAGCCTGGCTAGTCTCAACATTTGAAGTGTGGAATATTCGTTA	3022
Qy	2733	TTGTTATGCACTAGAGAGTCTCCCGAGGAAGGTGTGAAGGTTTAATTTCACTCACACA	2792
Db	3023	TTGTTATGCACTAGAGAGTCTCCCGAGGAAGGCTGGAAGTTTATCTTCACTCACAGA	3082
Qy	2793	GTTATTCATTAATATCTGTGAATGCTAACATGTTTACCGAGGAGATTGCACACTTAAC	2852
Db	3083	GTTATTTGTTGAACACTGTAACTATGCTTAATATGTTTACAGAGGATGTGCAGCACTTAAC	3142
Qy	2853	AGCCTTCAGAAATTTATCATGTTGAGTTTGTTCCAACTGCGCCAAAGCGGTGTGAAAGGG	2912
Db	3143	AACCTTCAGAAATTTAAAAATTCGGGGATGTCCCAACTGATCAAGCGGTGTGAAAGGG	3202
Qy	2913	AATAGGAGAAACTGTCAAAATTTGCTCAATTCCTGATGTTTATTTAT	2964
Db	3203	AATAGGAGAAACTGTCAAAATTTTCTCAACTTCTTATATGTAATATATAT	3254

RESULT 10
US-10-360

```

? Sequence 53, Application US/10360522
? Publication No. US20030221215A1
? GENERAL INFORMATION:
? APPLICANT: Allefs, Josephus J.H.M.
? APPLICANT: Vossen v.d., Edwin A.G.
? TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
? TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
? FILE REFERENCE: U 014413-9
? CURRENT APPLICATION NUMBER: US/10/360,522
? CURRENT FILING DATE: 2003-02-07
? PRIOR APPLICATION NUMBER: EP 02075565.8
? PRIOR FILING DATE: 2003-02-08
? PRIOR APPLICATION NUMBER: PCT/NL03/00091
? PRIOR FILING DATE: 2003-02-07
? NUMBER OF SEQ ID NOS: 63
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 53
? LENGTH: 3899
? TYPE: DNA
? ORGANISM: Solanum bulbocastanum
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(3899)
? OTHER INFORMATION: /note="RGc4-b1b"
? US-10-360-522-53

```

Query Match 58.5%; Score 1736.2; DB 17; Length 3899;

Best Local Similarity 82.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 428; Indels 33; Gaps 7.

QY	426	AACAGGTTTTGTTTGGATGAAACCAAGTTTATGGAAGAGACAAAGAAAGAGACGAGAT	485
Db	1361	AACGGTTTTGTGTTAACTGAAACCAAAAGTCTACGGAAGGAGCAAAAGGGAGATGAGAT	1420
QY	486	AGTGAATAATCTGATTAACAATGTTAGCAATGCGCAAACTTCAGCTCTCCCAATCT	545
Db	1421	AGTGAATAATCTGATTAACAATGTTAAAGTTGCGGAAGAACTTCAGCTTCCCTTAAT	1480
QY	546	TGGTATGGGGGAGCTAGGAAGAAGACGACTTTGCCCAAAATGGTCTTCAATGATCAGAGGT	605
Db	1481	TGGTATGGGGGAGCTAGGAAGAAGACGACTTGGCCAAATGATCTTCAACGATGAGAGGT	1540
QY	606	AATTGACATTTCCATCCCAAAATATGATTTTGTCTTCGGAAGATTTTAATGAGAAAG	665
Db	1541	AACATGACATTTCCATCCCAAAATATGAGTTTGTCTTCAGATGATTTTATGAGAAAG	1600

QY	666	GTTCATTAAGAAATTGTAGAACTCTATTGAAAGAAAGTCACTTGCGGCANTGACCTTGGC	725
Db	1601	GTTAATTAAGCAATTATAGAAATATTTGAAAGAGTCTCTCATGTGTAGAGACTTGGC	1660
QY	726	TCCACTTCAAAAGAGCTTCGGGACTTCGTAATGCAATGCAAAAATAATTTGCTCGCTTAGA	785
Db	1661	TTCAATTTCAAGAGAGCTCCAGGAGTTATGTAAATGAAAAACGATACCTTGCTTGCTTAGA	1720
QY	786	TGATGTTTGGATGAAATGAAATGAAATGAGGGCTTAAGTAAAGCAAGTCTTGAAGTGG	845
Db	1721	TGATGTTTGGATGATGATCTAAGAAAGTGGGGCTTAAGTAAAGCACTCTTAACCTGTTGG	1780
QY	846	AGCAAGTGGCGCTCTGTCTTAACCACTACTCGCTTGAAAAGGTGGAATCAATTAAGG	905
Db	1781	AGCAAGAGGTGCTCTATTCTAGCTACTACTCGCTTGAAAAGGTGGAATCAATTAAGG	1840
QY	906	AACATTCAACCAATATGAATTTGCAAAATTTGTCTCAAGAAAGATTGTGTTGTGTTTCAT	965
Db	1841	AACGTTGCAACCAATATCAATTTGCAAAATTTGTCTCCACATGATAGTTTACTTTTGTAT	1900
QY	966	GCAACGTGCAATTTGGGCAACAGAGAAATPAACTTTAATCTTGTGGCTATCGAAAGGA	1025
Db	1901	GCAACGGGCATTTGGGCAACAAAAGAACAAATCTTAATCTAGTGGCCATTTGGAAGGA	1960
QY	1026	GATTGTGAAAAATGTGTGTGTGTGCTCTTAAGCAAGCTTAAACTCTTGGAGTATTTGGC	1085
Db	1961	GATTGTGAAAAATGTGTGTGTGTGCTTTAAGCAAGCCMAACCTTGGTGTCTTTTACG	2020
QY	1086	CTTTAAGAGAGAAAGAACAGTGGGAAACATGTGAGAGATAGTGAAGTTTGGAAATTGGC	1145
Db	2021	CTTCAAGAGAGAAAGATGATGATGAGAAACATGTGAGAGATATGAGATTTGGAGTCTGCC	2080
QY	1146	TCAAGAAAGAAAGTCTATTCTGTGCTGCTGCGCAGACTTAAGTAAACATCACCCTTCCACTGA	1205
Db	2081	TCAAGATGAAGAAAGTCTATTGCTGTGCTGCTTAAGCTGATTAATCATCACCCTTCCACTGA	2140
QY	1206	TTTGAAGCAATGCTTTACATATTGTGCAATTTCCCAAGATATCCGAATTGAAAAAGG	1265
Db	2141	TTTGAAGCAATGCTTTCCGTAATGTGCAATTTCCCAAGAACCCAAAATGATTAAGGA	2200
QY	1266	AAATCTAATCTCTCTCGATGAGGCAATGGTTTTATTATTCGAAGAGAACTTGAAGCT	1325
Db	2201	AAATCTCAATCTCTCTCGAATGGCGAATGGTTTTCTTTATTCGAAGGAAACTTGAAGCT	2260
QY	1326	AGAGATGATAGTAAATGAATGAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT	1385
Db	2261	AGAGATGATAGTAAATGAATGAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT	2320
QY	1386	TGAAGTAAATCTGTGCAAACTTATTCGAAGTCAATCTCATTAATGATCTGGCAAC	1445
Db	2321	TGAAGTAAATCTGTGCAAACTTATTCGAAGTCAATCTCATTAATGATTAATTAATTAATTAAT	2380
QY	1446	ATCTCTAATTTTGGCAAGCAATCAAGCAGCAATATCCAGAAATTAATTTGAAAAATTA	1505
Db	2381	ATCTCTGTTTTGGCAAGCCGATATGCGGCATATTCGGGAATTAATTAATTAATTAATTAAT	2440
QY	1506	CATACATATGATGTCCATGTGTTTCACTAAAGTGTATCTTCTTACTCTCTTCCACTT	1565
Db	2441	TAAACATATGATGTCCATGTGTTTCCGTGCAAGTGTCTTCTTACTCTCTTCCACTT	2500
QY	1566	GCAGAAGTTGTCTGTGTAAGGGTCTTAACTTAAGTACATTAATTAATTAATTAATTAATTAAT	1625
Db	2501	GAAAAAGTTGTCTGTGTAAGGGTCTTAACTTAAGTATTAATTAATTAATTAATTAATTAAT	2560
QY	1626	GCTTTCATTTGGAATCTAGTACATTTAAGATCTTAACTTGTGTGCAATTAATTAATTAAT	1685
Db	2561	GCTTTCATTTGGAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2617
QY	1686	TGCTAAGTCTTCCAAACCAATTAAGCAAGTTCGAATCTGCAAGCTTGTATCTAATTAATTAAT	1745
Db	2618	CCGTAAGTCTTCCAAAGAGGTTGTGCAAGCTTCGAATCTTCAAGCTCTGTATGATCAATTAAT	2677
QY	1746	CTGTCAATTCATTTGTTGTTTGGCCAAAAAGCAAGCAAACTTGATGATCTTGCAGAACT	1805

Db	475	CGTGAAGAGGTGCTCATCTTAACGTGTTTAAAGCAAGTACTTAATAGCTAGTTT	534
Oy	426	-----	425
Db	535	TATATTCACTTTTGTAGTACCAGATCTTATACATGTTGTTCCATGTCAGCCCTTCC	594
Oy	426	-----	425
Db	595	TTGTGCTTTTTGTTTGCAAAAATCTTATTAATTCGTCTACCTCTTTTAACTGAGCT	654
Oy	426	-----AAGGTTTGTGTTGAATGAACCA	450
Db	655	TGAATTTAATAAATTTGTGTTCGATTCCTTGGAACAAGTTTTTTTAAAGCAGAGCTT	714
Oy	451	CAAGTTTATGGAAGACAAAGAAAAGACGAGATAGTAAATCTCTGATTAACATGTT	510
Db	715	AAAGTTTATGGAAGGACAAAGAGAGATGATGATGTAATCTTGATTAACAGTGT	774
Oy	511	AGCAATGCCCAACACTTCACGTCTCTCCCATACTTGTGTATGGGGGAGCTTGAAAGCG	570
Db	775	AGTATGCGCCAAAGAACTTATAGTGTCTCCCAATCTTGATATGGGGGAGCTTGAAAGCA	834
Oy	571	ACTGTGCGCCAAATGAGTCTCAATGATCAGAGAGTAAATGAGCAATTCATCCCAATA	630
Db	835	AACCTGCGCCAAATGATTTTATGATCAGAGCGTGAAGCTGACATTTCAATCTTAAGATA	894
Oy	631	TGATTTTGTCTCGAGAGATTTTATGAGAAAGAGTGTATTAAGAAATGTAGATCT	690
Db	895	TGGTTTGTCTCAGATGATTTTGAATGAAAGAGTGTATTAAGCAATTTGTAGATCT	954
Oy	691	ATTGAGAAAAGTCACTGTGTGCGACATGACCTTGCTCCACTTCAAGAGAGCTTGGGAC	750
Db	955	ATTGAAAAGAGCCACTGTGTGACATTAACCTTGCTCCCTCCAGAGAACCTTCAGAG	1014
Oy	751	TTGCGATGAGAAAATAATTTGTGCTCTTAATGATGTTGGAAATGAAGATCAAGAT	810
Db	1015	TTGTGATGAGAAAAGATCACTTCTTGTTTAGTGAATGTTGAAATGAAGATCAGAA	1074
Oy	811	AAGTGGCGTAAGTTAAGACAAGCTCTTGAAGGTTGAGCAAGTGGCGCTTCTGTTCAAC	870
Db	1075	AAGTGGCGTAAGTTAAGACAAGCTCTTGAAGGTTGAGCAAGTGGCTTCTTATCTAGCC	1134
Oy	871	ACTACTGCTCTTGAAGAGTTGATCAATTAATGGAACATTGCAACCATATGAATTTGTA	930
Db	1135	ACTACTGCTCTTGAAGAGTTGATCAATTAATGGAACATTGCAACCATATCAATATCA	1194
Oy	931	AATTTGCTCAAGAGATTTGTTGTTGTTTCATGCAAGTGCATTTGGGCAACCAAGA	990
Db	1195	ATTTTGTCTCAGAGATTTGTTGTTGTTGTTTCAGCAACGTGCATTTGGGCAACCAAG	1254
Oy	991	GAAATTAATCTTAATCTTGTGGCTTTCGAAAGAGATTTGTGAAAAATGTGTTGTTG	1050
Db	1255	GAAACAAATCTGCGCTTGTGGGATTTGAAAAGAGATTTGTGAAGAAATGTGGGGTGTG	1314
Oy	1051	CCTCTAGACGATAAACTCTTGAAGTATTTTGGCTTTAAAGAGAAAGACAAGTG	1110
Db	1315	CCTCTAGACGCAAGACTCTTGAAGTCTTTTAAAGCTTCAAGAGAGAAAGTGAATGG	1374
Oy	1111	GAACTGTGAGAGATAGTGAATTTGAAATTTGCTCAAGAGAAAGTTCTATTTCTGCT	1170
Db	1375	GAACTGTGAGAGATAGTGAATTTGAAATTTGCTCAAGAGTGAATTTCTGTTTGGCT	1434
Oy	1171	GCCCTGAGACTTGAATTAACATCACTTGCATCTGATTTTGAAGACATGCTTTAACAATATG	1230
Db	1435	TCCCTGAGGCTGAATTAATCACTTGCATCTTAATTTGAGACAAATGTTTGCATATTTG	1494
Oy	1231	GCAATATTCCAAAGGATACGAAATGAAAAAGGAAATCTAATCTCTCTGTGATGGCA	1290
Db	1495	GCGGATATCCAAAGGACCCAAATTAAGAAAAGAAATATTCATCACTCTCGATGGCA	1554
Oy	1291	CATGCTTTATTTTATGAAAAGAACTTGAAGTGAAGATGTAAGTATGAGTATGG	1350

Dp	1555	CATGTTTCTTTTATCAAAAAGAAATTCAAGCTAGAGATGGGGTAATGAAGTATGG	1614
QY	1351	AATGAATATATCTAGAGCTCTTCTTCCAGAGATTGAAG---TTAAATCTGCGCAACT	1407
Dp	1615	AAAAGAAATTAATCTTGAGAGCTCTTCTTCCAGAGAGTCCAGAAATATATAATTTGGTAATCT	1674
QY	1408	TATTTCAAGATGAGATGATCTCATCTATCTGGCAATCTCTATTTTGGGCAAGACA	1467
Dp	1675	TATTTCAAGATGAGATGATCTCATCTATCTGGCAATTTGGCTACATCTCTGTTCTCACAAAACACA	1734
-QY	1468	TCAAGCAGCATATATCCGAGAAATATGTAGAAAATTACATACATATGATGTCATTTGGT	1527
Dp	1735	AGGAGCAGCAAAATTTGCGTCAAAATAGAGTGAACA---CAGAAAAATACAAATTCCTATTTGGT	1791
QY	1528	TTCACTAAAGTGGTATCTTCTTACTCTCTTTCCCACTTGCAGAAAGTTGTCTGTAGG	1587
Dp	1792	TTTCTGAGAGTGGGCGCTTCTTATCTTCCCTTAATCTTTAAAGGTTTGTCTGCTTAAGG	1851
QY	1588	GTGCTTAATCTAAATGACATTAATACTTAAGAGATTACCGCTTCATTTGGAGATCTAGTA	1647
Dp	1852	GTCTCTGATATGAATTTTCAAACTTTGATTCAGTTATCATCTTCCATCGAGATCTAATA	1911
QY	1648	CATTTAAGATATCTAAACTGTCTGCGAATACTAGATTTCGTAGTCTTCCAAACAGATTA	1707
Dp	1912	CATTTAAGGTGTGAACTTGACCTTGGCGTGC---AGTAGATTTGGTAGCTTCCAAAGAGTTA	1968
QY	1708	TGCAAGCTTCAAAATCTGCAGACTCTTGATCTACATGCGTGTCTATCACTTTGTTTGG	1767
Dp	1969	TGCAAGCTTCAAAATCTGCAGACACTTGATATATCATGTTGTTCTCATCTTCTTAATTT	2028
QY	1768	CCAAAGAAACAACAACAATTTGAGTCTTCGAAATCTTTTACATGATGGTGTATAGA	1827
Dp	2029	CCAAAGCAAAATAGATTAATTAAGTAGTCTTGAATCTTGTGTTCAAGTGTG---TCAA	2085
QY	1828	TTGACTTGTATGCGACCAAGAGATAGATCTTTTGACATGCGTTAAGACTCTAAGTAGATT	1887
Dp	2086	ATATCTTCTATGCCACCAAGAAATAGATATATGACATGCGCTTAAGACTCTAAGATTACTTT	2145
QY	1888	GTGCTGGGAATTCAGAGAAAAGTTGTCAACTTGGTGAATTAGAAACCTGAATCTCTAT	1947
Dp	2146	ATGTGCG---CGAGAGAAAAGTTATTCAACTTGGTAGACTACGGAATCTTAAGCTTCAAT	2202
QY	1948	GGCTCAATTTGAAATCAGCACTCTTGAGAGTGAAGATATATATGATGCAAAAAGAAAGCC	2007
Dp	2203	GGTTCACCTTTCMACTCACAATCTTGAGAGTGAAGGTGAAGAGATGCAAAAAGAAAGCT	2262
QY	2008	AATTTATCTGCAAAAAGAAATCTGCATCTTTTACATGCAAAATGGATGACATGAACGT	2067
Dp	2263	AATTTATCTACAAAACAAAATTTTCAATTTATGATGATGGATATTAAGGCCATAT	2322
QY	2068	CCAGCTATATATGAAATCAGAAAAAGTTG---AAGTGTGAAAGCTCTCAAAACCACTCC	2124
Dp	2323	GGATATGAAATCAGAAAAACAATTTGGATGAAAAGTGTGTAAGGCTTCAGACCACTCC	2382
QY	2125	AATCTGACTTGTTTAAACAATCAGGGGCTTCAGAGGAATCCGTCTCCAGACTGATGAAT	2184
Dp	2383	AACCTGAATCACAATCAAGCTCATCTATGGCTTCAGAGGTTTCAATTTCCAAATTTGATTAAC	2442
QY	2185	CACTCAGTTTGAAAAAGTGTGCTCTAATGAATCATCATGTTGCAAAAACCTGCTATGC	2244
Dp	2443	GCTTGGGTTTGAAAAAGTGTGCTCTAATGAATTTGAA---TGTGAAAACCTGTGGCGT	2499
QY	2245	TTACACACCTTTGGTGAAGTGCCTTGTCTAAAAAGTCTAAGATTGAGAGGGGCTTGGC	2304
Dp	2500	TTTACACACATTTGAGAGGCTGCGCTTGTCTAAGAAAGTTAATCAACGGAATCTGGC	2559
QY	2305	GAACTGAGATATGTT---GATTCTGGAATCCCTTACAGAAAGAGTTTCCATCTCTGAGA	2361
Dp	2560	GAGGTGAGATATATTTGAAGAGAGATGATGATCTTCCACATTAAGTTCCCATCTTGAAA	2619
QY	2362	AAACTTAAATATAGCGCAATTTGATATCTGAAAAGATTTGCTGAAAAAGAAAGAGAGAG	2421
Dp	2620	CGACTTGTATGAAGATTTTCCAAATCTGAAGAGACTGCTGAGATGAAAGAGAGAG	2679

QY 2422 CAATGCCCTGCTTGAAGAGATGAGATTAATGTGCCCCATGTTTATTCCAAAC 2481
Db 2680 AATTTCTTCATGCTTGAAGAAATGAAATTTGGCAATGCCCTATGTTTGTTCACCA 2739
QY 2482 CTTTCTTCTGCAAGAAATTTGATAGTGGGCAAGATGATGCAATAGGTTTCACT 2541
Db 2740 TTCTCTTCTGCAAGAAATTTGATAGTGGGCAAGATGATGCAATAGGTTTCACT 2796
QY 2542 TCCATATCTAATCTCATGAGCTTATCTTCCCTCCAAATTCGCTATTAACAAAGAGATCT 2601
Db 2797 TCCATATCTAATCTCATGAGCTTATCTTCCCTCCAAATTCGCTATTAACAAAGAGATCT 2856
QY 2602 TCACCTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTCAATATCTGATATCTTTT 2661
Db 2857 ACTCTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTGATATCTGATATCTTTT 2916
QY 2662 TACTTCAATCTTAAAGAGCTGCTACAGCCTGCTAGTCTCAATGCTTTGAAGCATCTG 2721
Db 2917 TTCAAAAACTCAGAGAGTTCGCAAGCAGCCTGCTAGTCTCAATGCTTTGAAGCATCTG 2976
QY 2722 GAATTCATGATTTGTATGCTAGAGAGTCTCCCGAGAGAGTGTGAAGGTTTAAAT 2781
Db 2977 AAAATTCATTTATTTGTAGCACTAGAGAGTCTCCCGAGAGAGTGTGAAGGTTTAAAT 3036
QY 2782 TCACCTCAGAGAGTTCATCAATACATCTGTAAGATGTTTACCGAGAGGATTTG 2841
Db 3037 TCACCTCAGAGAGTTCATCAATACATCTGTAAGATGTTTACCGAGAGGATTTG 3096
QY 2842 CAGCAGCTTAACAGCCTTCAAAATTTTACGTTGTTTTCACAGCTGCGCAAGCGG 2901
Db 3097 CAGCAGCTTAACAGCCTTCAAAATTTTACGTTGTTTTCACAGCTGCGCAAGCGG 3156
QY 2902 TGTGAGAGAGAGATGAG 2961
Db 3157 TGTGAG 3216
QY 2962 TATTAG 2967
Db 3217 TGTTAG 3222

RESULT 12
US-10-437-963-67879
; Sequence 67879, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Mei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 67879
; LENGTH: 2409
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68697C.1
US-10-437-963-67879

Query Match 9.2%; Score 274.4; DB 18; Length 2409;
Best Local Similarity 53.2%; Pred. No. 3.1e-61;
Matches 756; Conservative 0; Mismatches 636; Indels 30; Gaps 7;

QY 58 GAATTCGATGATCTTGTGTTTAAAGATGAGTTCGAAAAGCTTCAAGCAGCTTTACT 117
Db 76 GACATTAATTTGCTTGAAGATGTTAAGAGTACGTGAAAAGTTGAAAACCTCATTTGGGA 135
QY 118 ACAATTCAGCTGTCTAAGAGATGCTCAGAGAGCAATTTGAAGAGCAGGCAATAGAA 177
Db 136 GCTATTTGTGCTTCTGAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
QY 178 AATGTTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 234
Db 196 CATTTGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 255
QY 235 TGTAAAATGAGCAGCAATTTAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294
Db 256 GAGACAGAGATTTGAGCAG 315
QY 295 GTTATCATTTTGTCTCAGAGATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 354
Db 316 CTAACTCATTTTCTTTTGAAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375
QY 355 GTATTCAGCGAGAGAGATTTAAGTTTCAATTTGATGAGAGAGAGAGAGAGAGAGAGAGAG 408
Db 376 GAATTCAGCTGCTTAAAGAGATTTGAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 435
QY 409 ---CAGTTGCTACAGCAGCAAGAGTTTGTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAG 465
Db 436 GATCAATTTTGGCCAG 495
QY 466 GACAAAG 522
Db 496 GATTAAGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 555
QY 523 ACACTTCAGCTTCCCAATATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 582
Db 556 ACCCTGCTAGCTTCTCACTAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
QY 583 ATGCTCTCAATGATCAGAGATTAATGAGATTTCCATCCCAATTAATGAGATTTGTCTC 642
Db 616 CTGTTATTTATGATTAATCAACCAAGATTAATGATTAATGATTAATGATTAATGATTAAT 675
QY 643 TCGAAGATTTTATGAG 702
Db 676 TCTAATGCTTTGACCTTAAACATATTTGTAATTAATTAATTAATTAATTAATTAATTAAT 735
QY 703 TCACTTGTGAGATGAGCTTGTCTCCTCACTTCAAAAGAGCTTGGAGCTTGTGATAGAG 762
Db 736 AGCAATTAACCAATTAACCTTGAAGAGATTAACAAAGAGAGAGAGAGAGAGAGAGAGAG 795
QY 763 AAAAATATTTGCTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 822
Db 796 AAGAGATCTTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 852
QY 823 TTAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 882
Db 853 TTGATTAACCTGCTACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
QY 883 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942
Db 913 ACMAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972
QY 943 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002
Db 973 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1032
QY 1003 AATCTTGTGCTATCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062
Db 1033 GAGTTACTTAATAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1092
QY 1063 AAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1122
Db 1093 AGAATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1149
QY 1123 GATAGTGAATTTGAAATTTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1182

Db 1150 GAAATATATTTGCTGAGTACTGCGAAGGTAAGATGATATCTGTCAGTATTTAAACCTC 1209
Qy 1183 AGTTACGATCACTCCGCTGATTTGAGCAATGCTTACATATTTGAGAGTATTC 1242
Db 1210 AGTTATGATGACCTTCCATCTGATTTAAACTGTTTTTCTGGTATTCACCTTTTCCA 1269
Qy 1243 AAGATACCGAATGTAAGAAAGGAAATCTAATCTCTCTGATGAGCAGATGCT---TTT 1299
Db 1270 AAGAGCTATGATTTTTCAGAGAACTTATATATATGATATGATGAGCAATGGCTTATTTG 1329
Qy 1300 ATTTTATGAAAGAAAGAACTTGAGCTAGAGAAATGATGATATGAAATGAAATGTA 1359
Db 1330 AATCCAGCTAGTCACTAGAGGAGCAATTAAGAGTGGAGAGAAATATCTTATATAGCTT 1389
Qy 1360 TACTGAGCTCTTTTCTCCAGAGATGATGATGATTAATCTGTCGAA-----CTTATTTG 1413
Db 1390 GCTGGAAGATCTTTTCTCCAGACTATGTTTTTAATCATGATGGAGCAATCTCACATTGC 1449
Qy 1414 AAGATGATGATCTCATTCATGATCTGCAACATCTCTATTT 1455
Db 1450 AAATGATAGCTTGTCTTCTCATGATCTAGCAATATCTGTCT 1491

RESULT 13

US-10-437-963-79971
Sequence 79971, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boudharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 79971
LENGTH: 3333
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1
US-10-437-963-79971

Query Match 9.1%; Score 269; DB 18; Length 3333;

Best Local Similarity 52.1%; Pred. No. 1e-59;
Matches 748; Conservative 0; Mismatches 645; Indels 42; Gaps 5;

Qy 7 GAAGTTTCCCTCAAGTCTGTAGACAATCGACTGTTTTCATCCAGGGGAACTTGA 66
Db 22 GAGGCTTTCATGCAACCCCTCTTCCAGAAATTTGAGAGCAACCTTGATCATTTCTA 81
Qy 67 TTGATTTCTGTTTAAAGATGATTCGAAAAGCTTCAAGCAGCTTTACTACATCCAA 126
Db 82 TCTTGAAGAGCATATCATGAGAGCTAGAGCCCTCTTCCACATCTCTCAAGTTACG 141
Qy 127 GCTGTCTAGAGATGCTCAGAGAGCAATTTGAAGCAAGAGCAATTAAGAAATTTGTTG 186
Db 142 GCTTCTCTTGAAGAGCTGAGAGAGCAATTTGAAGATGATCATCTGTAGAGGAGTGGCTA 201
Qy 187 CAGAACTCATATGCTGCTGATGATGAGGCTGATGATCTTGAAGAGATGTAATGAG 246
Db 202 GCGAAGCTCAAGATATGCGTACGACCTTGTATGATCTGCTGAGAGCTATTCAGCCAA 261
Qy 247 GCACCAATTAGACAGAGAGAAACAATATGAGGTGTATCATCCAAAGTTATCATCTTT 306

Db 262 AGTATGCGCATGAAGACAGAGGAGGTATATTTCCCAACAAAGCAAGTTTCTTTCTCC 321
Qy 307 -----CGTCAAGATTTGGGAAAGAGATGAAAGATATATG 342
Db 322 TCTTTCTGATGAGAAATCTGTACAGCATATGATTAAGCATTAAGATTAACATCATTTG 381
Qy 343 GAGAACTGATGATTTTTCAGCGGAAAGCAATTAAGTTTCAATTTGATGAAAGACTATA 402
Db 382 GAGAGATTAATGATTTGCGCAAGAACGCAACATTTGGGCTTCAGATATATGTGA 441
Qy 403 GAGAGCAAGTTGCTAC-----ACGCCAAACAGTTTGTTTTCAATGAAACCAAA 453
Db 442 ATGAGACGATATGATCTTCAAGCGTCCGAATCAAGTTCTCTTGTATGATATGTTCCGCT 501
Qy 454 GTTATGAGAAAGACAAAGAAAGAGAGATGAGAAATCTGAT---AAACAAATGT 510
Db 502 GTATTTGTAG 561
Qy 511 AGCAATGCCAAACATCTCCAGTCTCCCAATCTGATGAGGAGAGCTAGAAAGAG 570
Db 562 CATATATCTGCACTTATGATGATTCAGATGTTGGCATGGGCTTGTAAACT 621
Qy 571 ACTCTGCGCAATGCTTCAATGATCAGAGATTAATGAGCATTTCCATCCAAATA 630
Db 622 ACTCTTATGAGATGGTGTACATGATGACAGAGTAAGAGAACTTTGACTTGAGATC 681
Qy 631 TGAATTTGTCTGGAAGATTTAATGAGAAAGGTTGATTAAGAAATGTATGAAATCT 690
Db 682 TGAATCTATGATGTTGAAAGTTTGAATGAGAAAGCTTAACAAAGAACTTTGAGCT 741
Qy 691 ATTTG---AAGAAAGTCACTGTGAGATGAGTCTGCTCCACTTCAAAAGACCTTCG 747
Db 742 TCTGATATGACCAATCTGTTGATGATCTAATGATATGATCAAGAGAAACCTCTCC 801
Qy 748 GACTTCTGATGAGAAATTAATTTGCTGCTCTTATGATGATGTTGATGAAAGATCA 807
Db 802 AGAGTATTTGCGGGGCAAGAGGTACTGCTGCTTGAATGATGATGATGAAAGACCTT 861
Qy 808 GATATGAGGCTAATTAAGCAAGTCTGTAAGGTTGAGAGAGTGGCGCTTCTGTTCTA 867
Db 862 GATTAATGACACACTATAGAGAGCTTAAATTTCAAGAGGTTTGGAGAGAGATAGT 921
Qy 868 ACCACTACTGCTCTTGAAGAGTGTGATCAATTAAGGAACTTGAACCATATGAAATG 927
Db 922 GTGATCAGAGAAATGAGAAATGTTGGCAGATCATGAGAGAAATAGAGCCCTCAAGATTA 981
Qy 928 TCAATTTGTCTCAAGAGATTTGTTGTTTTCATGCAAGCTGATTTGGGCACTAA 987
Db 982 CAGAACTATCAGATGATGACAGCTGCTGTATTAAGAGCCATGCAATTTAGGAGATG 1041
Qy 988 GAGAAAT---TAATCTTAATCTGTGCTATGAGAAAGAGATTTGAAATTAATGTGCT 1044
Db 1042 GACTGACGCGCACATCCGAGTTGAGGCGATGAGAAATGAGAAATGAGAAAGCTGAAG 1101
Qy 1045 GGTGTGCTCTAGAGCTTAAACTCTTGAAGATTTTTCGCTTTAAGAGAGAAAGAA 1104
Db 1102 GGATTTGCTCTGATCAAGAGCATTTAGAGAGCTCTGTTTTCGAAACGATGAGAG 1161
Qy 1105 CAGTGGAAACATGTGAGAGATGATGAAATTTGAAATTTGCTCAAGAGAAAGTTCTATT 1164
Db 1162 GAGTGAAGAGACATATGCAAAATGACATATGAGAGTTACCGGAGATTAAGAAATACATC 1221
Qy 1165 CTGCTGCGCTGAGACATTAATGATCAATCACTTCCACTGATTTGAGCAATGCTTACA 1224
Db 1222 CTGCAAGCTTCACTTGAATTAACCACTTTTACACACATCTTAAAGCAATGCTTGCA 1281
Qy 1225 TATGTCAATATTTCCAAAGATACCGAAATGAGAAAGGAAATCTAATCTCTCTG 1284
Db 1282 TTCTGTTCTGTAATCTTAAGATTAATATGTTACAGAGAGAAACGTGTTAATATCTG 1341
Qy 1285 ATGCAATGATTTTATTTATTTATGAAAGAACTTGAAGCTAGAGAAATGATGAA 1344
Db 1342 CTAGCACTTGTGTTTCAATCAGACAGTATGAGAAAGAGAAATGAGATATCTGAAATGCA 1401

OY 1345 GTATGGAATGATTAATTAAGGCTTTCTTCCAGAGATTGAAGTTAAATCG 1339
DB 1402 TACTTAAATGAGTAAATTAAGCAGGCTTTCTTCCAGCCATATGAAATTAATGATG 1456

RESULT 14

US-10-437-963-33626
; Sequence 33626, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33626
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3771C.1
US-10-437-963-33626

Query Match 9.1%; Score 268.6; DB 18; Length 3615;
Best Local Similarity 57.0%; Pred. No. 1.4e-59;
Matches 553; Conservative 0; Mismatches 409; Indels 9; Gaps 3;

OY 421 CGCCAAACAGGTTTGTGTTGAATGAACACAGATTGAGAGCAAGAAAGAGAC 480
DB 814 CCCAAGACCACTGTTAATGACAGCTGAGTGTATGTAGAGAAAGATTAAGAG 873
OY 481 GAGATAGTGAATAATCTGATTAACAGATGTAGCAATGCCCA---AACACTTCAGTCTCT 537
DB 874 GTCTTTGTAACATGTTACTCACCACGATTAACCAATGCAACTTTTATTTCTT 933
OY 538 CCAATCTTGTATGAGGGGAGCTAGGAAAGACGACTCTTGGCCAAATGCTTCAATGAT 597
DB 934 CCCATAGTGGGTATGAGGAGTAGGAGAAACAATTAAACACAGCTCTACAAATGAT 993
OY 598 CAGAGAGTAATGAGCAATTCATCCCAAAATATGAGATTTGTCTGAGAAATTTTAT 657
DB 994 GTGAGAGTAAGAAAGCAATTTCCAGTTAAGATGTGGCTGTGTCTTCTGAAAACCTTGAT 1053
OY 658 GAGAAAGGTTGATTAAGAAATTTGAAATCTATTG---AAGAAAGTCACTTGTGGC 714
DB 1054 GAGGCCAAACTTACCAAGAGAAACGATAGATCAGTGTGAGCGGATTTATCTCGCCACA 1113
OY 715 ATGACCTTGGCTCCACTTCAAAAGAGCTTGGGACTTGTCTGAATGAAAAAATATTGG 774
DB 1114 ACAAACATGAACCTGCTTCAAGAGACCTCTCAACAGCTGAAAGGAAAAAGGTTTCTT 1173
OY 775 CTGCTTTAGATGATGTTTGGATGAGATCAAGTAAAGTGAAGGCTAAGTTAAAGCAAGTC 834
DB 1174 CTAGTATTTGAGTATGATGAGATGAGATCTCTGATGATGAGTAAAGTACCGATGTGCT 1233
OY 835 TTGAAGTTGAGCAAGTGGCGCTTCTGTTAAACCACTACTGCTTGAAGAGTTGGA 894
DB 1234 CTATTTGCTGGTGCAAAAGAGTAATAATTTATGATCTACTCGAAATGAAAAATGTTGG 1293
OY 895 TCAATTTAGGCAACATTGCAACATATGATTTGCAAAATTTGTCTCAAGAAAGATTGTTGG 954
DB 1294 AAATTAAGTGGCGGGTGAATCTTACTATCAAAAACAGTTATCATATCAATGATGTGCTG 1353

OY 955 TTGTTTCATGCAACGCGCATTTGGGACCAAGAAAGAAA---TAAATCTTAATCTTGTG 1011
DB 1354 CATTTATTCAGACGATATGATTTTGCAGATGTGATCTCCAGTGACACCCAAATTTGGAA 1413
OY 1012 GCTATCGAAAAGAGATTGAAAAAATGTGTGTGCTCTAGACGCTAAAACTCTT 1071
DB 1414 ATGATCGCAAGAAATTTGCTCATATGATGTAAGAGCCCTACCATATAGCTGCAAGAGCTTTA 1473
OY 1072 GGAAGTATTTTGGCTTTAAGAGAAAGAAAGACAGTGGAAACATGTGAGATATGAG 1131
DB 1474 GGTGCTTATTTATGTGTTAAGGACACAGAGATGACTGAAAAATATCTTAAGAAAGTAA 1533
OY 1132 ATTGAAATTTGCTCAAGAAAGAAAGTTCTATTGCTGCTGCTGAGACTAGTTTACAT 1191
DB 1534 ATATGGAATTTGCTCATGACAAAGAAATATATCTTACAGCTGCGAGACTAGTTACAT 1593
OY 1192 CACCTTCACCTGATTTGAGCAATGCTTTACATATTTGTGCAATTTCCAAAGATACC 1251
DB 1594 CATCTTCACCCATATTTGAAGCCGATGCTTGTGATTTGCTGCTGCTTCAACAAAGACTAT 1653
OY 1252 GAAATGAAAAAGGAATCTAATCTCTCTGATGTGCAATGCTTTTATTTATCGAAA 1311
DB 1654 GTGTTTGAAGAAACATATTTGTTCAGATCTGAGTGGCAAGTTGGTACATCAGCTCAA 1713
OY 1312 GGAATCTTGAAGCTAGAGAAATGTAGTAAATGATGAAATTAATCTTGAGGCTCT 1371
DB 1714 GGGCGGAGAAAGATGAGAAAGATTTGGGAATATATCTTATGATTAATCTGAGAGATCC 1773
OY 1372 TTCTTCCAAG 1382
DB 1774 TTCTTCCAAA 1784

RESULT 15
US-10-437-963-33659
; Sequence 33659, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33659
; LENGTH: 3852
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3774C.1
US-10-437-963-33659

Query Match 9.1%; Score 268.6; DB 18; Length 3852;
Best Local Similarity 57.0%; Pred. No. 1.4e-59;
Matches 553; Conservative 0; Mismatches 409; Indels 9; Gaps 3;

OY 421 CGCCAAACAGGTTTGTGTTGAATGAACACAGTTTATGGAAGAGCAAGAAAGAGAC 480
DB 827 CCCAAGACCACTGTTAATGACAGCTGAGTGTATGTAGAGAAAGATTAAGAG 886
OY 481 GAGATAGTGAATAATCTGATTAACAGATGTAGCAATGCCCA---AACACTTCAGTCTCT 537
DB 887 GTCTTTGTAACATGTTACTCACCACGATTAACCAATGCAACTTTTATTTCTT 946
OY 538 CCAATCTTGTATGAGGGGAGCTAGGAAAGACGACTCTTGGCCAAATGATGTCTCAATGAT 597

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2005, 14:12:11 ; Search time 8497 Seconds
(without alignments)
13291.360 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967

Sequence: 1 atggctgaagcttcctcca.....ctcgctgcttattattag 2967

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_eat1:
2: gb_eat2:
3: gb_hcc:
4: gb_esc3:
5: gb_esc4:
6: gb_esc5:
7: gb_esc6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610.8	20.6	670	7	CR61977 33106 In
2	540.4	18.2	594	4	BG096938 EST161457
3	510	17.2	729	4	BG890602 EST16453
4	483	16.3	717	5	BQ111670 EST597246
5	473.6	16.0	732	6	CV499954 64358.1 M
6	472	15.9	664	4	BG097566 EST462085
7	462.8	15.6	808	7	CN214760 28498.8
8	449.8	15.2	618	4	BT191903 EST139826
9	421.2	14.2	935	7	CV434731 58221.1 S
10	415	14.0	668	4	BG593905 EST492583
11	414	14.0	577	5	BQ117360 EST602936
12	402	13.5	631	2	AM035144 EST76112
13	399.8	13.5	598	5	BM011700 EST619115
14	385	13.0	592	2	AM907068 EST143100
15	383.2	12.9	668	7	CV496683 60822.1 M
16	369.6	12.5	575	2	AM032553 EST176112
17	346.2	11.7	885	9	CG944135 MBEN024TF
18	325.8	11.0	882	9	CG939127 MBERT46TF
19	325.4	11.0	571	7	CM644273 7934.1 Af
20	315.4	10.6	424	2	AM928868 EST137656
21	308.2	10.4	418	2	BE342109 EST194950
22	304.8	10.3	787	9	CG956037 MBEC53TF
23	291.6	9.8	504	2	BE920178 EST423947
24	289	9.7	686	8	AZ773501 T221249b

C 25	288.8	9.7	819	9	CG972611 MBEL43TF
C 26	285.8	9.6	886	2	CG965962 MBEP65TR
C 27	282	9.5	407	2	AM032184 EST175638
C 28	280.8	9.5	716	7	CV469963 42731.1 C
C 29	276	9.3	2409	9	CL979800 OBIFCC04
C 30	275.4	9.3	875	9	CG960374 MBEGK4TF
C 31	270.6	9.1	3333	9	CL960744 OBIFCC037
C 32	266.4	9.0	712	9	CR494610 Medicago
C 33	262.2	8.8	375	4	BG096371 EST460890
C 34	258.6	8.7	872	9	CG927653 MBEBP90TR
C 35	253.8	8.6	680	9	AZ773502 T221250b
C 36	253.2	8.5	1902	9	CL979799 OBIFCC04
C 37	251.4	8.5	454	2	AM979927 EST134581
C 38	251	8.5	863	9	CG931272 MBEG87TF
C 39	246.8	8.3	932	9	CG944419 MBECG67TF
C 40	246.4	8.3	1714	9	CL955053 OBTRU000
C 41	240.4	8.1	2499	9	CL944015 OBIFSB01
C 42	240.4	8.1	2499	9	CL965216 OBIFCC01
C 43	238.8	8.0	804	9	CG919643 MBEGH93TR
C 44	237.6	8.0	432	5	BO505531 EST612946
C 45	236.8	8.0	368	2	AM979626 EST141225

ALIGNMENTS

RESULT 1
CR61977
LOCUS 33106 In vitro Root Solanum tuberosum cDNA, mRNA sequence.
DEFINITION CR61977
ACCESSION CR61977.1 GI:45291634
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 670)
Flinn, B., Kothwell, C., Sardana, R., Griffiths, R., Laque, M., De
Koeper, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruksa, G. and Regan, S.
Generation of ESTs from in vitro root tissues of potato
Unpublished (2004)
COMMENT
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

source
Location/Qualifiers
1..670
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/issue_type="Root"
/lab_host="XL10-Gold"
/clone_lib="In vitro Root"
/note="Vector: pBluescript II SK(+) XR, Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Sterile stem
sections from pathogen-free Solanum tuberosum var.
Shepody, clone 1756, nuclear stock were cultured in
Magenta boxes containing 1/10 strength MS medium,
solidified with 0.8% (w/v) Phytagar. Roots of all sizes,
originating from the stem bottoms were collected from
these cultures, washed to remove residual Phytagar, and
used in RNA isolations and library construction."

ORIGIN

Query Match 20.6%; Score 610.8; DB 7; Length 670;
Best Local Similarity 94.5%; Pred. No. 2.1e-149;
Matches 633; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Cy 889 GTTGACATCATTTGGACATTCGACACATGATTCGCAATTTGTCTCAAGAGAT 948

Source	Organism	Reference Authors	Title	Journal	Comment
Solanum tuberosum (potato)	Solanum tuberosum	Bukarjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.	1 (bases 1 to 729)	van der Hoeven R., Bezzerides J., Ewing E., Cho J., Chienlingo A., Bougri, O., Buell, C.R., Ronning, C., Tankeley, S. and Baker, B. Generations of ESTs from dormant potato tubers Unpublished (2001)	Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potato-array@igr.org This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/ Seq primer: M13F-R.
Location/Qualifiers					
1..729					
/organism="Solanum tuberosum"					
/mol_type="mRNA"					
/cultivar="Kennebec"					
/db_xref="taxon:4113"					
/clone="cSTID18P22"					
/tissue_type="dormant tuber"					
/dev_stage="one month post-harvest"					
/lab_host="SOLR"					
/clone_lib="cSTD"					
/note="Vector: pBluescript SK(-), Site_1: EcoRI, Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tankeley lab notebooks."					
ORIGIN					
Query Match	17.2%; Score 510; DB 4; Length 729;				
Best Local Similarity	82.9%; Pred. No. 8,3e-123;				
Matches	607; Conservative	0; Mismatches	120; Indels	5; Gaps	2
QY	76 GGTTTAAGATGAGTTCGAAAGCTTCAAGACGTTTACTACATCCAAAGCTGTGCTA	135			
Db	1 GGTTCCTCAAAATGAGTTCGAAAGCTTCAAGACGTTTACTACATCCAAATCCGTCCT	60			
QY	136 GAAGTGTCTGAAAGACCATTTGAAGACCAAGGCAATAGAAATTTGGTTCGAAATCTC	195			
Db	61 GAAGTGTCTGAAAGACCATTTGAAGACCAAGGCAATAGAAATTTGGTTCGAAATCTC	120			
QY	196 AATGCTGTCATATGAGCTGATGACATCTTGACAAATGTAATCGAGGACCAAT	255			
Db	121 AAGCTGTCATATGAGCTGATGACATCTTGACAAATGTAATCGAGGACCAAT	177			
QY	256 AGACGAAAGAAACCAATATGGGTATATCATCCAAAGT-TATCATCTTTCGTACA	313			
Db	178 CGATTCCTCCAGTCTGATATGGCCGTATATCATCCAAAGTATATCTTCCTTCGTACA	237			
QY	314 AGATTTGGAAAAGATGAAAAAGATTTAGGAAATCTGATGTAATTCGACGGAACGA	373			
Db	238 AGGTCGGGAAAAGATGGAACCAAGGATGCAAAAGCTTAAATGCAATTCGAGGAAGAA	297			
QY	374 TTAAGTTTCATTTGGATGAAGACATATAGAGAGACAAAGTTCATGACGCCAAACAGGT	433			
Db	298 AGAATTTTCATTTGACGAAATATATATACAGAGACATCTGTTAGTAGAAGAAACAGTT	357			
QY	434 TTGTTTGAATGAACCAAGTTTATGGAAGAGCAAAAGAAAGACGAGTATGTAA	493			
Db	358 CTGATATTAATGAACCAAGTATATGGAAGGACAAAGAGAGATGAGTATGTAA	417			
QY	494 TCCGATTAACAAATGTTAGCAATGCCCAACATTCAGTCTCCCATATCTTGGTATGG	553			

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	B011670	EST597246 mixed potato tissues Solanum tuberosum cDNA STWC32	B011670	5'	end, mRNA sequence.	B011670	Solanum tuberosum (potato)	1	(bases 1 to 617)	Buelli, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Reestepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and Karamycheva, S.A.	Generation of a set of potato cDNA clones for microarray analyses unpublished (2002)	On Apr 17, 2002 this sequence version replaced gi:20163632.
Qy	554	GGGACATGAGAAAGACGACTCTTCCCAATGGTCTTCAATGATCAGAGATTAATGAC	613									
Db	478	GGGACATGAGAAAGACGACTCTTCCCAATGGTCTTCAATGATCAGAGATTAATGAC	537									
Qy	614	ATTTCATCCCAAAATATGATTTGTGTGCTCGAAGATTTTAATGAGAAAGGTTGATTA	673									
Db	538	ATTTCATCCCAAAATATGATTTGTGTGCTCGAAGATTTTAATGAGAAAGGTTGATTA	597									
Qy	674	AGGAATTTGTAGATTCATTTGAGAAAGAAAGTCACCTTGGTGAGTGGACTTGGCTCCATTC	733									
Db	598	AGGAATTTGTAGATTCATTTGAGAAAGAAAGTCACCTTGGTGAGTGGACTTGGCTCCATTC	657									
Qy	734	AAAAGAAGCTTGGGACTTGGTGAATGAGAAAAATATTTTCTGCTTGAATGATGTTT	793									
Db	658	AAAAGAAGCTTGGGACTTGGTGAATGAGAAAAATATTTTCTGCTTGAATGATGTTT	717									
Qy	794	GGATGAAAGATC 805										
Db	718	GGATGAAAGATC 729										
RESULT 4												
LOCUS	B011670	617 bp	mRNA	linear	EST 07-MAR-2003							
DEFINITION	B011670	EST597246 mixed potato tissues Solanum tuberosum cDNA STWC32										
ACCESSION	B011670											
VERSION	B011670.2	GI:21915068										
KEYWORDS	EST.											
SOURCE	Solanum tuberosum (potato)											
ORGANISM	Solanum tuberosum											
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.											
AUTHORS	Buelli, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Reestepo, S., Griffiths, H., van der Hoeven, R., Tsai, J., and Karamycheva, S.A.											
TITLE	Generation of a set of potato cDNA clones for microarray analyses unpublished (2002)											
JOURNAL	On Apr 17, 2002 this sequence version replaced gi:20163632.											
COMMENT	Contact: Robin Buelli The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Email: potato-array@tigr.org This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL: http://genome.arizona.edu/orders/ Seq primer: T3. Location/Qualifiers											
FEATURES												
SOURCE	1..617											
	/organism="Solanum tuberosum"											
	/mol_type="mRNA"											
	/cultivar="Kennebec or Binje"											
	/db_xref="taxon:4113"											
	/clone="STM32"											
	/tissue_type="mixed tissues"											
	/lab_host="SOLR"											
	/clone_id="mixed potato tissues"											
	/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Supplier: Combination of untreated and Phytoptophora infestans-treated libraries of scions, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."											
ORIGIN												
Query Match	16.3%;	Score 483;	DB 5;	Length 617;								
Best Local Similarity	87.4%;	Pred. No. 1e-115;										
Matches 541;	Conservative 0;	Mismatches 75;	Indels 3;	Gaps 1;								

Db 2 GGATGCGGTAATGAGTATGAAACAATTATCTGAGGCTCTTTTCCAAAGATTGA 61
Qy 1389 AGTTAAATCTGCGCAAACTTATTTCAAGATGCAATCTCATTCATGATCTGGCAATC 1448
Db 62 AGTTAAATCTGCGCAAACTTATTTCAAGATGCAATCTCATTCATGATCTGGCAATC 121
Qy 1449 TCTATTTTGGGCAAGACATCAAGCAATATCCAGAAATTAATTGTAGAAATATGACAT 1508
Db 122 TCTGTTTGGGCAAGACATCAAGCAATATCCAGAAATTAATTGTAGAAATATGACAT 181
Qy 1509 ACATATGATGCTCATTTGTTTCACTAAAGTGTATCTTCTCTTTCCCACTTGA 1568
Db 182 ACATATGATGCTCATTTGTTTCACTAAAGTGTATCTTCTCTTTCCCACTTGA 241
Qy 1569 GAAGTTGCTGCTGAGGAGTGTATATCATGATGCAATAAATTAACCACTTACCGTC 1628
Db 242 GAACCTTGTCTGTTAGGAGTGTATCTGATATTTCTTAAATCAATCACTTACCGTC 301
Qy 1629 TTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGTGCAATATCTAGTATTCG 1688
Db 302 TTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGTGCAATATCTAGTATTCG 361
Qy 1689 TGTCTTCCAAACAGATTATGCAAGCTTCAAAATCTGCAAGCTCTTGTATCTATGCTG 1748
Db 362 TGTCTTCCAAACAGATTATGCAAGCTTCAAAATCTGCAAGCTCTTGTATCTATGCTG 421
Qy 1749 TCATTCACCTTGTGTTTCCAAAGAAACAGCAAACTTGTATCTTCCAAATCTTT 1808
Db 422 CACCTCATTCTTGTGTTTCCAAAGAAACAGCAAACTTGTATCTTCCAAATCTTT 481
Qy 1809 ACTTATGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1868
Db 482 ACTTATGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Qy 1869 TAAGACTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1928
Db 542 TAAGACTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
Qy 1929 AGCAAACTGATCTAT 1947
Db 599 AGCAAACTGATCTAT 617

RESULT 5
CVA99954/c 732 bp mRNA linear EST 04-OCT-2004
LOCUS 64358.1 Mixed Leaf Solanum tuberosum cDNA clone 64358 5', mRNA
DEFINITION
ACCESSION CVA99954.1 GI:53782311
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 732)
Film, B., Rochwell, C., Sardana, R., Griffiths, R., Jague, M., De
Koeber, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Puski, G., and Regan, S.
Generation of ESTs from a normalized developing leaf library
Unpublished (2004)
Contact: Barry Film
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bfilm@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
1..732
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultiVar="Shepody"
/db_xref="taxon:4113"

FEATURES
source

/clone="64358"
/cisse_type="Leaves"
/lab_host="XL10-Gold"
/clone_id="Mixed Leaf"
/note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Plants from
pathogen-free Solanum tuberosum var. Shepody, clone 1756,
nuclear stock were grown in a greenhouse under natural
conditions. Emerging, expanding and mature leaves were
harvested along the length of the plant and pooled. RNA
was isolated and used for library construction. A
normalized library was constructed following a modified
protocol of Bonaldi et al. (1996). Genome Research 6:
791-806."

ORIGIN

Query Match 16.0%; Score 473.6; DB 7; Length 732;
Best Local Similarity 88.9%; Pred. No. 3.3e-113;
Matches 523; Conservative 0; Mismatches 64; Indels 1; Gaps 1;

Qy 2379 ATTGTTATCTGAAAGATTTGCTGAAAGAAAGAAAGCAATGCCCTGCTTGA 2438
Db 732 ATTGTTATCTGAAAGATTTGCTGAAAGAAAGAAAGCAATGCCCTGCTTGA 674
Qy 2439 AGAGATGAGATTAATGTTGCTGCTATGTTTATTCACACCTTTCTGCAAGAA 2498
Db 673 AGAGATGATTTATTTACATGCTGCTATGCTTATTTCCACCTTTCTGCAAGAA 614
Qy 2499 ATTGTTATGTTGAGGAGCAATGATGATGATGATGATGATGATGATGATGATGAT 2558
Db 613 ATTGTTATGTTGAGGAGCAATGATGATGATGATGATGATGATGATGATGATGAT 554
Qy 2559 GGCTTACTTCTCCCTCAATTTGCTATTAACAAGAAAGCTTCTCCCAAGAGAT 2618
Db 553 GGCTTACTTCTCCCTCAATTTGCTATTAACAAGAAAGCTTCTCCCAAGAGAT 494
Qy 2619 GTTCAAAAGCTTCAAAATCTCAATTTGCTATTTTACTTCAATTTTAAAG 2678
Db 493 GTTCAAAAGCTTCAAAATCTCAATTTGCTATTTTACTTCAATTTTAAAG 434
Qy 2679 GCTGCTACCAAGCTGCTGCTATGCTATGCTTGAAGCATCTGGAATTCATGTTGTTA 2738
Db 433 ATTGCTTACCAAGCTGCTGCTATGCTATGCTTGAAGCATCTGGAATTCATGTTGTTA 374
Qy 2739 TGCACTAGAGAGCTCCCGAGAGAGTGAAGGTTTAAATTTCACTACAGTTATC 2798
Db 373 TGCACTAGAGAGCTCCCGAGAGAGTGAAGGTTTAAATTTCACTACAGTTATC 314
Qy 2799 CATPACATCTGTAATGCTACATGTTTACCGAGAGATTCAGACACCTTACAGCCCT 2858
Db 313 CATPACATCTGTAATGCTACATGTTTACCGAGAGATTCAGACACCTTACAGCCCT 254
Qy 2859 CACAAATTTATCTGATGTTTGTCCACACCTGCGCAGCGGTGAGAAAGGAATAG 2918
Db 253 CACAAATTTATCTGATGTTTGTCCACACCTGCGCAGCGGTGAGAAAGGAATAG 194
Qy 2919 AGAAGACTGGTCAAAATTTGCTACATTTCTGCTGTTTATTTATTA 2966
Db 193 AGAAGACTGGTCAAAATTTGCTACATTTCTGCTGTTTATTTATTA 146

RESULT 6
BG097566 664 bp mRNA linear EST 07-MAR-2003
LOCUS EST462085 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION
ACCESSION BG097566
VERSION BG097566.1 GI:12587601
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Bakeryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;


```

Db      195 TTGGTTGCAAAAACCTCAAGTTGCTACATATGAGTTGATGACATCTTGATGATATATA 254
Qy      240 AACTGAGGACCAATTAGACAGAAAGAAACAATATGGGTGTTATCATCCAAAGCTTAT 299
Db      255 AACTAAGGCGACA---CGTTTCTCCAGCTGTCATATGCGCTTATCATCCAAAGCTTAT 311
Qy      300 CACTTTTGTGCAAGATTTGGGAAAAGATGAAAAGATTAATGAGAACTAGATGATAT 359
Db      312 CCTTTTCCCTCAAGAGTGGGAAAAGATGAACTAGTATGAGAAACATAATGCAAT 371
Qy      360 TGCAGGGAACGAATTTAGTTTCATTTGGATGAAAAGACTATATAGAGACAAAGTTGTAAC 419
Db      372 TGCAAAAGAAAAGAAAGATTTTCATTTGACGAAAAGATTAATAGAGACAAAGTTGTAAC 431
Qy      420 AGCCCAAAAGAGTTTGTGTTTGAATGAAACCAAGTTTATGGAAGACAAAGAAAAGAA 479
Db      432 ATGTAAACAGAGTTCTGTATTTGACCGAACACAAAGTTTATGGAAGGACAAAGAAAGAA 491
Qy      480 CGAGATAGTAAATCTGTATTAACATGTTAGCAATGCCCAACACTTCCAGTCTCC 539
Db      492 TAAAGTATGTAATCTTGATTAATGATGTTGATGATGCCCAACACTTCCAGTCTCC 551
Qy      540 AATACCTTGATGGGAGGACTAGAAAGACGACTCTT-GCCCAATGCTCTTCAATGATC 598
Db      552 AATACCTTGATGGGAGGACTAGAAAGACGACTCTTGGCCGGAATGATCTTCAATGATC 611
Qy      599 AGAGAGTATGAGATTTCCATCCCAAAATATGATTTGCTGCTCGGAAGATTTATG 658
Db      612 AGAAAGTACTAAGAGATTTCTATCCCAAAATATGAGTTGCTGCTCGGAATGATTTGATG 671
Qy      659 AGAAGAGGTTGAT-AAAGGAAATTTAGATCTATTTGAAGAAAGTCACTTGTTG- 713
Db      672 AGAAGAGGTTGATTAAGGCAATTTAGATCTATTTGAAGAAAGGCACTTACTTGCGGGA 731
Qy      714 --CATGACTTGCTCCACTTCAAAAGAAAGCTTGGGAACTTGCTGATGAGAAAAATAT 771
Db      732 CATGGAGCTTGAGATCCCACTTCAAAAGAAAGTTCCAGAGCTTGTTGAATGGGAAAAAGAT 791

```

```

RESULT 8
BI919903      618 bp      mRNA      linear      EST 10-MAR-2003
LOCUS      EST539826 potato microtubers, in vitro-grown Solanum tuberosum cDNA
DEFINITION      clone CSTE23018 5' end, mRNA sequence.
ACCESSION      BI919903
VERSION      BI919903.1 GI:16215919
KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 618)
van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R.,
Karameycheva,S.A., Tsai,J., Van Aken,S., Uteerback,T., Chiemiango,A.,
Bougri,O., Buell,C.R., Romling,C., Tanksley,S. and Baker,B.
Generation of ESTs from in vitro grown microtubers (2001b)
Unpublished (2001)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

```

```

FEATURES
Source
1..618
Location/Qualifiers

```

```

/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"

```

```

/clone="CSTE23018"
/tissue_type="axillary buds of stem explants; growing
sink-tubers"
/dev_stage="7, 8 and 10 days"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cDNA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996). Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucrose medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds. The
first library, cST1 (1-20) consists of axillary buds
harvested on days 1-3. This targets those genes involved
in induction of the microtubers. The following libraries,
cST1 (21-40) and cST1 (41-60), capture genes involved in
tuber initiation and outgrowth. This library is noted as
p3 in Tanksley lab notebooks."

```

```

ORIGIN
Query Match      15.2%; Score 449.8; DB 4; Length 618;
Matches 521; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

```

```

Qy      39 GACTTGTTTATCCAGAGGGAACCTTGATGATCTTGTTTAAAGATGATGCAAAA 98
Db      1 GACTTCTTATCCAAAGGAACCTTGATGATCTTGTTTAAAGATGATGCAAAA 60
Qy      99 GCTTCAAGCAAGTTTACTTCAATCCAGCTGCTGTAAGATGCTCAAGAAAGCAATT 158
Db      61 TATTTGAGAGAGGTTTCTTCAATCAAGCCGCTTGAAGATGCTCAGAGAAAGCAACT 120
Qy      159 GAAGACAAAGCAATGAATAATGTTGTCAGAAAGTCAATGCTGCAATATGAGGCTGA 218
Db      121 AAAGACAAAGCAATTAATAATGTTGTCAGAAAGTCAATGCTGCAATATGAGGCTGA 180
Qy      219 TGACATCTTGAGCAATGTAATAATGAGGCAATTAAGACAGAAAGCAATATATGG 278
Db      181 TGACATCTTGAGCAATGTAATAATGAGGCAATTAAGACAGAAAGCAATATATGG 237
Qy      279 GTGTTATCAATCCAAAGCTTATCACTTTGCTCAAGATTTGGGAAAGATGAAAGAT 338
Db      238 GCGTTATCAATCCAAAGCTTATCACTTTGCTCAAGATTTGGGAAAGATGAAAGAT 297
Qy      339 TATGAGAAACATGATGTAATTCAGCGAAGCAATTAAGTTTCATTTGGATGAAAGAC 398
Db      298 GATGAGAAACATGATGTAATTCAGCGAAGCAATTAAGTTTCATTTGGATGAAAGAC 357
Qy      399 TATGAGAGCAAGATGCTACACGCCAAACAGGTTTGTGTTGAATGAACCAAGTTTA 458
Db      358 TATGAGAGCAAGATGCTACACGCCAAACAGGTTTGTGTTGAATGAACCAAGTTTA 417
Qy      459 TGAAGAGCAAGAAAGAGAGAGATGTAAGAAATCCGATTAACAATGTTAGCAATGC 518
Db      418 TGAAGAGCAAGAAAGAGAGATGTAAGAAATCCGATTAACAATGTTAGCAATGC 477
Qy      519 CCAAACTTCCAGCTCTCCCAATACCTTGATGAGGAGGACTAGAAAGACGACTTTGC 578
Db      478 CCAAGAGCTTTGAGTCTCCCAATACCTTGATGAGGAGGACTAGAAAGACGACTTTGC 537
Qy      579 CCAATGCTTTCATGATGAGAGATTAATGAGCAATTTCCATCCCAATATGATTTG 638
Db      538 CCAATGCTTTCATGATGAGAGATTAATGAGCAATTTCCATCCCAATATGATTTG 597
Qy      639 TGTCTCGAAGATTTTAATGA 659
Db      598 TGTCTCGAAGATTTTAATGA 618

```

RESULT 9
CV434731 935 bp mRNA linear EST 29-SEP-2004
LOCUS 58221.1 Suspension culture Solanum tuberosum cDNA clone 58221 5',
DEFINITION mRNA sequence.
ACCESSION CV434731 GI:52844021
VERSION CV434731.1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 935)
Plum, B., Rothwell, C., Sardana, R., Griffiths, R., Lagre, M., De
Koeijer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruksa, G., and Regan, S.
Generation of ESTs from potato suspension cultures
Unpublished (2004)
TITLE JOURNAL
COMMENT The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflim@bioatlantech.nb.ca
Seq primer: 73.
FEATURES
source
1..935
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="58221"
/issue_type="Callus-derived suspension culture"
/lab_host="XLI0-Gold"
/clone_lhb="Suspension culture"
/note="Vector: pBluescript II SK(+) XE; Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Callus was
induced from Shepody, Clone 1756, sterile stem sections by
culture on Callus Induction Medium (CIM), comprised of MS
medium (pH 5.6) containing 10 mg/L thiamine-HCl, 0.1 mg/L
kinetin and 3 mg/L 2,4-D solidified with .8% (w/v)
Phytagar. Suspensions were induced by placing callus from
the plates into 125 ml Erlenmeyer flasks with liquid CIM
(no Phytagar) at a density of 10% (w/v) in volumes of
approximately 30-35 ml. Cells were subcultured weekly by
transfer to fresh media, with the density remaining at 10%
(w/v) and the volume remaining around 30 ml. Cells were
collected for RNA isolations and library construction 5
days after subculture."

ORIGIN
Query Match 14.2%; Score 421.2; DB 7; Length 935;
Best Local Similarity 85.5%; Pred. No. 2.3e-99;
Matches 518; Conservative 0; Mismatches 78; Indels 10; Gaps 4;
1355 AATTATCTGAGGCTTTCTCCAGAGATGAATTAATCTGCAACTTATTTCA 1414
Db 1 AATTATCTGAGGCTTTCTCCAGAGATGAATTAATCTGCAACTTATTTCA 60
Qy 1415 AGATGATGATCTCATTCATGATCTGGCAACATCTCTATTTTGGCAAGACATCAACA 1474
Db 61 AGATGATGATCTCATTCATGATTTGGCTACATCTCTGTTTGGCAACATCAACA 120
Qy 1475 GCATATCCGGAATATTTGAGAAATTTACATCATGATGCGCATTTGGTTCACTA 1534
Db 121 GCATATCCGGAATATTTGAGAAATTTACATCATGATGCGCATTTGGTTCACTA 180
Qy 1535 AAGTGTATCTTCTACTCTCTTTTCCACTTGCAAGATTTGTCGTTGAGGGTGC 1591
Db 181 AAGTGTATCTTCTACTCTCTTTTCCACTTGCAAGATTTGTCGTTGAGGGTGC 240
Qy 1592 TTAATCTAAGTACATAAATTAAGAGTTACCGTCTTCCATTTGAGATCTAGTCA 1651
Db 241 TTAATCTAAGTACATAAATTAAGAGTTACCGTCTTCCATTTGAGATCTAGTCA 300

Qy 1652 TAAGATACCTAACTTGCTGCGCAATAGTATTCGTAGTCTTCCAAACCGATTATCA 1711
Db 301 TAAGATACCTAACTTGCTGCGCAATAGTATTCGTAGTCTTCCAAACCGATTATCA 357
Qy 1712 AGCTTCAAAATCTGCAAGCTTTGATATCTACATGCGCTGTCATTCATCTTTGTTGCCAA 1771
Db 358 AGCTTCAAAATCTGCAAGCTTTGATATCTACATGCGCTGTCATTCATCTTTGTTGCCCTA 417
Qy 1772 AAGAAACAGAACTTGATGCTTGAATCTTTTACTGATGATGTTGCATGATTTGA 1831
Db 418 AAAAAACAGAACTTGATGCTTGAATCTTTTACTGATGATGTTGCATGATTTGA 477
Qy 1832 CTTGTATGCCACCAAGATAGATCTTTGACATGCTTAAAGACTTAAAGATTTGTTGG 1891
Db 478 TTTGTATGCCACCAAGATAGATCTTTGACATGCTTAAAGACTTAAAGATTTGTTGG 537
Qy 1892 TGGCAATTCAGAGAAAGTTGCACTTGCTG- AATTACGAAACCTGAATCTTATGCGC 1950
Db 538 TTGGCA--AGAGAAAAAGTGTCACTTGCTGTAAGTACGAAATCTGAATCTTATGCGC 594
Qy 1951 TCATTT 1956
Db 595 TCAGTT 600

RESULT 10
BG593905 668 bp mRNA linear EST 07-MAR-2003
LOCUS EST492583 cSTS Solanum tuberosum cDNA clone STS5J14 5' sequence,
DEFINITION mRNA sequence.
ACCESSION BG593905
VERSION BG593905.1 GI:13612045
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 668)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chieningo, A.,
Bougrit, O., Buell, C.R., Romming, C., Tanksley, S., and Baker, B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
CONTACT: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
FEATURES
source
1..668
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="STS5J14"
/issue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone_lhb="cSTS"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

ORIGIN
Query Match 14.0%; Score 415; DB 4; Length 668;
Best Local Similarity 87.6%; Pred. No. 9e-98;

TITLE
JOURNAL
COMMENT

Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES

Source

Location/Qualifiers

1..631
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEC32D21"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato callus, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory; cLEC - cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

ORIGIN

Query Match 13.5%; Score 402; DB 2; Length 611;
Best Local Similarity 80.9%; Pred. No. 2.4e-94;
Matches 520; Conservative 0; Mismatches 111; Indels 12; Gaps 4;

1397 CTGGCAACATTTATTTCAAGATGATGATTCATTCATGATCTGGCAATCTCTATTT 1456
1 CCGGAATATCTTATTTCAAGATGATGATTCATTCATGATTTGGCTACATCTCTGTTT 60

1457 CGGCAAGACATCAAGACGATATCCGAGAAATATTGAAATTTACATACATATGA 1516
61 TGGCAAGGCAATCAAGACGATATCCGAGAAATATTGAAATTTACATACATCA 120

1517 TGTCCATTGGTTTCACTAAAGTGTATCTTCTTCTCTTCCACTTGGCAAAAGTTTG 1576
121 TGTCCATTGGTTTCCGTGAGTGTGTCTTCTTCTCTCTCCACTTGGAAAAAGTTTG 180

1577 TCTGCTTGAAGGTGGTTTATCTAAGTGAATTAACCTTAAGAGTTACCGTCTCCATTG 1636
181 TCTGCTTGAAGGTGGTTTATCTAAGTGAATTAACCTTAAGAGTTACCGTCTCTATTTG 240

1637 GAGATCTAGTACATTAAGTACCTAAACTGTCTGGCAATACCTAGTATTCGATGTTTC 1696
241 GAGATCTAGTACATTAAGTACCTAAACTGTCTGGCAATACCTAGTATTCGATGTTTC 297

1697 CAAACCACTTATGCAAGCTTCAAAATCTGCAAGCTCTTGAATCTAAGTGGTCTCATTCAC 1756
298 CAGAGAGGTATGCAAGCTTCAAAATCTGCAAGCTCTTGAATCTAAGTGGTCTCATTCAC 357

1757 TTTGTTGTTTGGCAAAAGAAACAGCAAACTTGGTGAAGCTTCTGAAATCTTTTACTGATG 1816
358 TTAATTTGTTTGGCAAAAGAAACAGCAAACTTGGTGAAGCTTCTGAAATCTTTTACTGATG 417

1817 GTTGCTATGATGATGCTGTATGACCAAGAGATAGATCTTTGACATGCTTAAAGATC 1876
418 ---GCTGTCATGATGCTGTATGACCAAGAGATAGATGTTGACATGCTTAAAGATC 474

1877 TAACTAGATTTGTGTGGAAATTCAGAAAGAAAGTTGCACTTGGTGAATTAAGAAAC 1936
475 TAGGTTTCTTATTTGTGGAAA---GCAAGAAAGGTCATCACTCGGTGAACGAAAAAC 531

1937 TGAATCTCTAAGGCTCAATTAAGATCAGCAATCTTGAAGAGTGAAGATTAATGATG 1996
532 TAAATCTTTGGGCTCAATTTCAATGCAACCTTGAAGAGTGAAGATTAATGATG 591

1997 CAAAGAAAGCAATTTATCTGCAAAAGAAATCTGATTTCTT 2039

Db 592 C---CGAAGCAATTTATCTGCAAAAGCAATCTGCAATCTTT 631

RESULT 13

BO511700

LOCUS

DEFINITION

BO511700 598 bp mRNA linear EST 07-MAR-2003
EST019115 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STMHT23
5' end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: T3.

FEATURES

Source

Location/Qualifiers

1..598
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Bintje"
/db_xref="taxon:4113"
/clone="STMHT23"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/clone_lib="generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

ORIGIN

Query Match 13.5%; Score 399.8; DB 5; Length 598;
Best Local Similarity 81.4%; Pred. No. 8.8e-94;
Matches 489; Conservative 0; Mismatches 107; Indels 5; Gaps 2;

76 GGTTTAAGATGATGTTGCAAAAGCTTCAAGACGTTTCTACATCAAGTGTGCTA 135
1 GGTTTAAGATGATGTTGCAAAAGCTTCAAGACGTTTCTACATCAAGTGTGCTT 60

136 GAAATGCTCAGAGAAAGCAATTCACGACGACCACTTGAATTTGGTCAAAAATC 195
61 GAAATGCTCAGAGAAAGCAATTCACGACGACCACTTGAATTTGGTCAAAAATC 120

196 AATGCTGCTGATTTGAGGCTGATGACATCTTGGACGAATTAACCTGAGCACCAAT 255
121 AATGCTGCTGATTTGAGGCTGATGACATCTTGGATTAATTAACCTGAGCACCA 177

256 AGACAGAAAGAAACAATATGGGTGTTATCATCAAGCT--TATCATTTTGTGACA 313
178 GATTTCTCCAGTGTGATATGCGGTTTATCATCAAGGTTATATCCCTTCCGTACA 237

314 AGATTTGAAAAAGATGAAAAAGTTATGAGAACTAGATGTAATTGACGCGAAGCA 373

238 AGTCGGGAAAGATGATGACCAAGTGATGACAAAGCTAAATGCAATTCGTGAGAAAGA 297
QY 374 TTAAGTTTATTTGATGAAAGACATATGAGAGACAACTTCTACGCCCAACAGGTT 433
Db 238 AGAATTTTCAATTTGACGAAATATTTATACAGAGCAATCTGTATGATGAGAAACAGGTT 357
QY 434 TTGTTTGAATGACACCAAGTTTATGAAAGAGACAAAGAAAGACGATATGAAAA 493
Db 358 CTGTTTATTTATGACCAAGATATATGAAAGGACAAAGAGAAATGATATGATGAA 417
QY 434 TCTGATTAACCAATGTTAGCAATGCCCAACCACTTCAGTCTCCCAATATCTGTATGG 553
Db 418 TCTGATTAACCAATGTTAGCAATGCCCAACCAATGCTCCCAATATCTGTATGG 477
QY 554 GGGGACTGGAAGAGCACTCTTGGCCCAATGCTCTTCAATGATGAGAGATGATGAGC 613
Db 478 GGGGACTGGAAGAGCACTCTTGGCCCAATGCTCTTCAATGATGAGAGATGATGAGC 537
QY 614 ATTTCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAAAGATGATTA 673
Db 538 ATTTCATCCCAAAATATGATTTGTCTCGAAGATTTTATGAGAAAGATGATTA 597
QY 674 A 674
Db 598 A 598

RESULT 14

AM907068 592 bp mRNA linear EST 10-MAR-2003
LOCUS EST343100 potato stolon, Cornell University Solanum tuberosum cDNA
DEFINITION clone cSTASM3, mRNA sequence.
ACCESSION AM907068
VERSION AM907068.1 GI:8071187
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 592)

van der Hoeven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R.,
Holt,I.E., Liang,F., Hansen,T.S., Uteback,T., Bowman,C.L.,
Doan,B., Bougri,O., Buell,C.R., Roming,C.M., Tankley,S.D. and
Baker,B.

Generation of ESTs from potato swelling stolons
Unpublished (1999)

TITLE JOURNAL

COMMENT

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.

FEATURES

source

Location/Qualifiers
1..592
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="cSTASM3"
/issue_type="axillary buds of stem explants, swelling stolons"
/dev_stage="1 to 3 days"
/lab_host="SOLR"
/clone_lib="potato stolon, Cornell University"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; RNA was supplied by Christian Bachem & Beatrix Horvath (Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem et

ORIGIN

Query Match 13.0%; Score 385; DB 2; Length 592;
Best Local Similarity 89.2%; Pred. No. 7e-90;
Matches 415; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

al. (Plant Journal 1996). Tissue samples were taken of
stages corresponding to growing stolons and the early
stages of tuber formation."

QY 733 CAAAGAAAGCTTGGGACTTGTCTGAATGAAAAAATATTTGCTGTAGATGATGT 792
Db 128 CAGAAAGAGCTTCAGCAGTTGTGAATGAAAAAGATACCTTGTCTTATGATGATGT 187
QY 793 TGAATGAAGATCAAGATTAAGTGGCTAAGTAAACAAGCTTGAAGCTTGAAGCAAGT 852
Db 188 TGAATGAAGATCAAGATTAAGTGGCTAAGTAAAGCTGTCTTGAAGCTTGAAGCAAGT 247
QY 853 GGCCTCTCTGTTCTTACACCACTACTGCTTGAAGAAAGTTGGATCAATATGGAACAATGG 912
Db 248 GGTGCTTCTGTTCTTACACTACTGCTTGAAGAAAGTTGGATCAATATGGAACAATGG 307
QY 913 CAACCATATGAAATGTCAAATTTGTCTCAAGAGATTTGGTGTTCATGCAACGT 972
Db 308 CAACCATATGAAATGTCAAATTTGTCTCAAGAGATTTGGTGTTCATGCAACGT 367
QY 973 GCATTTGGGACCAAGAAATTAATCTTAATCTTGTGCTATCGGAAGAGATGTTG 1032
Db 368 GCATTTGACATCAAGAAATTAATCTTACCTTGTGCTATCGGAAGAGATGTTG 427
QY 1033 AAAAAATGTTGTTGTTGCTGTAGCAGCTAAACTTGTGAGAGTATTTGGCTTTAAG 1092
Db 428 AAAAAATGTTGTTGTTGCTGTAGCAGCTAAACTTGTGAGAGTATTTGGCTTTAAG 487
QY 1093 AGAGAAAGAAACAGTGGGAACATGTAGAGATGATGATTTGGAATTCCTCAAGAA 1152
Db 488 AGAGAAAGAAACAGTGGGAACATGTAGAGATGATGATTTGGAATTCCTCAAGAA 547
QY 1153 GAAAGTCTATTCCTGCTGCTCGAGACTAGTTACCATCACTT 1197
Db 548 GAAATGCTATTTTGTGCTGCTCGAGACTAGTTACCATCACTT 592

RESULT 15

CV496683 668 bp mRNA linear EST 04-OCT-2004
LOCUS CV496683
DEFINITION 60822.1 Mixed Leaf Solanum tuberosum cDNA clone 60822 5', mRNA
sequence.
ACCESSION CV496683
VERSION CV496683.1 GI:53779040
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 668)

Keyser,D., Audy,P., Goyer,C., Li,X-Q., Wang-Prunki,G. and Regan,S.
Generation of ESTs from a normalized developing leaf library
Unpublished (2004)

TITLE JOURNAL

COMMENT

Contact: Barry Filim
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bfilim@bioatlantech.nb.ca

Seq primer: T3.
Location/Qualifiers

FEATURES

source

Location/Qualifiers
1..668
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="60822"
/issue_type="Leaves"

/lab host="Xl10-Gold"
 /clone lib="Mixed Leaf"
 /note="Vector: pBluescript II SK(+), XR, Site_1: EcoRI,
 Site_2: XhoI; supplier: Developmental series, Plants from
 pathogen-free Solanum tuberosum var. Shepody, clone 1756,
 nuclear stock were grown in a screenhouse under natural
 conditions. Emerging, expanding and mature leaves were
 harvested along the length of the plant and pooled. RNA
 was isolated and used for library construction. A
 normalized library was constructed following a modified
 protocol of Bonaldo et al. (1996). Genome Research 6:
 751-806."

ORIGIN

Query Match	Similarity	12.9%	Score 383.2	DB 7	Length 668
Best Local	Similarity	75.9%	Pred. No. 2.2e-89		
Matches	560	Conservative	0	Mismatches 103	Indels 75
				Gaps	4
Qy	2101	CTTGAAGCTCTCAAAACCACTCCATCTGA	CTTGTTTAACAATCAGGGGCTTCAGAGA	2160	
Dy	1	CTTGAAGCCTTCAAAACCAACCCCAATCTGA	CTTCTTTAACAATCAATGAGCTTCAGAGA	60	
Qy	2161	ATCCGCTCTCCAGACTGGATGTAATCAGT	CTTGTGGAAAAATGTTGCTCTAATGAAATC	2220	
Dy	61	TTCCGCTCTCCAGAGTGGATGAATCAGTCA	CTCAGCAATGAAAAATATGCTCTAATGTAAAT	120	
Qy	2221	ATCAGTTGCAAAAACTGCTCAATGCTTAA	CAACCTTTGGTGAAGTCCCTGCTCAAAAAGT	2280	
Dy	121	ACCGACTGCAAAAATCTGCTCTGCTTACCA	CCCTTTGGTGAATCTGCTCTGCTCAAAAAGT	180	
Qy	2281	CTAGAGT-----TGTGAGGGGGGTCTGG	AGAGTGAATGTTGATTTCTGGAATTCCTTA	2335	
Dy	181	CTAGAGTTACAAATATGGTGTGTGAGATAT	GTGATGTTGATGTTGATTCCTGATTTCCCA	240	
Qy	2336	CAABAAGAAGTTTCCATCTCTGAGAAAAC	TTAATATACGGAATTTGATATCTGAAAG	2395	
Dy	241	GAAATAATATGGGTTTCCATCCCTGAGAAA	CTTTGTATATCAATTTTGGATATCTGAAAG	300	
Qy	2396	GATTGCTGAAAAAGGAAGAAAGCAATGCC	TGCTGGAAGATAGATGATTAAT	2455	
Dy	301	GATTGATGAAAAAGGAAGAGAGCAATTCCT	GCTGCTTGAAGATGAGATTCAC	360	
Qy	2456	GTTGCCCTAATCTTGTATATTCAAACCTTT	CTTCTGTCAGAAATTGTAAGTGGGG	2515	
Dy	361	ATTTCCTCC-----TATTCGACCCCTTCT	-----	383	
Qy	2516	ACAAGTCAGATGCAATAGTTTCAAGTTCAT	ATCATCTGATGGCTTCACTTCCCTCC	2575	
Dy	384	-----	-----TCTAATCTTGAAGCTCTTATCTTCCCTCA	411	
Qy	2576	AAATTCGCTATATACAAAGAGATGCTTCACT	CCGAGAAAGAGATGTTCAAAAGCTTGCAA	2635	
Dy	412	ACATTAAGATATATGAGAAAGATATCTTCA	TATACAGAAAGATGTTCAATAGCTTGCAA	471	
Qy	2636	ATCTCAAAATCTTGAATATCTCTTTTATCTT	CAATCTTAAAGAGCTGCTTACAGCTCG	2695	
Dy	472	ATCTCAAAATCTTGAATATCTCTCTTTATCT	CAATCTTCAAAAGAGCTGCTTACAGCTCG	531	
Qy	2696	CTAGTCTCAATGCTTTGAAGCATGCGAAAT	TTCAATGTTATGATGTTATGCACTAGAGATCTCC	2755	
Dy	532	CTAGTCTTAAATGCTTTGAAGAGCTTCCAA	TTTGAATTTTCGAGACCATAGAGAGCTCC	591	
Qy	2756	CCGAGGAAGGTGTGAAAGGTTTAATTTCACT	CACAGACAGTATTCATATACATATCTGTAAA	2815	
Dy	592	CAGAGGAAGGGGTGAAAGG--TTAACTTCA	TTCACCGAGTATTCGTTAATCTGTAAAG	650	
Qy	2816	TGCTACAATGTTTACCGG	2833		
Dy	651	TGCTAAAATGTATACCGG	668		

Search completed: April 16, 2005, 20:33:49
Job time : 8504 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2005, 20:42:26 ; Search time 9229 Seconds
(without alignments)
5187.318 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFGLVLDNLTCFIQGE.....EKIGEDWYKIAHPRVFIY 988

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/p/US10647266/runat_15042005_154719_26473/app.query.fasta_1.1159
-DB=genbml -QMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647268.cogn_1.1_6279_@runat_15042005_154719_26473 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genbml:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ats:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3774	73.6	79178	8	AY303170 Solanum b
2	3766.5	73.5	2913	6	AX814112 Sequence
3	3766.5	73.5	2913	6	AX816331 Sequence
4	3648	71.2	3260	6	AX814115 Sequence

5	3648	71.2	3260	6	AX816334
6	3648	71.2	3260	8	AY426260
7	3642	71.0	163635	8	AY303171
8	3638.5	71.0	3592	6	AX814113
9	3638.5	71.0	3592	6	AX816332
10	3638.5	71.0	5191	6	AX816333
11	3638.5	71.0	6824	6	AX336128
12	3638.5	71.0	7349	6	AX814114
13	3638.5	71.0	7349	6	AY426259
14	3606.5	70.3	3971	6	AX814116
15	3606.5	70.3	3971	6	AX816335
16	3606.5	70.3	3971	8	AY426261
17	3604.5	70.3	3641	8	AY426266
18	3594	70.1	3344	8	AY426265
19	3543	69.1	3196	8	AY426263
20	3518.5	68.6	3689	8	AY426264
21	3420.5	66.7	163635	8	AY303171
22	3400	66.3	3899	8	AX814117
23	3400	66.3	3899	6	AX816336
24	3400	66.3	3899	6	AY426262
25	3400	66.3	79178	8	AY303170
26	2048.5	40.0	53203	8	AP006683
27	2020.5	39.4	118130	2	AC148359
28	2011.5	39.2	122089	8	AC137552
29	2000.5	39.0	119925	8	AC123572
30	1993.5	38.9	124758	2	AC133864
31	1987.5	38.8	114098	8	AC144459
32	1977.5	38.6	148813	2	AC135162
33	1961	38.2	65807	2	AC146556
34	1951	38.1	122167	2	AC146806
35	1945.5	37.9	120197	2	AC124216
36	1938	37.8	124857	2	AC134049
37	1936	37.8	133198	2	AC137553
38	1916.5	37.4	120576	8	AC136141
39	1903	37.1	114576	8	AP004490
40	1898	37.0	135702	2	AC126785
41	1846.5	36.0	133198	2	AC137553
42	1839.5	35.9	122058	2	AC135312
43	1726.5	33.7	125127	8	AC146971
44	1580.5	30.8	187651	8	AC129718
45	1517	29.6	172541	8	AP003073

ALIGNMENTS

RESULT 1
AY303170/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanales; Solanum.
1 (bases 1 to 79178)
Song,J., Bradeen,J.M., Naess,S.K., Raasch,J.A., Wielgus,S.M.,
Haberlach,G.T., Liu,J., Kuang,H., Austin-Phillips,S., Buell,C.R.,
Heigeson,J.P., and Jiang,J.
Gene RB cloned from Solanum bulbocastanum confers broad spectrum
resistance to potato late blight
Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)
JOURNAL
PUBMED
REFERENCES
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

repeat_region
16833 .16854
/rpt_family="AT_rich"
complement(<18598 .>21580)
/locus_tag="CB3A14.2"
/note="contains Pfam profile PF04819 (plant viral response family)"
complement(join(<18598 .19075,21234 .>21580))
/locus_tag="CB3A14.2"
/product="putative plant viral-response family protein"
complement(join(18598 .19075,21234 .21580))
/locus_tag="CB3A14.2"
/codon_start=1
/product="putative plant viral-response family protein"
/protein_id="AAP45159.1"
/db_xref="GI:32470632"
/translation="MGSPFGCHVLPGLFLVIGVGMHTMSALVYRSSNPKSRFRVWSP
PGRGDQKYELELVVIAIGGIDPCIELFSTHRLRVHGVLANVNNNEBHAGMLLM
VIRGLVYLSEKTSFLPDRGALCLAAVAFSEYFLPFHSTTHGLGYYHLILV
LIGLCITLTITAGALMPTSPDILASGISVALQGLMFWQYAPFLYGMWPDGOLKGN
VMORSDBSEVRGGLLNLQLFMSIFPLVLAATTGAYGFAASETHKDIRMSH.PLOG"
19594 .19617
/rpt_family="AT_rich"
20891 .20925
/rpt_family="AT_rich"
22568 .22692
/rpt_family="(T)n"
22954 .23034
/rpt_family="AT_rich"
23085 .23140
/rpt_family="AT_rich"
23319 .23371
/rpt_family="AT_rich"
23685 .23705
/rpt_family="AT_rich"
23772 .23821
/rpt_family="A-rich"
24167 .24292
/rpt_family="(TTA)n"
24312 .24369
/rpt_family="AT_rich"
complement(<24447 .>26791)
/locus_tag="CB3A14.3"
/note="similar to transposase related protein GB:CAB51950
GI:5690095 (Zea mays)"
25874 .26005,26221 .26418,26711 .>26791)
/locus_tag="CB3A14.3"
/product="putative transposase-related protein"
complement(join(24447 .24871,24982 .25195,25412 .25663,
25874 .26005,26221 .26418,26711 .26791))
/locus_tag="CB3A14.3"
/codon_start=1
/product="putative transposase-related protein"
/protein_id="AAP45161.1"
/db_xref="GI:32470634"
/translation="MKESQLVLAAYKTDNSDKFRGQNNIIFKIMTVAFVVAAGSDYIG
VWEIEPKKMWKPSFKTLPALRCNGSYDMMASVIAKADLTCEPNDLSIIGNSNBSE
LSDHSNNIHDPPTVKNQPADPEBPCEEMQARKYECSDRFRIKYTGHSCEGVA
EHANSHSRKISIKVASCNNMVRDGGKPNVCLIORAFNSFHGSPSYKCMKGVAGL
KEMGLLVAASDDDNHNYPIVFCVVDKENASMSFPREKIKETVDEPNI.CFISDRH
KSIANGVYNNHMLRQMPDAALVLEHDIPEKMSRAHBSGNRYDWTNTIASLVNV
MLINRKYPMESIPNLAKRFGELFRFHAIILSLMGQNVPAHEKTLARKMTGDSL
YVRANTGNGQTVFVGCVTVLVLDLEKSCSKRYDLIKH"
27359 .27432
/rpt_family="(CATATA)n"
27448 .27499
/rpt_family="CT-rich"
complement(<28031 .>32001)
/locus_tag="CB3A14.4"

mRNA

CDS

/note="similar to NBS LRR resistance like protein B11
GB:AAK6316 GI:14348616 (Phaseolus vulgaris)"
complement(join(-28031..30681,31575..32001))
/locus_tag="CB3A14.4"
/product="putative disease resistant protein RGA1"
complement(join(28031..30681,31575..32001))
/locus_tag="CB3A14.4"
/codon_start=1
/product="putative disease resistant protein RGA1"
/protein_id="AAP45163.1"
/db_xref="GI:32470636"
/translation="MAEAFIQVLDNLTSLFKELVLLFGQDEFQRSLSMFTTQAV
LEDAQEQKNDKPLEMLQKLNAAVEYDDILDEKTAFTPLQSEYRYPKPIPR
HKVGKMDQVMKLNALAEERKFKLOKIEROAAETYSMTSCSSHPYLFIVQ
NPSLFWYLPPTPKLEKNLILMTLLAGSLTEPOVGRKEDDEIKYLINVASDA
OKLSVPLIMGSGIGKTTLSQVPRDQVTRFPKIMICISDPEREKLKALVEST
EGKSLSDMDLAPLOKQDELNGKRFYVLVDVWEDDHKRNAPNVALKVASGAFVY
TTTLERKVSIMGTLOPYELNLSPEDCWFLPMQRAFGHOEINPNTMALIGKETVKK
CFVYCAVEPKDTAKENLAFMMAHGFLSGNLELDENYENNELYLKSPROIE
VESGKTYRQMDLIHDLATSLFSANTSSNREINANDGYMMSIGFAVVSYSPL
LQKVSARVNLBNSNQLPSSIGDVLHLYLIDSGFRIRNPKEKCKQNTCTID
LHYCDLSCLPKQTSKLSLKNLLDGSLSLTPPRIGLCLSLSCFVIGKRGHQ
LGBLKNMLYGSISITKLDKRVKQTDAAKANLSAKANLHSLCLSDWLDGKRYDEVL
EALKPHSNLKYLEINGFGIRLPDMNOSVLKNVSIIRIGCENCSCLPPEGEPLCLE
SLEHTGSADVEYEDNVHGRPSPLRKLVIWDSPLKIDMGEKQFVLEEMTFY
WCPMFVLPITSSVTKLVIVTDATVLRISLRLALSLDISDNVBAISPEMKKSLA
NLKTKLISFFRNKELPISLASLNALSKLRFCDALBSLEBEVKGLSLTELVSIN

Alignment Scores:

Pred. No.: 1.28e-286 Length: 79178
Score: 3774.00 Matches: 778
Percent Similarity: 70.07% Conservative: 79
Best Local Similarity: 63.61% Mismatches: 127
Query Match: 73.61% Indels: 239
DB: Gaps: 7

US-10-647-268-2 (1-988) x AY303170 (1-79178)

QY 1 MetAAGTUAIApHeleuGlnValleuLeuAAspAenLeuThrCyPheIleGlnGlyLeu 20
DB 42527 ATGGCTGAAGCTTTCATCAAGATGAGTTCTGCTAGCAATCTCCTTCTTCCAAAGGGGAA 42468
QY 21 LeuGlyLeuIleleuGlyPheLeuAAspGluPheGlyLeuGlnInsErThrPheThrThr 40
DB 42467 CTGTGATTTGCTTTTCGCTTTTCAGATGAGTTCCAAAGGCTTTCAAGCATGTTTCTACA 42408
QY 41 IleGlnAValleuGlnAAspAlaGlnLysLysGlnLeuLysAAspLysAlaIleGlnAAsn 60
DB 42407 ATTCAGACCGCTCTTGAAGATGCTCAGAGAAAGCACTCAACAACAACCTCTGAAGAAAT 42348
QY 61 TrpLeuGlnLysLeuAAspAlaAlaAlaTyrgLualAAspAAspIleLeuAAspGluCyLys 80
DB 42347 TGGTTGCAAAATCAATGCTGCTACATATGAAAGTCGATGACATCTTGATGAAATATATATA 42288
QY 81 ThrGlnAAspProIleArgGlnLysLysAAspLysTyrgLysCyTyrgLysProAAsnValIle 100
DB 42287 ACCAAGGCC--ACAAAGATTCTCCAGTCGAAATATGCGCTTATCATTCACAAAGGTATAC 42231
QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlnLysLeuAAspValIle 120
DB 42230 CCTTTCCTCCACAAAGCTCGGAGAAAGATGAGCAAGATGAGAAATACTAAAGGCATTT 42171
QY 121 AlaAlaGlnAAspIleLysPheHisLeuAAspGluArgThrIleGlnAAspGlnValAlaThr 140
DB 42170 GCTGAGGAAAGAAAGAAATTTTCATTTGACGAAATAATTGTAGAGAGCAAGCTGTTAGA 42111
QY 141 ArgGlnThrGly----- 144
DB 42110 CGGGAAACAGGACTCATCTTAATTAAGTATTAACAACAACTAAGTTTATTAATTCATTTT 42051
QY 144 ----- 144

DB 42050 TGGCAATTATGAATTCAGAAAAAGGTTAAATATATCATGCTCCTATCTGAATATAGTGA 41991
QY 144 ----- 144
DB 41990 AATATACCTCTCGTTGATCTTGCATCTGAATATATCTTGTCAATCTGGCAAGCTCAGAA 41931
QY 144 ----- 144
DB 41930 TCAAATTATGACCCCAACTTTTAATATCTGATATCTTTAGAAATCCACCTGTCTAACT 41871
QY 144 ----- 144
DB 41870 CATCCACTACCCACTTCCCTTGTCTTGAATCTTTTCTTAACTTAACCTGAGAACACT 41811
QY 144 ----- 144
DB 41810 CGATCCGTTTTCCTTTCTTAAACAAGACGCTCAGAGAAAAGAGTTTCTTCTATTCTG 41751
QY 144 ----- 144
DB 41750 TTTCTGTGTGCTGCACCTGGGCTTAAATCCATTAAAAACAGGCGATGTATATCCA 41691
QY 144 ----- 144
DB 41690 ACGACGGTAGCCTTCTCTGACAGCTGACTGTAAATTTTGTCTAACAAAAGAAAAAAGA 41631
QY 144 ----- 144
DB 41630 TTAGACATGTTTTTCTTGTTCATTGATTAGGCTGAGATTTCTTCAAGATGSAACATAGGG 41571
QY 144 ----- 144
DB 41570 GATATATTGACCAAAAGTAGAATGGGTATATTTAAAGTATTTCTGATGAACAGAG 41511
QY 144 ----- 144
DB 41510 TATATGTCGCAAAATATATCTCTATTTTCTGTGCTCTCTAATGATGATTGAATGATAA 41451
QY 145 -----Phe-ValLeuAAsnGluProGlnValIleTyrgL 154
DB 41450 TATTTCTCATGTGACATGCTTGTGCAACAGGTTCTGATTAACCAACCGCAGGTTTATGG 41391
QY 154 YArgAAspLysGlnLysAAspGluIleValIleLysIleLeuIleAAsnAAsnValIleSerAAsnAlaG 174
DB 41390 AAGAGACAAAGAGAAAGATGATGATGAAATCTATATAACAATGTATAGTAGGCCCA 41331
QY 174 nThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLysGlyLysThrThrLeuAlaG 194
DB 41330 ACACCTTTCAGTCTCCCAATATCTTGATGAGGAGATTAGGAAAAACGACTCTTGCCCA 41271
QY 194 nMetValPheAAspAAspGlnArgValIleGlnHisPheHisAProLysIleTrpIleCyVal 214
DB 41270 AATGCTCTTCATATACAGAGATGATGACATTTCCATTCCAAAATATGATGATTTGCT 41211
QY 214 IserGlnAAspPheAAsnGlnLysArgLysLysIleLysGlnIleValGlnSerIleGlnGlnLys 234
DB 41210 CTCGGAAGATTTTATATGAGAGAGCTTATATAGCAATGTATAGATCTATATGAAGAGAG 41151
QY 234 sSer--LeuGlyGlyMetAAspLeuAlaProLeuGlnLysLysLeuArgAAspLeuAAs 253
DB 41150 GCCACTACTTGGTGAATGAGCTTGCTGCCACTTCAAAAGAAAGCTTCAGAGGTTGCTGAA 41091
QY 253 nGlyLysLysTyrgLeuLeuValIleAAspAAspValITrpAAsnGluAAspGlnAAspLysTrpAl 273
DB 41090 TGGAAAAAGATCACTGCTGTGTAGATGATGTTGGAATGAATCAACAGAAAGTGAGC 41031
QY 273 AlveLeuArgGlnValIleuLysValIleGlnAlaSerGlyAlaSerValIleuThrThrThr 293
DB 41030 TAAATTAAGACACTCTTGAAGAGTTGAGAGCAAGTGGTCTTCTTCAACCACTACCTCG 40971
QY 293 gLeuGlnLysValIleSerIleMetGlyThrLeuGlnProTyrgLysLeuSerAAsnLeuSe 313
DB 40970 TCTTGAAGAAAGTTGATCAATTAATGAGAACATTCGCAACATATGAACTGTCAATCTGTCTC 40911

QY 313 rGIngluAspCySTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluLeu 333
 Db 40910 TCAGAGAGATGTTGGTGTGTTTCATGACAGCGATTTGGACACCAAGAAATATAA 40851
 QY 333 nLeuAsnLeuValAlaIleGlyLeuGluLeuValLeuAlaLeuGlyValProLeuAl 353
 Db 40850 TCCAAACTTGTGGCAATCGAAGAGAGATTTGAAAGAAAAAGTGGTGGTCCCTAGC 40791
 QY 353 aAlaLeuThrLeuGlyGlyIleLeuArgPheLeuValArgGluGluGlnIleHisVa 373
 Db 40790 ACCCAAACTCTGGAGGATATTTGGCTTCAAGAGAGAAAGAAAGCAATGGCAATGT 40731
 QY 373 lArgAspSerGluIleTrpLeuLeuProGlnGluGlnSerSerIleLeuProAlaLeuArg 393
 Db 40730 GAGAGACAGTCGGATTTGGAAATTTGCTCAGATGAAGAAATTTATTCCTGCCCTGAG 40671
 QY 393 gLeuSerTyThrHisIleLeuProLeuAspLeuArgGlnCysPheThrTyrcysAlaValPh 413
 Db 40670 GCTTAGTTACCATCAACTTCCACTTGATTTGAAACAATGCTTGGCTATGTGGCGTGT 40611
 QY 413 eProAspThrGluMetGluLeuGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPh 433
 Db 40610 CCCAAAGATGCCAAATGAGAAAGAAAGAAAGCTAATCTCTCTGGATGGCGCATGTGTT 40551
 QY 433 eIleLeuSerTySGlyAsnLeuGluLeuGlnAsnValGlyAsnGluValTrpAsnGluLe 453
 Db 40550 TCTTTATCAAAAGAAACATGAGACTAGAGATGTGGCGCATGAGATGAGAAAGATTT 40491
 QY 453 uTyLeuArgSerPhePheGlnGluIleGluValIysSerGlyGlnIleTyrcPheIysMe 473
 Db 40490 ATACTTGGGCTCTTTTCCAAAGATTTGAAGATTGAAGATTGAAGCTTTTTCAGAT 40431
 QY 473 CHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerAs 493
 Db 40430 GCATGATCTCATTCATGATTTGGCAACATCTCTGTTTTCACAAACACATCAAGACGAA 40371
 QY 493 nIleArgGluIleIleValGluAsnTyrcIleHisMetSerSerIleGlyPheThrIysVa 513
 Db 40370 TATCCGTAAATTAATAACACAGTTACACATATGATGTCCATTTGGTTTCCGCGAAGT 40311
 QY 513 lValSerSerTyrcSerLeuSerHisIleGlnIlePheValSerLeuArgValIleAsnLe 533
 Db 40310 GGTGTTTTCATCTCTTCCCTGGGAAAGTTATCTCGTTAAGAGTCTTAATCT 40251
 QY 533 uSerAspIleLeuSerGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTy 553
 Db 40250 AGCGATTCGACATTTAATAGTTACCATCTTCATTTGGAGATCTAGTACATTTAAGATA 40191
 QY 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysIysLeuG 573
 Db 40190 CTTAACCCTGTATGGC--AGTGGCAGTGGTATGCTTCCAAAGCAAGTTATGCAAGCTTCA 40134
 QY 573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysPheLeuProIysGluTh 593
 Db 40133 AAATCTGCAACTTTATCTATCAATTTGACCAACAGCTTTGTGTTCGCAAAAGAAAC 40074
 QY 593 rSerTyLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrcGlyLeuThrCysMe 613
 Db 40073 AAGTAACCTTGGTATGCTCCGAATCTTTAATCTTGATGGTAGCCAGTCATTTGATAT 40014
 QY 613 tProProArgGluIleGlySerLeuThrTyrcGlyLeuThrLeuSerArgPheValAlaGlyI 633
 Db 40013 GCCACCAAGATAGATCATTTGATGCTTAAAGACTCTAGCTCAATTTGTGTGGA-- 39956
 QY 633 eGlnTyLeuSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrcIysSerIleG 653
 Db 39955 -AGAGAAAGGTTATTAACCTTGGTGAATTAAGAAACCTTAATCTTATGCTCAATTA 39897
 QY 653 uIleThrHisLeuGluArgValIysAsnAspMetAspAlaIysGluValAsnLeuSerAl 673
 Db 39896 AATCTGCATCTTGAAGAGATTAAGATTAAGAGCAAAAGAACCAATTTATCTGC 39837

QY 673 alyGluAsnLeuHisSerLeuSerMetIysTrpAspAspGluArgProArgIleTy 693
 Db 39836 AAAAGGATCTGCATCTTTAAGCATGAGTTGG--AATAACTTTGGACCAATATATA 39780
 QY 693 rGluSerGluIysValGluValIleGluValAlaLeuIysProHisSerAsnLeuThrCysLe 713
 Db 39779 TGAATCGAAGAACTTAAGTGCCTTGAAGCCCTCAACACACATCCCATCTGACTCTTT 39720
 QY 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValLeuTy 733
 Db 39719 AAAATCTATGGCTTCAGAGAAATCCATCTCCAGATGATGAATCACTAGATTGAA 39660
 QY 733 sAsnValValSerIleGluIleIleSerCysIysAsnCysSerCysLeuProPheG 753
 Db 39659 AAATATGTCTCTATTTTAATTAGCACTTCAGAACTGCTCATGCTTACCACTTTGG 39600
 QY 753 yGluLeuProCysLeuIysSerLeuGluLeuTyrcArgGlySerAlaGluValGlyTyrcVa 773
 Db 39599 TGATCTGCTTGTCTAGAAAGTCTAGAGTTACACTGGGGGTCTGGCGGATGTGGAGTATGT 39540
 QY 773 lAsp-----SerGlyPheProThrArgArgPheProSerIle 786
 Db 39539 TGAAGAGTGAATATTGATGTTCATTTCTGATTTCCCAAGAAATAGGTTTCATCTCT 39480
 QY 786 uArgTyLeuAsnIleArgGluPheGlyAsnLeuIysGlyLeuLeuIysGlyGlyI 806
 Db 39479 GAGAAACTTGATATATAGGACCTTTGTAGTCTGAAAGATTTCTGAAAGAAAGAGAGA 39420
 QY 806 uGluGlnCysProValIleGluGluIleGluIleIysCysCysProMetPheValIlePr 826
 Db 39419 AGAGCAATTCCTGCTGTCGAAAGATGAGATTAATAGTGCCCTATGTTGTATTC 39360
 QY 826 oThrLeuSerSerValIysLeuValIleSerGlyAspIysSerAspAlaIleGlyPh 846
 Db 39359 GACCTTTCTTCTGTCAAGAAATGGTAGTCTGTGGGACAACTCGAATGCAATAGGTT 39300
 QY 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTyrcAsnIysGluAs 866
 Db 39299 CAGTTCATATCTAATCTCAGAGGCTCTTACTTCCCTCAATATTACTTTAACAAGAAC 39240
 QY 866 pAlaSerLeuProGluGluMetPheIysSerLeuAlaAsnLeuTyrcTyrcLeuAsnIleSe 886
 Db 39239 TACTTACCTCCCAAGAGATGTTCAAAAGCCCTTGCAAACTCTTCAATAATCTTC 39180
 QY 886 rPheTyrcPheAsnLeuIysGluLeuProThrSerSerAlaSerLeuAsnAlaLeuIysHis 906
 Db 39179 TTCTTTAGGAATCTCAAGAGCTGCTTACAGCTGCTGCTAGTCTCAATGCTTTGGAGAG 39120
 QY 906 sLeuGluIleHisSerCysTyrcAlaLeuGluSerLeuProGluGluValIysGlyLe 926
 Db 39119 TCTGACAAATTGAACATTTGTGAGCGCACTAGAGAGTCTCCAGAAAGAGGGGTGAAGGTTT 39060
 QY 926 uIleSerLeuThrGlnLeuSerIleThrTyrcGlyMetLeuGlnCysLeuProGluG 946
 Db 39059 AACTTACTACCGAAGTGTCTGTCCAGAGCTGAGAGAGCTTAATATGTTTACCGGACGG 39000
 QY 946 yLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaI 966
 Db 38999 AATGACGACCTTAACAGCTCTCAACAAGATTAGCAATTTGGGAGATCTCCACAAGTGTGGA 38940
 QY 966 sArgCysGluTyrcGlyIleGlyGluAspTrpTyrcIysIleAlaHisIleProArgValPh 986
 Db 38939 GCGGTATGAGTACGGAATGAGGAAGACTGGCAAAATTTGCACACATTTCTAATGTGGA 38880
 QY 986 eIleTyrc 988
 Db 38879 TTATATAT 38873
 RESULT 2
 AX814112 2913 bp DNA linear PAT 05-DEC-2003
 LOCUS AX814112
 DEFINITION Sequence 35 from Patent EP1334979.
 ACCESSION AX814112

VERSION AX814112.1 GI:39103414
 KEYWORDS Solanum bulbocastanum
 SOURCE Solanum bulbocastanum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE 1
 AUTHORS Van der Vossen, E.A. and Allefs, J.J.
 TITLE Gene conferring resistance to phytophthora infestans (late-blight) in Solanaceae
 JOURNAL Patent: EP 1334979-A 35 13-AUG-2003;
 Week-en Researchbedrijf Agrico B.V. (NL)
 FEATURES
 source 1..2913
 /organism="Solanum bulbocastanum"
 /mol_type="unassigned DNA"
 /db_xref="taxon:147425"
 misc_feature 1..2913
 /note="Rpi-b1b"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,266-288 Length: 2913
 Score: 3766.50 Matches: 753
 Percent Similarity: 83.43% Conservative: 78
 Best Local Similarity: 75.60% Mismatches: 130
 Query Match: 73.46% Indels: 35
 DB: 6 Gaps: 8
 US-10-647-268-2 (1-988) x AX814112 (1-2913)
 QY 1 MetAlaGluAlaPheLeuGluValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
 DB 1 ATGGCTGAAGCTTATTCATCAAGTCTGCTAGACAACTCACTTCTTCTCAAGGGGAA 60
 QY 21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
 DB 61 CTGTGATTTGGCTTTGGTTTCAAGATGATGATCCAAAGGCTTTCAAGATGTTTCTCA 120
 QY 41 IleglnAlaValLeuGlnAspAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn 60
 DB 121 ATTCAGAGCGCTCTTGAAGATGCTCAGAGCAAGCAACTCAACAGAGCTCTAGAAAAT 180
 QY 61 ThrLeuGlnLysLeuAsnAlaAlaIleTyrgLysAlaAspAspIleLeuAspGluCysLys 80
 DB 181 TGGTTGCAAAAACCTCAATGCTGCTACATATGATGATGATCTTGTGATGATATATA 240
 QY 81 ThrGlnAlaProIleArgGlnLysLysAsnLysTyrgLysCysTyrgLysProAsnValIle 100
 DB 241 ACCAAGGCC---ACAAAGATTCCTCCAGCTCTGAATATGGCCGTTATCATCCAAAGCTTATC 297
 QY 101 ThrPheArgGlnLysGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
 DB 298 CCTTCCCTGCTCAAGGTCGGGAAAGATGAGCAAGATGATGAAATACTAAAGGCATTT 357
 QY 121 AlaAlaGluArgLysPheIleLeuAspGluLysGlnIleGluArgGlnValAlaThr 140
 DB 358 GCTAGAGAAAGAAAGAAATTTTCATTTTGACAGAAAATAATGTAGAGACCAAGCTGTGTA 417
 QY 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValTyrgLysArgAspLysGluLysAsp 160
 DB 418 CGGAAACAGGTTCTGTATTAAACGACCGCAGGTTTATGAAAGAGACAAAGAAAGAT 477
 QY 161 GluIleValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
 DB 478 GAGATAGTGAAGAAATCTATATAACATGTAGTATGCCCAACCTTTCAGTCTCTCCCA 537
 QY 181 ILeuGlnMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGln 200
 DB 538 ATACTGTGATAGGGGGGATAGGAAAGACACTTGTGCCCAATGCTTCAATGATCAG 597
 QY 201 ArgValIleGlnIlePheIleProLysIleTrrIleCysValSerGluAspPheAsnGlu 220

DB 598 AGAGTTACTGAGCATTTCCATTCCAAAATATGATTTGTGCTCGAGATTTTGTATGATAG 657
 QY 221 LysArgLeuIleLysGluIleValGlnSerIleGlnGluLysSer---LeuGlyGlyMet 239
 DB 658 AAGAGTTAATAAAGGCAATTTGTAATCTATTAAGAGAAAGCCACTATCTTGATGATG 717
 QY 240 AspLeuAlaProLeuGlnLysLysLeuAspLeuAsnGlyLysLysTyrrLeuLeu 259
 DB 718 GACTTGGCTCAGCTTCAAAAGACCTTCAGAGAGTTGCTGTAATGAAAAAGATCTGCTT 777
 QY 260 ValLeuAspAspValTTPAsnGlnAspGlnAspLysTTPAlaLysLeuArgGlnValIleu 279
 DB 778 GTCTTAGATGATGTTTGGATGAAGATCAACAGAAAGTGGCTTAATTAAGAGCATCTTG 837
 QY 280 LysValGlyAlaSerGlyValaSerValLeuThrThrArgLeuGluValGlySer 299
 DB 838 AAGGTTGAGCAAGATGGCTTCTGTTCTTAACCACTCTGCTTGAAGAGTTGATCA 897
 QY 300 IleMetGlyThrLeuGlnProTyrgLysLeuSerAsnLeuSerGlnGluAspCysTrrLeu 319
 DB 898 ATTATGGAGACATTGCAACCATATGAACTGCTCAATCTCTCAAGAAATGTTGGTGG 957
 QY 320 LeuPheMetGlnArgAlaPheGlyHisGlnGluIleAsnLeuAsnLeuValAlaIle 339
 DB 958 TTGTTCAATGCAACGTCATTTGACACCAAGAAATAATCCAAACCTTGTGGCAATC 1017
 QY 340 GlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGly 359
 DB 1018 GGAAGAGATTTGAAAAAAAGTGGTGTGCTCTTACAGAGCAAAACCTTGGAGGT 1077
 QY 360 IleLeuArgPheLysArgGluGluArgGlnTrrPgluHisValaArgAspSerGluIleTrr 379
 DB 1078 ATTTTGGCTTCAAGAGAGAAAGAAAGCATGGAAACATGTGAAGACAGTCCGATTTGG 1137
 QY 380 LysLeuProGlnGlnLysSerSerIleLeuProAlaLeuArgLeuSerTyrgHisIleLeu 399
 DB 1138 AATTGGCTCAAGATGAAGATTTATCTATCTGCTGCTCCGAGGCTTAGTACATCAACTT 1197
 QY 400 ProLeuAspLeuArgGlnCysPheThrTyrgValAlaPheProLysAspThrGluMet 419
 DB 1198 CCACCTTGAATTTGAACAATGCTTTGCGTATGTCGGTGTCCCAAGAGATGCCAAATG 1257
 QY 420 GluLysGlyAsnLeuIleSerLeuTrrPheAlaHisGlyPheIleLeuSerLysGlyAsn 439
 DB 1258 GAAAAAGAAAGCTAAATCTCTCTGATGCGCATGCTTTCTTTATCAAAAGAAAC 1317
 QY 440 LeuGluLeuGluAsnValGlyAsnGluValTrrPasnGluLeuLysArgSerPhePhe 459
 DB 1318 ATGAGGCTAGAGATGTGGCGGATGAAAGTATGAAAGATTAATCTTGAGGCTTTTTC 1377
 QY 460 GlnGluIleGluValLysSerGlyGlnThrTyrgLysMetHisAspLeuIleHisAsp 479
 DB 1378 CAAGAGATTTGAATGAAGATGTTAAACTTATTTCAAGATGCAATGATCTCATCATGAT 1437
 QY 480 LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleVal 499
 DB 1438 TTGGCAACATCTCTGTTTTCAGCAACACATCAAGCAGCAATATCCGTGAATATAATA 1497
 QY 500 GluAsnTyrrIleHisMetMetSerIleGlyPheThrLysValaLysSerTyrrSerLeu 519
 DB 1498 CACAGTTACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
 QY 520 SerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLys 539
 DB 1558 CCCCCCTTGAAGAAAGTTATCTGTTAAGATGCTTATATCAAGGTGATTCACATTAAT 1617
 QY 540 GluLeuProSerSerIleGlyAspLeuValHisLeuArgTyrrLeuAsnLeuSerGlyAsn 559
 DB 1618 AAGTTACATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674
 QY 560 ThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAsp 579

Db 1675 AGTGCATGCTAGTCTCCAAAGCAGTTATGCAAGCTTCAAATCTGCAATCTTGAT 1734
 QY LeuHISGLYCYSHisSerLeuCYsLeuProGluThrSerLeuLeuGlySerLeu 599
 Db 1735 CTACAAATATGCAAGCTTTGTTGTTGCCAAAAGAAACAAAGTGGTGGTCTC 1794
 QY ArgAsnLeuLeuLeuAspGlyCYsTyrGlyLeuThrCYsMetProProArgIleGlySer 619
 Db 1795 CGAAATCTTTACTTGATGTCAGCCAGTCATGATCTTGATGCCAACAGATAGATCA 1854
 QY LeuThrCYsLeuLeuThrLeuSerArgPheValValGlyIleGlnLysLysSerCYsGln 639
 Db 1855 TTGAATGCTTAAAGACTTACGATTTGTTGTTGA---AGAGAAAGAAAGTTATCAA 1911
 QY LeuGlyGlyLeuLeuArgAsnLeuAsnLeuTyrGlySerIleGlnIleThrHisLeuGlnArg 659
 Db 1912 CTGAGTGAACCTAGAAACCTTAATCTTAATGCTCAATTAATATCCGATTTAGAGA 1971
 QY ValLysAsnAspMetAspAlaLysGlnAlaAsnLeuSerAlaLysGlnAsnLeuHisSer 679
 Db 1972 GTGAAGATGATTAAGAGAGCAAAAGAGCAATTTATCGCAAAAGGAGATCTGATCT 2031
 QY LeuSerMetLysTTPAspAspAspGlnArgProArgIleTyrGlySerGlnLysValGln 699
 Db 2032 TTAAACCATGAGTTGG---ATACTTTGAGCCACCATATATATGAAATCAGAAAGCTTAA 2088
 QY ValLeuGlnAlaLeuLysProHisSerAsnLeuThrCYsLeuThrIleArgGlyPheArg 719
 Db 2089 GTGCTTGAAGCCCTCAACACACCTCCATCTGATCTTTAAAAATCTATGGCTTCGA 2148
 QY GlnLysLeuLeuProAspTyrMetAsnHisSerValLeuLysAsnValValSerIleGln 739
 Db 2149 GGAATCCATCTCCCGAGTGTGATGATCATCATGATTAATAAATATGTCTATCTCA 2208
 QY IleIleSerCYsLysAsnCYsSerCYsLeuProArgPheGlyGlnLeuProCYsLeuLys 759
 Db 2209 ATTGCAACCTTCAGAACTGCTCATGCTTACCACTTGTGGATCTGCTGTCTGAA 2268
 QY SerLeuGlnLeuTyrArgGlySerAlaGlnValGlnTyrValAsp----- 774
 Db 2269 AGTCAAGATTAACCTGGGGGTCTCCGAGTGTGAGATGTTGTAAGAGTGGATTTGAT 2328
 QY -----SerGlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArg 792
 Db 2329 GTTCATCTTGATTTCCCAAGAAATAGGTTTCATCTTGAGAGAACTTGATATATG 2388
 QY GlnPheGlyAsnLeuLysGlyLeuLeuLysLysGlnGlnGlnGlnGlnGlnGlnGln 812
 Db 2389 GACTTTGGTACTGGAAGAGATGCTGTAAGAAAGAGAGAGAGCAATTCCTGTGCTT 2448
 QY GlnGlnIleGlnIleLysCYsCYsProMetPheValIleProThrLeuSerSerValLys 832
 Db 2449 GAAGAGATGATTAATTCACGAGTGCCTTTCTG-----ACCTTTCT----- 2490
 QY LysLeuValValSerGlyAspLysSerPheAlaIleGlyPheSerSerIleSerAsnLeu 852
 Db 2491 -----TCATATCTT 2499
 QY MetAlaLeuThrSerLeuGlnIleArgTyrAsnLysGlnAspAlaSerLeuProGlnGln 872
 Db 2500 AGGCTCTTACTTCCCTCAGAAATTTGCTATATATAAGTACTTCTCCAGAAAG 2559
 QY MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
 Db 2560 ATGTTCAAAAACCTTGCAAAATCTCAAAATATCTGCAATCTCGTGCAATTAATCTCAA 2619
 QY GlnLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGlnIleHisSerCYs 912
 Db 2620 GAGTGTCTACCGAGCTTGCTAGTCTAATGCTTGAAGAGTCTAAAAATTCATTTGCT 2679
 QY TyrAlaLeuGlnLeuSerLeuProGlnGlnGlnValLysGlyLeuIleSerLeuThrGlnLeu 932
 Db 2680 TGGCACTAAGAGTCTCCCTGAGAGAGGCTGAGAGCTTTATCTTCACTCAGAGATTA 2739

QY 933 SerLeuThrTyrCYsGlyMetLeuGlnCYsLeuProGlnGlnLysLeuThrAla 952
 Db 2740 TTGTGTGAACCTGATACATCTTAATGTTTACAGAGGGATGGACACCTTAACACC 2799
 QY LeuThrAsnLeuSerValGlnPheCYsProThrLeuAlaLysArgCYsGlnLysGlyIle 972
 Db 2800 CTCACAGCTTTAAAAATTCGGGAGATGTCACACTGATCAAGCGGTGTGAGAAAGGAATA 2859
 QY GlnGlnAspTyrTyrLysIleAlaHisIleProArgValPheIleTyr 988
 Db 2860 GGAGAGAGCTGGCAAAATTTCTCAATTCCTATGATATATATAT 2907
 RESULT 3
 AX816331
 LOCUS AX816331 2913 bp DNA linear PAT 09-DEC-2003
 DEFINITION Sequence 48 from Patent WO03066675.
 ACCESSION AX816331
 VERSION AX816331.1 GI:39646822
 KEYWORDS
 SOURCE
 ORGANISM
 Solanum bulbocastanum
 Solanum bulbocastanum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 Allefs, J. J. and van der Vossen, E. A.
 Gene conferring resistance to phytophthora infestans (late-blight)
 in solanaceae
 Patent: WO 03066675-A 48 14-AUG-2003;
 Kweek- en Researchbedrijf Agrico B. V. (NL)
 LOCATION/Qualifiers
 FEATURES
 source
 1..2913
 /organism="Solanum bulbocastanum"
 /mol_type="unassigned DNA"
 /db_xref="taxon:147425"
 1..2913
 misc_feature
 /note="#Rp1-D1b#"

ALIGNMENT Scores:
 Pred. No.: 5.26e-288 Length: 2913
 Score: 3766.50 Matches: 753
 Percent Similarity: 83.43% Conservative: 78
 Best Local Similarity: 75.60% Mismatches: 130
 Query Match: 73.46% Indels: 35
 DB: 6 Gaps: 8

US-10-647-268-2 (1-988) x AX816331 (1-2913)

QY 1 MetAlaGlnAlaPheLeuGlnValLeuLeuAspAsnLeuThrCYsPheIleGlnGlyIle 20
 Db 1 ATGGCTGAAGCTTCAATCTCAAGTTCTGCTAGACAAATCTTCTTCCCAAGGGGAA 60
 QY 21 LeuGlyLeuIleLeuGlyPheLysAspGlnPheGlnLysLeuGlnSerThrPheThr 40
 Db 61 CTGTATTCCTTTCCGTTTCAAGATGATTCCAAGGCTTTCAAGCATGTTTCTCA 120
 QY 41 IleGlnAlaValLeuGlnLysAspAlaGlnLysGlnLeuLysAspLysAlaIleGln 60
 Db 121 ATTCAGCGCTCTTAAAGAGTCTCAGAGAGCAACTCAACAAAGCCTTAAGAAAT 180
 QY 61 TrpLeuGlnLysLeuAsnAlaAlaValTyrGlnAlaAspAspIleLeuAspGlnCYsLys 80
 Db 181 TGGTTCCAAAACATCATATGCTGTATATAGAGTGAATCTTGGATGAATTA 240
 QY 81 ThrGlnAlaProIleArgGlnLysLysAsnLysTyrGlyCYsTyrHisProAsnValIle 100
 Db 241 ACCAAGGCC---ACAAGATTTCTCCAGTCTGAATATAGCGCTTATCATCAAGGTTATC 297
 QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlnLysLysAspValIle 120
 Db 298 CCTTTCCTCAAGAGTCCGGAAGAGATGACCAAGTATGAATAAATTAAGGCAATT 357

QY	121	AlaAlaGluArgIleLeuPheHisLeuAspGluAgtGlnIleGluValAlaIaThr	140
Db	358	GCTGAGAAAGAAAGAAATTTTCATTGTGACGAAAAAAATTGTAGAGACAGCTTGAGA	417
QY	141	ArgGlnThrGluPheValLeuAsnGluProGlnValTyrGluYAspAspGluYAsp	160
Db	418	CGGAAACAGGTTCTGTATTAAACGACCGCAGGTTTATGAAAGACAAAGAAAGAT	477
QY	161	GluIleValLeuIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro	180
Db	478	GAGATATGGAATAATCTCTAATAACAATGTTAGTAGGCCAACACTTTCAGTCTCCCA	537
QY	181	IleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGln	200
Db	538	ATACTTGATAGGGGGGATTTAGAAAACGACTCTTGCCCAATGCTCTTCATATACAG	597
QY	201	ArgValIleGluHisPheHisProLysIleTrpIleCysValSerGluAsnAspGln	220
Db	598	AGAGTACTGAGCAATTCCTTCATTCGAAATATGAAATTTGTGTCCGAAAGATTTGATAG	657
QY	221	LysArgLeuIleLysGluIleValGluSerIleGluGluYSer---LeuGlyLysMet	239
Db	658	AAAGGCTTATTAAGGCAATGTGTAAATCTATTTAGAGAGAGCCACTTGCTGATAGTG	717
QY	240	AspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeu	259
Db	718	GACTTGCTCCCACTTCGAAAGAGCTTCAGAGTGCTGAATGAAAAAGATACCTTGCTT	777
QY	260	ValLeuAspAspValTyrAsnGluAspGlnAspGlyTyrAlaLysLeuArgGlnValLeu	279
Db	778	GCTTATGATGATGTTTGAAATGAAATCAACAGAAATGGGCTTAAATTAAAGCACTCTTG	837
QY	280	LysValGlyAlaSerGlyAlaSerValLeuThrThrArgLeuGluLysValGlySer	299
Db	838	AAAGTTGAGCAAGTGTGTCTTCTGTCTTAAACCACTACTCGCTTGAAAAGGTTGATCA	897
QY	300	IleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnLysAspCysTrpLeu	319
Db	898	ATTATGGGAACATTGCACCATATGACATGTCGCAATCTGTCGAAAGATTTGTTGGTTG	957
QY	320	LeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIle	339
Db	958	TTGTTCATGCAACGCGATTTGACACCAAGAAATTAATCCAAACCTTGCGCAATC	1017
QY	340	GlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGly	359
Db	1018	GGAAGAGGATTTGTAATAAAAGTGTGTGTGCTCTAGACGCCAAACCTTTGGAGCT	1077
QY	360	IleLeuArgPheLysArgGluGluArgGlnTrpGluHisValArgAspSerGluIleTrp	379
Db	1078	ATTTTGTGCTTCAGAGAGAGAAAGAAAGACATGGGAACATGTAGAGACAGTCCCATTTGG	1137
QY	380	LysLeuProGlnGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrHisLeu	399
Db	1138	AAATTGCTCAAGAGAAAGATTCTATTTCGCTGCGCTCGAGGCTTAGTTACATCAACTT	1197
QY	400	ProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMet	419
Db	1198	CCACTGTGATTTGAAACAATGCTTTGGATTTGTGGGGGTTCGCCAAAGATGCCAAATG	1257
QY	420	GluLysGlyAsnLeuIleSerLeuTrpPheLysIleAspGlyPheIleLeuSerLysGlyAsn	439
Db	1258	GAAAAAGAAAAGCTATCTCTCTCTCGAATGGCGCATGTTTTCTTTATCAAAAGAAAC	1317
QY	440	LeuGluLeuGluAsnValGlyAsnGluValTyrAsnGluLeuTyrLeuArgSerPhePhe	459
Db	1318	ATGAGGCTAAGAGATGGGCGCATGAAGATGAAAGAAATTAATCACTGAGGCTTTTTTC	1377
QY	460	GlnGluIleGluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAsp	479
Db	1378	CAAGGATTTGAATTAAGATGTGTAACCTATTTCAGATGCAATGATCATCATCAT	1437

QY	440	Leu1a1aThrSerLeuPheSer1a1aSerThrSerSerSer1a1aLeuGlu1a1aLeu1a1a	499
Db	1438	TTGGCAATCTCTGGTTTTCAGCAAAACATCAAGCAGCATATCTCCGGAATATATAA	1497
QY	500	GluAenTyr1Le1aMetMetSer1a1aGlyPheThrLysVal1aSerSerTyrSerLeu	519
Db	1498	CACAGTTACACACATATATATCTCCATTTGGTTCCGCCAAGTGGTGTCTTTTACACTCTT	1555
QY	520	Ser1a1aSerGlu1aPheValSer1a1aArgVal1aLeuAenLeuSerAsp1a1aLysLeuLys	539
Db	1558	CCCCCTTGGAAAAGTTATCTCGTTAAGATGGCTTATCTAAGTGATTCAGCATTTTAA	1617
QY	540	GluLeuPProSerSer1a1aGlyAspLeuVal1a1aLeuArgTyrLeuAenLeuSerGlyAen	559
Db	1618	AAGTTACCATCTTCCATTTGAGATCTAGTACATTTAAGATCTTGAACCTGTATAGGC---	1674
QY	560	ThrSer1a1aGSerLeuProAenGluLeuCybLysLeuGlu1aAenLeuGlu1aThrLeuAsp	579
Db	1675	AGTGGCAGCGAGTACTTCCAAAGCATTTAAGCAAGCTTCAAAATCTGCAAACTCTTGAT	1734
QY	580	Leu1a1aG1aCyb1aSerLeuCybSerLeuProLysGlu1aThrSer1a1aLeuGlySerLeu	599
Db	1735	CTACAAATTCGACCAAGCTTGTGTTTGGCAAAAGAAACAATTAACCTGGTATGCTC	1794
QY	600	ArgAenLeuLeuLeuAspGlyCybTyrGlyLeuThrCybMetProProArg1a1aGlySer	619
Db	1795	CGAAATCTTTTACTTGATGTAGTGGCAGCATGTGACTTGTATGCCACCAAGCATATGATCA	1854
QY	620	LeuThrCybLeuLysThrLeuSerArgPheVal1aGly1aLeuGlu1aLysLysSerCybGlu	639
Db	1855	TTGCATGCTTTAAGACTTGAAGTCATATTTGTTTGA---ACGAAAGAAAGTTATCA	1911
QY	640	LeuGlyGluLeuArgAenLeuAenLeuTyrGlySer1a1aLeu1a1aThr1a1aLeuGluArg	659
Db	1912	CTTGCTGAACACAGAAACCTTAATCTCATGGCTCAATTAATCACTCGCATCTTGAGAGA	1971
QY	660	ValLysAenAspMetAsp1a1aLysGlu1aAenLeuSer1a1aLysGluAenLeuHisSer	679
Db	1972	GTGAAGAATGATTAAGACGCAAAAGAACCAATTTATCTGCAAAAGGAATCTCATCTT	2031
QY	680	LeuSerMetLys1a1aPheAspAspGluArgProArg1a1aTyrGluSerGluLysValGlu	699
Db	2032	TTAAGCAGTGAAGTTGG---AATTAACCTTTGACACATATATATGATGATCAAGAAAGTTAA	2088
QY	700	ValLeuGlu1a1aLeuLysProHisSerAenLeuThrCybLeuThr1a1aLeuGlyPheArg	719
Db	2089	GTGCTTGAAAGCCCTCAAAACCACTCCATCTGACTCTTTAAAATCTAAGGCTTCAGA	2148
QY	720	Gly1a1aLeuLeuProAspTyrMetLeuAsnHisSerVal1aLeuLysAenVal1aSer1a1aGlu	739
Db	2149	GGAAATCCATCTCCGAGATGGATGATCACTCAGTATTTGAAAATATATGTCTTATCTTA	2208
QY	740	1a1aLeuSerCybLysAenCybSerCybLeuProProPheGlyGluLeuProCybLeuLys	759
Db	2209	ATTGACCACTTCACAAACTGCTCATGTCTTACACCCCTTGGTGAATGTCCTTGTCTGAA	2268
QY	760	SerLeuGluLeuTyrPheGlySer1a1aGluVal1aGluTyrVal1aAsp-----	774
Db	2269	AGCTTAGAGTTACACTGGGGGTCTGCGGATGTGAGTATGTGAAGAACTGATATTCAT	2328
QY	775	-----SerGlyPheProThrArgArgArgPheProSerLeuArgLysLeuAen1a1aLeuArg	792
Db	2329	GTTCATCTTGGATTCGCCCAAGAAATTAAGGTTTCATCTCTTGAGAGAACTTGATATATGG	2388
QY	793	GluPheGlyAenLeuLysGlyLysLeuLysLysGluGlyGluGluGluGluGluGluGluGlu	812
Db	2389	GACCTTGGTACTCTGAAGAATTCCTGTAAGAAAGAAAGAAAGCAATTCCTCGTGTCTT	2448
QY	813	GluGlu1a1aGlu1a1aLysCybCybProMetPheVal1a1aProThrLysSerSerValLys	832
Db	2449	GAAAGATGATATATTCACGAGTGCCTTTTCTG-----ACCTTTCT-----	2490
QY	833	LysLeuValValSerGlyAspLysSerAsp1a1a1aGlyPheSerSer1a1aSerAenLeu	852

Db 2491 -----TCTAATCTT 2499
QY 883 MetAlaLeuThrSerLeuGlnIleArgTyrAnlySGluAspAlaSerLeuProGluGlu 872
Db 2500 AGGGCTTACTTCCCTCGAAGATTGCTATATTAAGTAGCTACTTCCCAAGAG 2559
QY 873 MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
Db 2560 ATGTTCAAAACCTTGCAATCTTCAAAATCTTGACAACTCTCGGTGCAATATCTCAAA 2619
QY 893 GluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysSHiSLeuGluIleHisSerCys 912
Db 2620 GAGTGCCTACACAGCTTGCTAGTCTGAATGCTTTGAAAAGCTTAAATCAATGTGCT 2679
QY 913 TyrAlaLeuGluSerLeuProGluGluVallySGlyLeuIleSerLeuThrGluLeu 932
Db 2660 TGGCAGCTAGAGAGTCTCCCTGAGAGAGGGCTGAGAGGTTATCTTCACTCAGACAGTTA 2739
QY 933 SerIleThrTyrCysGluMetLeuGlnCysLeuProGluGluIleGluGlnHisLeuThrAla 952
Db 2740 TTGTGTGAACACTGTGAACGTGAATGTTTACAGAGGAGTTGACACCTTAACACC 2799
QY 953 LeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyTle 972
Db 2800 CTCACAAAGTTAAATAATTCGGGGATGTCACAACTGATCAAGCGGTGAGAGAGGAATA 2859
QY 973 GlyGluAspTyrTyrLysIleAlaHisIleProArgValPheIleTyr 988
Db 2860 GGAGAAAGCTGGACAAATAATTTCTCAATCTCTAATGTGAATATATATAT 2907
RESULT 4
AX814115 3260 bp DNA linear PAT 05-DEC-2003
LOCUS AX814115
DEFINITION Sequence 38 from Patent EP1334979.
ACCESSION AX814115
VERSION AX814115.1 GI:39103417
KEYWORDS
SOURCE
ORGANISM Solanum bulbocastanum
Solanum bulbocastanum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS van der Vossen, E.A. and Allefs, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
JOURNAL Patent: EP 1334979-A 38 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1..3260
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
misc_feature
1..3260
/note="RGCT-b1b"
ORIGIN
Alignment Scores:
Pred. No.: 1.47e-278 Length: 3260
Score: 3646.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
Query Match: 71.15% Indels: 114
DB: Gaps: 9
US-10-647-268-2 (1-988) x AX814115 (1-3260)
QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyIle 20
Db 1 ATGGCTGAAGCTTCCCTTCAAGTCTGCTAGATATCTCACTTTTTCATCCAAAGGGAA 60
QY 21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40

Db 61 CTTGATTCGCTTTTGTGTTTCGAGAGAGTTTAAAAAAGTTTCAAGTATCTTTCATG 120
QY 41 IleGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn 60
Db 121 ATCCAGCTGCTAGAGAGATGCTCAAGAGAGCACTGAAGTCAAGAGCAATTAAGAC 180
QY 61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
Db 181 TGGTTACGAAACCTCAATGTTGCTGCATATGAAAGTTATGACATCTTGAGACTGTAAA 240
QY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
Db 241 ACTAGGCA---GCAAGATTCAGACAGAGCTGATATGGGGGGTTATCATCCAGGACCATC 297
QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
Db 298 ACTTTCGTGTACAAAGGTGGGAAAAAGAAATGATGAAAAAAGTATGAGATGCAT 357
QY 121 AlaAlaGluArgGluLysPheHisLeuAspGluLysThrIleGluArgGlnValAlaThr 140
Db 358 GCAGAGAGAGAGAGAAATTTTCATTTAGTGAAGGATTTTAGAGAGACAAAGCTGTAGA 417
QY 141 ArgGlnThr----- 143
Db 418 CGGCAAC-AGTGCTCATCTTAATTTTAAACAAATAGATTAACAATTCAG 476
QY 143 ----- 143
Db 477 AGAAACGAGAGAAATTATATTCATTTTATTTTGGCAATTAACAAGCATTTGTGTT 536
QY 143 ----- 143
Db 537 TTAAAGCTGGGGGGAAGTTTCAATATTTTCTAGTCTTAATGTTTCTCACTCACTCA 596
QY 143 ----- 143
Db 597 GCATGATTTTCTCATTCCTTCACTTCAACTCCCCCTACTGTCAAAATATCTTCTAT 656
QY 144 -----GlyPheVal 146
Db 657 TTCTGTGACTCCTAATGACCTGAATGAATGAACAACATCTTGTGGAGAGAGTTTGT 716
QY 147 LeuAsnGluProGlnValTyrGlyLysArgAspLysGluLysAspGluIleValLysIleLeu 166
Db 717 TTAACTGAGCCAAAGTTTATGAGAGGAAAAAGAGAGATGAGATAGTGAATCTTG 776
QY 167 IleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGly 186
Db 777 ATAAACATGTGTATGTTATTCGAAAGAAAGTCCAGTACTCCCAATTACTTGATGGGGGA 836
QY 187 LeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPhe 206
Db 837 CTAGAAAGAGCACTAGCCCAATAGTCTTAAAGATCAAAAGAAATTAAGTGCATTTTC 886
QY 207 HisProLysIleTrpIleCysValSerGluAspPheAsnGluLysArgLeuIleLysGlu 226
Db 897 AATCTAAAGATATGGGTGTGTCTCAGATGATTTTGATGAGAGAGTTGATTAAGCA 956
QY 227 IleValGluSerIleGluGluLysSerLeuGlyMetAspLeuAlaProLeuGlnLys 246
Db 957 ATGTGTGAATCTATTGAAGAAAGTCACTGGGTGACATGACTTGCTCCCTCCAGAAA 1016
QY 247 LysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeuValLeuAspAspValTTPAsn 266
Db 1017 AAGCTTCAGAGAGTGTGATGAGAAAAAGATACTTCTTGTTGATGATGTTGGAAAT 1076
QY 267 GluAspGluAspLysTrpAlaLysLeuArgGlnValLeuLysValGlyLysArgGlyAla 286
Db 1077 GAGATCAAGAAAGTGGGATATCTTAGAGCAGTATGAGATTTGAGAGTGTGCTGT 1136
QY 287 SerValLeuThrThrThrArgLeuGluLysValGlySerIleMetGlyThrLeuGlnPro 306

ACCESSION	AX816334
VERSION	AX816334.1
KEYWORDS	GI:39646825
SOURCE	
ORGANISM	Solanum bulbocastanum Solanum bulbocastanum Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE	1 Allefs,J.J. and van der Vossen,E.A. Gene conferring resistance to phytophthora infestans (late-blight) in solanaceae Patent: WO 0306675-A 51 14-AUG-2003; Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES	Location/Qualifiers 1..3260 /organism="Solanum bulbocastanum" /mol_type="unassigned DNA" /db_xref="taxon:147425"
misc_feature	1..3260
ORIGIN	/note="#RGCL-blb#"
Alignment Scores:	
Pred. No.:	1..47e-278 Length: 3260
Score:	3648.00 Matches: 745
Percent Similarity:	76.58% Conservative: 92
Best Local Similarity:	68.16% Mismatches: 143
Query Match:	71.15% Indels: 114
DB:	Gaps: 9
US-10-647-268-2 (1-988) x AX816334 (1-3260)	
Dn	1 MetAlGluNlAphLeuGlInValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGu 20
Dc	1 ATGGCTGAAGCTTCCCTTCAGATTGCAGAAATATCACTTTTTCATCCAAAGGGAAA 60
Dy	21 LeuGLYleuILleuGLYPhelYsaSPGiUpheGLYLSleuGInserThrPheThrThr 40
Dd	61 CTGGATTGGTTTTTGCGTTTCGAGAAGAGGTTTAAAAAACCTTCAAGTAGTTTTCATG 120
Dq	41 IileGlnAlaValleuGluAspAlaGlnLYsLYSGInLeuLYSaAPLYSAIleGluAsn 60
Df	121 ATCCAAGCTGTGTATMAAGATGCTCAAGAGAAAGCAAAGCAAGTAACAAGGCATTAAGAC 180
Dg	61 TTrPLEuGInLYsLeuSnAlaIalaTYrGUalaaSPAPIleAspAGLUcYSlys 80
Dh	181 TGSTTCAAGAAACTCAATGTCTGCAATGAAGTGATGAACHTTGGATGACTGTAAA 240
Di	81 ThrGluAlaProIleArgGInLYsLYSaenLYTyrgLYCYsTYrHIsproAsnValIle 1000
Dj	241 ACTGAAGGCA---GCAAGATTCAAGAGAGGCTGATTTGGGGCTTATCCACGAGCATC 297
Dk	101 ThRPheARHisLYsIleGlyLYsaRomeLYsLYSIleMeGLYLSleuAspValIle 1200
Dl	298 ACCTTGTGTTACAAGTGGGAAAAAGAAAGAAAGAAAGTGAAGAAAACTAGATGCAATT 3577
Dm	121 AlaAlaGluArGIleYsPheHIsleuAspGIuaTYrTrIIleGIuaRGInValAlaThr 140
Dn	358 GCAGAGAAACGGAGAAATTTTCATTATAGTAGAAAGATTATAGAGAGACAAGCGCTAGA 417
Dp	141 ArgGInTh----- 143
Dq	418 CGGCAAAC-AGGTGCTCATCTTAATTTATTTTAAAACAATAAGTATTCAAATTGCGAG 476
Dd	143 ----- 143
De	477 AGAAACGAAGAAATTATATTATTTTATTTTGGCAATTATCAAAAGCTATTTTGCTTT 536
Df	143 ----- 143
Dg	537 TTAAAGCTGGGGGAAAGTTTCAAAATATTTTCTAGTCTTAATGTTTGTCTCACTCACTCA 596

QY	143	-----	143
Db	597	GCATGATTTTTCATCAATTCCTTCACTTCACTCCCCCTCCTAGCGAATATCTCTCATT	656
QY	144	-----	GlyPheVal 146
Db	657	TTTCGTGTACTCCTAATGAGCTTGAAATGAAACAATCTTGTTGGACAGGTTTTGTT	716
QY	147	LeuAsnGluProGlnIValTyrGlyValArgAspIlySerGluIleValIysIleLeu	166
Db	717	TTAACTGAGCCAAAGATTATGAAAGGGGAAAAAGAGAGATGAGATGATGAAATCTTG	776
QY	167	ILAsnAsnValSerSerMetIagInnhThreupProValLeuProIleLeuGlnMetGlyI	166
Db	777	ATAAACAATGTTATGTTATTCGAGAAGAGTTCCAGTACTCCAAATCTTGATATGGGGGA	836
QY	187	LeuGlyIlySerThrThreuValIagInMetValPheAsnAspGlnArgValIleGluHisPhe	206
Db	837	CTAGAAAAGCGACTTACGCCAAATGGCTTCAATGATCAAGAATATGTAAGCATTTTC	896
QY	207	HisProIylIleThrIleCysValSerGluAspPheAsnGluValArgLeuIleIysGlu	226
Db	897	AAACTAAAGATATGGGTTTGTCCTCAATGATTTTGTATGAGAAAGAGTTGATTAAGCA	956
QY	227	ILValGlySerIleGluIlySerIeuGlyGlyMetAspLeuValProLeuGlnIys	246
Db	957	ATTGTGATTCATTATGAAGAAGCATCTGGGTGACATGACCTTGGCTCCCTCCAGAA	101
QY	247	IlyLeuValArgAspLeuLeuAsnGlyIlyIlySerIleuValLeuAspAspValTyrAsn	266
Db	1017	AAACCTCAGAGATGTTGTGATGAGAAAAAGATATCTTCTGTTTGTGATGATGTTTGGAT	1077
QY	267	GluAspGlnAspIlySerThrAlaIysLeuArgGlnValLeuIysValGlyAlaSerGlyAla	286
Db	1077	GAAGATCAAGAAAAGTGGGATTAATTGAGACAGATTTGAAGATTTGAGCTAAGTGGCT	113
QY	287	SerValLeuThrThrThrArgLeuGluIlySerIleMetGlyThrLeuGlnPro	306
Db	1137	TCAAATTCATATTACTACCTCGCTTGAAAAAATTTGAGTCAATTAATGAGAACTTTGCAACTA	119
QY	307	TyrGluIlySerAsnIlySerGlnIlyAspCysThrIleuIleuPheMetGlnArgAlaPhe	326
Db	1197	TATCAAGTATCAAAATTTGTCACAAAGATATGTTGGTTGTTGTTCAAGCAAGCTGCAATT	125
QY	327	GlyHisGlnGluGluIleAsnIleuAsnIleuValAlaIleGlyIysGluIleValIlyIys	346
Db	1257	TGCCAACCAACCGAAACAAGTCTCTAACTTAATGAGAAATCGGAAAGAGATTTGGAAGAAA	131
QY	347	CysGlyIlyValProLeuAlaIalIysThrIleuGlyIleValIleuAspPheIysArgGlu	366
Db	1317	TGGGGGGGTGCTCTTAGCACGCCAAACTCTTGGAGGCTTTTATCCCTTCAGAGGGAA	137
QY	367	GluArgGlnThrGlnHisValAlaArgAspSerGluIleTyrIlyLeuProGlnIlyIlySer	386
Db	1377	GAAAGGAGATGGGAACATGTGAGATAGTGAGATTTTGAATTACTCAAGATGAAAT	143
QY	387	SerIleLeuProAlaIleuArgIlySerTyrHisIleuProLeuAspLeuArgGlnCys	406
Db	1437	TCGTGTTTCCGCCCTTAGGCTGAGTATCATCATCTTCCACTGTGATTTGAAACAATGT	149
QY	407	PheThrTyrCysAlaValPheProIlyAspThrGlnIleuMetGluIysGlyAsnIleIleSer	426
Db	1497	TTTGCATATGGCGCATTTCCCAAGGACACCAAAATAGAAAAAGAAATATCTCATCTGCT	155
QY	427	LeuTyrMetAlaHisGlyPheIleIeuSerIysGlyAsnIleuGluIleuGluAsnValGly	446
Db	1557	CTCTGGATGGCACACAGATTTCTTTTATCAAAAGAAACATGAGAGCTAGAGAGATGGGCGC	161
QY	447	AsnGluValTyrAsnGluIlyLeuArgSerPhePheGlnGluIleGlyValIlyIysSer	466
Db	1617	AATGAAGATGGAATGAATTAATCTAGGCTTTTTCAGAGGATGGAATTAATCT	167
QY	467	GlyGlnThrTyrPheIlyMetHisAspLeuIleHisAspLeuAlaThrSerIleuPheSer	486

```

Db      1677 GGTAAACTTATTTCAAGATCATGATCATTCATGATTTGGCTACATCATATGTTTCA 1736
Qy      487 AlaserThrSerSerSerAsnIleArgGluLe----- 497
Db      1737 GCAGGCCATCTACAGAGATATGACCAATAATGTAAGATGATGAAGATATGATG 1796
Qy      498 ---IleValGluAsnIleLeIleMetMetSerIleGlyPheThrIleValIleSerSer 516
Db      1797 TTCATTGTAACAATTATTAAGATATGATATGATTCATGCTGTTCTCTCGAAGTGTCTTCT 1856
Qy      517 TySerLeuSerHisIleGluIleLysPheValSerIleuArgValIleuAsnIleuSerAspIle 536
Db      1857 TACTCTCCTTCGCTTTAAAGAGTTTGTCGTTAAGGGTGTAAATCTAAGTAACCTCA 1916
Qy      537 LysIleuArgGlnLeuProSerSerIleGlyAspIleValHisIleuArgIleuAsnIleu 556
Db      1917 GAATTTGAACGTTAACCGTCTTCCTCGTAGAGATCTAGTACATTTAAGATACCTTGACCTG 1976
Qy      557 SerGlyAsnThrSerIleArgSerIleuProAsnIleuCysIleuGlnAsnIleuGln 576
Db      1977 TCTGTAAT---AAATTTGATGCTCTTCCAAAGAGTTTGCAAGCTTCAAAATCTCGAG 2033
Qy      577 ThrIleuAspLeuHisGlyCysHisSerIleuCysCysIleuProLysGluThrSerLysIleu 596
Db      2034 ACTCTGATCTATTAATTAATGTCACGACTTCTTGTTGGCGAAACAACAAAGTAAGCTT 2093
Qy      597 GlySerIleuAsnIleuLeuLeuAsnIleuArgIleuSerIleuThrCysMetProProArg 616
Db      2094 TGTGATCTCCGGAATCTTGAATCTGATCAGTGT---CCATTGACTTCTATGCCACAGAA 2150
Qy      617 IleGlySerIleuThrCysLeuIleuThrIleuSerArgPheValIleGlyIleGlyIleVal 636
Db      2151 ATAGGATTTGTTGACATGCTTTAAGACACTAGTACTTTGTTGAGGC---GAAGAGAA 2207
Qy      637 SerCysGlnIleuGlyIleuLeuArgAsnIleuAsnIleuThrIleGlyIleGlyIleHis 656
Db      2208 GGTATCAACTGTTGGAACCTAGCAATTTAAACCTCGTGTGCAATTTCAATCACAAT 2267
Qy      657 LeuGluArgValIleuAsnAspMetAspAlaLysGluIleuAsnIleuSerAlaLysGluAsn 676
Db      2268 CTTGAGAGAGTGAAGAAATGATATGAGGCAAAGAACCAATTTATCTGCAAAAGCAAAAT 2327
Qy      677 LeuHisSerIleuSerMetIleuThrAspAspArgGluArgProArgIleuThrGluSerGlu 696
Db      2328 CTACACCTTTTAAGATGATGTTGGAT-----ACACCAAAACAGTATGAAATCCGAA 2378
Qy      697 LysValGluValIleuGluAlaLeuLysProHisSerAsnIleuThrCysLeuThrIleArg 716
Db      2379 GAATTTAAAGGCTTGAAGCCCTCAACACATCCCAATCTGAATAATTTAGAAATCATTT 2438
Qy      717 GlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValIleuLysAsnValIle 736
Db      2439 GACTTCTGTGATTTCTGTCTCTCGACCTGAGTGAATCACTAGTTTGAAGAAATGTTGTC 2498
Qy      737 SerIleGluIleIleSerCysValAsnCysSerCysLeuProProPheGluGluLeuPro 756
Db      2499 TCTATTTCTAATTAGCGGTTGTAAGAACTGCTGCTGCTTACCACTTTGGAGCTGCT 2558
Qy      757 CysLeuLysSerIleuGluLeuThrArgIleuSerAlaGluValIleGlyIleVal---AspSer 775
Db      2559 TGTCTAAGAACTCTGAGATTCAAGACCGGCTCTGAGAGGAGTATGTTGAAGATTCT 2618
Qy      776 GlyPheProThrArgArgArgPheProSerIleuArgIleuLysLeuAsnIleArgGluPheGly 795
Db      2619 GGATTTCTGACAAAGAAAGATTTCCATCCCTGAGAAAACTCATATATGTGGCTTTTGT 2678
Qy      796 AsnIleuArgGlyLeuLeuLysGluGlyIleGluGlnCysProValIleuGluGluIle 815
Db      2679 AATCTGAAGGATTTGCAAGATGAAAGACACAGACCAATTCCTCCGTCCTTGAAGAGTGT 2738
Qy      816 GluIleLysCysCysProMetPheValIleProThrIleuSerSerValIleLysLeuVal 835

```

```

Db      2739 AAGATTTCCGATGCGCTAATGTTGTTTCCGACCCCTTCTCTGTGCAGAAATTAAGA 2798
Qy      836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnIleuMetAlaIleu 855
Db      2799 ATTTGGGGGGAG---GCAGATGCAGAGAGTTTGAGCTTCATATCTATCTCAGACACTTT 2855
Qy      856 ThrSerLeuGlnIleArgIleAsnIleGluAspAlaSerIleuProGluIleMetPheIle 875
Db      2856 ACATCCCTCAAGATTTTCAGTAACACACAGTCACTCACTACGAAAGAGATGTTCAA 2915
Qy      876 SerIleuAlaAsnIleuSerIleuAsnIleSerPheThrPheAsnIleuLysGluLeuPro 895
Db      2916 AACCTTAAATCTCAATATCTGATGAGTCTCTTTTGGAGAAATCTCAAGAGCTGCT 2975
Qy      896 ThrSerIleuAlaSerIleuAsnAlaLeuIleHisIleuGluIleHisSerCysIleValIleu 915
Db      2976 ACCAGCTGGCTAGTCTCAACAATTTGAAGTGTGATATTCCTTATGTAGCACTA 3035
Qy      916 GluSerIleuProGluGluIleValIleGlyLeuIleSerIleuThrGlnIleuSerIleThr 935
Db      3036 GAGAGTCTCCCGAGAGAGGCTGGAAGTTTATCTTCACTCAGACAGATTTTGTGA 3095
Qy      936 TyrCysGluMetIleuGlnCysLeuProGluIleGluGlnHisIleuThrAlaIleuThrAsn 955
Db      3096 CACTGTACATGCTTAAATGTTTACAGAGGAGATTCAGACCTTACAAACCTTCAACAGT 3155
Qy      956 LeuSerValGluPheCysProThrIleuAlaLysArgCysGluLysGlyIleGlyIleAsp 975
Db      3156 TTAAATAATGGGGAGATTCCAACATGATCAAGCGGTGTGAGAGGGAATGAGAAAGAC 3215
Qy      976 TrpTyrIleLysIleAlaHisIleProArgValPheIleTyr 988
Db      3216 TGGCAAAATTTCTCACTTCTCAATGTGAATATATAT 3254

RESULT 6
AY426260 3260 bp DNA linear PLN 16-DEC-2003
LOCUS Solanum bulbocastanum blight resistance protein RGA1 gene, complete cds.
DEFINITION
ACCESSION AY426260
VERSION AY426260.1 GI:39636722
KEYWORDS Solanum bulbocastanum
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
REFERENCE 1. An ancient R gene from the wild potato species Solanum
AUTHORS Van Der Voosen, E., Sikkema, A., Hekker, B., Gros, J.,
Stevens, P., Muskens, M., Wouters, D., Pereira, A., Sikkema, W. and
Allefs, S.
TITLE Solanum bulbocastanum confers broad-spectrum resistance to Phytophthora
JOURNAL Plant J. 36 (6), 867-882 (2003)
PUBMED 14675451
REFERENCE 2. (bases 1 to 3260)
AUTHORS van der Voosen, E. and Allefs, S.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
FEATURES
location/Qualifiers
1..3260
/organism="Solanum bulbocastanum"
/mol_type="genomic DNA"
/db_xref="taxon:147425"
/join("<1..427,709..>3260)
/product="Blight resistance protein RGA1"
/note="confers broad-spectrum resistance to Phytophthora
infestans in potato and tomato"
/codon_start=1
/product="Blight resistance protein RGA1"

```

/protein_id="AAR29070.1"
/db_xref="gi:39636723"
/translation="MAEAFIQVLNDLTFPIQGLGVFGEKEFKLLSMSEMIQAV
LEDQOEKQIKYKAKIKMLOKINVAAYEVDDILDQCKTEAARPKQAVIGRHYPRITTC
YKVKRMEKMEKIDALAEERNFHLDERIIERQARQQTQFVLTEPRVGRKEBDE
IVKLIINNVSEBEVPVLPIMQGLQYTTIAQWVENDQRTHEFHNIKIVCVDDPD
EKRLIKAIIVESIIEKSLGDMQAPLOKLOELNGKRFVLVDVMDQEKMNLA
GLTKIGASGASITITRLEKISGMGTLOLYLSNMGODCVLLEKQRAFCQETSPK
LMETGKELVKGCGVPLAAKTLGILPRKRESEMEHRLSDINLPDENVLPAR
LSTHHLPDLAQCFAYCAVPKPKDKEKEYIILAMMAHSRLDSGNMLEDVEMVNVN
ELVYRFPQELIEVSGKTYFRMDLIHDLATSMFSASBSKISQINMLEDVEMFV
TNKDDMSIGFSEVSVSPSLFKRPSVLRLNLSNSEFQLPSSVGLVLRLLDS
GNKICSLPKRLCKLQNLQTLIDLYNCQSLCPQKTSKCSLRNVLHCPKLTSPRI
GLTKLTGIFVYVGERKQYQGLRLNLEGAISITLBEVKNDMEKEXNLSAKX
LHSLMSMDRPNRYSESEVKYIHALKHPNLIKYLEIIDPGECFLPDMMNHSVLKNVS
ILISGCNCSCLPRPGEIPCLISLELDQSGEVEYVDSGLTRRPPNSLPKLTIGP
CNLGLQMKGAQEPVLEBKISDCPFVFPVPTSSYKKEITWBDAGISLSDINS
TLTSLKIFSNHTVTSLEMPKLENILYLSVPLEMKELPFLASLNMKCLDIR
CYALESLPEBGLISLTLELPVHECNMLKCLPGLQHLTLTSLIKRGCPQLIKRCE
KGIGEDWIKISHIENVNIIYI"

ORIGIN

Alignment Scores:
Pred. No.: 1.47e-278 Length: 3260
Score: 3648.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
Query Match: 71.15% Indels: 114
DB: 8 Gaps: 9
US-10-647-268-2 (1-988) x AY426260 (1-3260)
QY 1 MetIaGluAlaPheIeuGluValIleuEuAspAsnIeuThrCysPheIleGluGlyIu 20
Db 1 ATGGCTGAAGCTTTCCTTCAAGTCTGCTAGATTAATCTCACTTTTATCAAGAGGAA 60
QY 21 LeuGlyIeuIleLeuGlyPheIysAspGluPheGluIuIysLeuGlnIserThrPheThr 40
Db 61 CTTCGATTGGTTTTCGTTTTCGAGAGAGGTTTAAACCTTCAAGTATGTTTTCATG 120
QY 41 ILeGlnAlaValIleuGluAspAlaGlnIuIysGlnIeuIuIysAspIysAlaIleGluAsn 60
Db 121 ATCCAGCTGTGCTAGAGATGCTCAAGAGAAACAATGAAAGTACAAAGCATTAAGAAC 180
QY 61 ThrIeuGlnIuIysLeuAsnAlaAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 80
Db 181 TGGTTACGAAATCTCAATGTGCTGCATATGAAGTTGATGACATCTGGAGACTGTA 240
QY 81 ThrGluAlaProIleArgGlnIuIysLeuAsnIuIysTyrgIuIysTyriHisProAsnValIle 100
Db 241 ACTAGAGCA---GCAAGATTCAAGCAGGCTGTATTTGGGCGTTTATCATCCACGACCATC 297
QY 101 ThrPheArgHisIysIleGlyIysArgMetIuIysIleMetGluIuIysLeuAspValIle 120
Db 298 ACTTTCGTTCACAGCTGGGAAAAAGATGAAGAAATGATGAAAAAACTAGATGCATTT 357
QY 121 AlaIaIaGluArgIleIysPheHisIleuAspGluIuArgThrIleGluIuArgIuValIaIaThr 140
Db 358 GCAAGAGAACGAGAGAAATTTTCATTTAGATGAAGATTATAGAGACAAAGCTGCTAGA 417
QY 141 ArgGlnThr----- 143
Db 418 CGGCAAC-AGGTGCTCATCTTAATTTTATTTAAAACAAAATAGATATTACAAATTGAG 476
QY 143 ----- 143
Db 477 AGAAACGAGAGAAATTTATATTCATTTTATTTTGGCAATTATCAAAAGTATTTGTGTTT 536
QY 143 ----- 143
Db 537 TTAAAGTGGGGGAGATTCAAAATATTTTCTAGTCTTAAATGTTTGTCTCACTCATCTCA 596
QY 143 ----- 143

Db 597 GCATGATTTTCTCAATCCTTCACTTCAATCCCCCTACTGTGCAAAATCTCTCATTT 656
QY 144 ----- GlyPheVal 146
Db 657 TTCTGTTGACTCCTAATAGACCTGAATGTAAACAATCTTGTGTTGAGACAGGTTTGT 716
QY 147 LeuAsnGluProGlnValTyrgIuIysArgAspIysGluIysAspGluIleValIysIleIeu 166
Db 717 TTAATGAGCCAAAGTTTATGAGAGGAAAAAGAGAGGATGATGATGAATATCTTG 776
QY 167 ILeuAsnValIserAsnAlaGlnThrIeuProValIeuProIleIeuGlyMetGlyIy 186
Db 777 ATAAACAATGTAGTTATTCGAAAGAGTTCCAGATCTCCCAAACTTGATGTGAGGAG 836
QY 187 LeuGlyIysThrThrIeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPhe 206
Db 837 CTAGAAAGACGACTAGCCCAATAGTCTTCATATATCAAAAGATTAATGACATTTTC 896
QY 207 HisProIysIleThrIleCysValIserGluAspPheAsnGluIysArgLeuIleIysGlu 226
Db 897 AATCTAAAGATATGCGTTTGTGTCTCAGATGATTTTATGAGAGAGGTTTAAAGCA 956
QY 227 ILeuAluIserIleGluGluIysSerIeuGlyGlyMetAspLeuAlaProIeuGluIys 246
Db 957 ATGTAGAATCTTATGAAAGAAAGTCACTGGGTGACATGACCTTGCTCCCTCCAGAAA 1016
QY 247 LysIeuArgAspIeuLeuAsnGlyIysIysIysIysIysIysIysIysIysIysIysIys 266
Db 1017 AAGCTTCAAGAGTGTGAATGAGAAAGAAAGTCTTGTGTTGATGATGATGTGAAT 1076
QY 267 GluAspGlnAspIysTyrgAlaIysLeuArgGlnValIleuIysValIglAlaIserGlyAla 286
Db 1077 GAGATCAAGAAAGTGGGATTAATCTTAAGCAGATATGAAGATGTGAGGTAGTGCT 1136
QY 287 SerValIeuThrThrIaIrgIeuGluIysValGlySerIleMetGlyThrIeuGlnPro 306
Db 1137 TCAATCTCAATTTACTACTCGCTTGAAAAAAATGGATCAATTAAGGAAACTTGGCACTA 1196
QY 307 TyrgIuIuIserAsnIeuIserGlnGluAspCysTyrgIeuIeuPheMetGlnArgAlaPhe 326
Db 1197 TATCAGTATCAAAATTTGTCTCAAGAAAGATTTGTTGTTGTTTCAAGCAACGTGCATTT 1256
QY 327 GluIysIleGlnIuIleAsnIeuAsnIeuValAlaIleGlyIysGluIleValIysIys 346
Db 1257 TGCACCAAAACGAAACAAGTCTTAATTAAGAAATCGGAAAGAGATGTGAAAGAA 1316
QY 347 CysGlyIysValProIeuAlaAlaIysThrIeuGlyIyIleIeuArgPheIysArgIu 366
Db 1317 TGTGGGGGTGTGCTCTAGACGCCAAAACCTTGGAGGCTTTTACCTTCMAAGAGGAA 1376
QY 367 GluArgGlnTyrgIuHisValArgAspSerGluIleTyrgIysIeuProGlnIuIuIser 386
Db 1377 GAAAGTAAATGGAAACATGAGAGATATGAGATTTGAATTTAATCTCAAGATGAATAAT 1436
QY 387 SerIleIeuProAlaIeuArgIeuSerTyriHisIleuProIeuAspLeuArgGlnCys 406
Db 1437 TCTGTTTGGCTGCTCGAGGCTGAGTTATCATATCTTCCACTGATTTGAGCAATGT 1496
QY 407 PheThrTyrgValAlaPheProIysAspThrGluMetGluIysGlyAsnIeuIleIser 426
Db 1497 TTTGCATATGGCGAGATATCCCAAGACCAAAATAGAAAAGAAATATCTCATGCT 1556
QY 427 LeuThrMetAlaHisGlyPheIleIeuSerIysGlyAsnIeuGluIuAsnValGly 446
Db 1557 CTTCGATGGCACAGTTTTCCTTATCAAAAGAAACATGAGGCTAGAGAGTGGGC 1616
QY 447 AsnGluValTyrgAsnGluIeuTyrgIeuArgSerPhePheGlnIuIleGluValIysSer 466
Db 1617 AATGAAGTATGAGATGATTAATTAATGAGCTTTTTCAGAGGATTTGAAGTTAAATCT 1676
QY 467 GlyIleThrTyrgPheIysMetHisAspLeuIleHisAspLeuAlaThrSerIeuPheSer 486

Db 1677 GGTAAACCTTATTCAGATGATGATCTCATCCATGATTTGGCTACATCTATGTTTCA 1736
 Qy 487 AAlaserThrsSerSerSerAsnIleArgIuile----- 497
 Db 1737 GCAAGCGCATCAAGACAGATATACGCCAATTAATGTAAGATGATGAAGATATGATG 1796
 Qy 498 ---1leValGluAsnTyrlleHlsmetMetSerIleGlyPheThrLyValValSerSer 516
 Db 1797 TTCATTGTAAACAATTATTAAGATATGATGTCATGTTCTCCGAAGTGGTGTCTTCT 1856
 Qy 517 TySerLeuSerHlsleGlnIlyPheValSerLeuArgValLeuAsnLeuSerAspIle 536
 Db 1857 TACCTCTCTGCTTCTTAAAGGTTTGTCTGTTAAGGGTCTTAACTAAGTAACCA 1916
 Qy 537 LysLeuLysGlnLeuProSerSerIleGlyAspLeuValHlsleArgTyrlleAsnLeu 556
 Db 1917 GAATTGTGAACGTTACCGCTTCTCGTGAAGTCTAGTACATTAAAGTACCTTGACCTG 1976
 Qy 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCySlyLeuGlnAsnLeuGln 576
 Db 1977 TCTGGTAT---AAATTGTAGTCTTCCAAAGAGTTGTGCAAGCTTCAAAATCTGCAG 2033
 Qy 577 ThrLeuAspLeuHlsGlyCyHlsSerLeuCySlyLeuProLysGlnThrSerLyLeu 596
 Db 2034 ACTCTGTATCTATTAATTAATGGCAGTCACTTCTGTGGCCGAAACAAACAGTAAGCTT 2093
 Qy 597 GlySerLeuArgAsnLeuLeuAspGlyCySerTyrlleLeuThrCyMetProProArg 616
 Db 2094 TGTAGTCTCCGGAATCTGTACTGATCACTGT---CCATTGACTTCTATGCAACCAAGA 2150
 Qy 617 IleGlySerLeuThrCySlyLeuThrLeuSerArgPheValValGlyIleGlnIlyLys 636
 Db 2151 ATAGAGTTGTGACATGCTTAAAGACATAGTATCTTGTGTAGGC---GAGAGGAA 2207
 Qy 637 SerCySglnLeuGlyGlnLeuArgAsnLeuAsnLeuTyrlleGlySerIleGlnIleThrHls 656
 Db 2208 GGTATATCAACTGTGTAAGTCACTGAAATTTAAACCTCGGTGCAATTTCAATCACTACAT 2267
 Qy 657 LeuGlnArgValLysAsnAspMetAspAlaLysGlnValAsnLeuSerAlaLysGlnLysn 676
 Db 2268 CTTAGAGAGGTAAGAAATGATATGAGGCAAAAGGCAATTTATCTGCAAAAGCAAT 2327
 Qy 677 LeuHlsSerLeuSerMetLysTrpAspAspArgIuArgProArgIleTyrlleGlySerGln 696
 Db 2328 CTACACTCTTAAAGATAGTGGAT-----AACCAACAGATATGATCCGAA 2378
 Qy 697 LysValGlnValLeuGlnAlaLeuLysProHlsSerAsnLeuThrCySlyLeuThrIleArg 716
 Db 2379 GAAGTTAAAGTGTGAAGCCCTCAACCATCCCATCTGAATATTTTGAATCAAT 2438
 Qy 717 GlyPheArgGlyIleArgLeuProAspTrpMetAsnHlsSerValLeuLysAsnValVal 736
 Db 2439 GACTTCTGTGATCTGTCTCCCTGACATGATCACTCAATTTTAAAAAGTGTCTC 2498
 Qy 737 SerIleGlnIleIleSerCySlyLeuAsnCySlyLeuProProPheGlyGlnLeuPro 756
 Db 2499 TCTATTCTAAATTAAGCGTGTGAAGAACCTGCTGCTTAAACCTTTGGTGAAGCTGCT 2558
 Qy 757 CySlyLeuSerLeuGlnLeuTrpArgIlySerAlaGlnValGlyTyrlleVal---AspSer 775
 Db 2559 TGTCTAGAAAGTCTGAGATTAACAAGCGGTCTGAGAGGTAGATATGTTGAAGATCTT 2618
 Qy 776 GlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIleArgGlnPheGly 795
 Db 2619 GGATTCTCGAAGAAAGATTTCCATCCCTGAAAAAATTCATATGATGGTGGCTTTGT 2678
 Qy 796 AsnLeuLysGlyLeuLysGlnIlyGlnGlnGlnCySlyProValLeuGlnIlyLeu 815
 Db 2679 AATCTGAAGATTTCAAGATGAAGAGAGCAATTCCTCCGTCTTGAAGAGATG 2738
 Qy 816 GlnIleLysCySlyProMetPheValIleProThrLeuSerSerValLysLeuVal 835
 Db 2739 AAGATTTCGATGCTATGTTGTGTTTCCGACCTTTCTTGTCTCAAGAAATTAAGAA 2798

Qy 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
 Db 2799 ATTGGGGGAG---GCAGATGCAAGAGGTTTGAGCTTCATATCTCAAGACTCTT 2855
 Qy 856 ThrSerLeuGlnIleArgTyrlleAsnLysGlnAspAlaSerLeuProGlnIlyMetPheLys 875
 Db 2856 ACATCCCTCAAGATTTTCAATTAACACACAGTGAATTCATCACTGGAAGATGTTCAAA 2915
 Qy 876 SerLeuAlaAsnLeuLysTyrlleAsnIleSerPheTyrlleAsnLeuLysGlnLeuPro 895
 Db 2916 AACCTTGAATTCATATTAAGTGTCTTCTTGGAGAACTTCAAGAGCTGCTT 2975
 Qy 896 ThrSerLeuAlaSerLeuAsnAlaLeuLysHlsleGlnIleHlsSerCySlyTyrlleVal 915
 Db 2976 ACCAGCTCGGTATCTTCAACAATTTGAAGTGTGATATTCGTTATTTAGCACTA 3035
 Qy 916 GluSerLeuProGlnIlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThr 935
 Db 3036 GAGAGTCTCCCGAAGAGGCTGAAGGTTTATCTTCACTCAAGAGATTGTTTGA 3095
 Qy 936 TyrlleGlnMetLeuGlnCySlyLeuProGlnIlyLeuGlnHlsleThrAlaLeuThrAsn 955
 Db 3096 CACTGTAAACATGCTAAATATGTTTACAGAGGATTCAGACCTTAAACCTCAAGAT 3155
 Qy 956 LeuSerValGlnPheCySlyProThrLeuAlaLysArgCySlyLysGlyIleGlyGlnAsp 975
 Db 3156 TTAAAAATTCGGGAGATGTCACAACTGATCAAGCGGTGTGAAAGGAATGAGAAAC 3215
 Qy 976 TrpTyrlleAlaHlsIleProArgValPheIleTyrlle 988
 Db 3216 TGGCAAAAATTTCTCAATCTTCAATGTAATATATAT 3254
 RESULT 7
 AV303171
 LOCUS 163635 bp DNA linear PLN 15-AUG-2003
 DEFINITION Solanum bulbocastanum chromosome 8 clone 177013, complete sequence.
 ACCESSION AY303171
 VERSION AY303171.1 GI:32470640
 KEYWORDS HTG.
 SOURCE Solanum bulbocastanum
 ORGANISM Solanum bulbocastanum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 163635)
 Song,J., Bradeen,J.M., Naess,S.K., Raesch,J.A., Wielgus,S.M., Haberlach,G.T., Liu,J., Kuang,H., Austin-Phillips,S., Helgeson,J.P., Helgeson,J.P., and Jiang,J.
 Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight
 Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)
 JOURNAL 2 (bases 1 to 163635)
 PUBMED 12872003
 AUTHORS Song,J., Bradeen,J.M., Naess,K.S., Raesch,J.A., Wielgus,S.M., Haberlach,G.T., Kuang,H., Austin-Phillips,S., Helgeson,J.P., Liu,J., Tallon,L.J., Zaborisky,J., Buell,C.R. and Jiang,J.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAY-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT Address all correspondence to: rbuel1@tigr.org
 Clone 177013 is from Solanum bulbocastanum chromosome 8. The orientation of the sequence is from SPE to T7 end of the clone. Genes were identified by a combination of several methods: Gene prediction programs including GENSCAN+ (Chris Burge, http://CCR-081.mlt.edu/GENSCAN.html), GenemarkHM (Mark Borodovsky, http://genemark.biology.gatech.edu/Genemark/), and GeneSplicer (Michaela Perera and Steven Salzberg, contact mperer@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/db/cgi.shml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide

similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SS (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arjan Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

SOURCE

```
1.163635
/organism="Solanum tuberosum"
/mol_type="genomic DNA"
/db_xref="taxon:147425"
/chromosome="8"
/clone="177013"
<1..>811
/locus_tag="177013.24"
/join(<1..345,682..>811)
/locus_tag="177013.24"
/product="hypothetical protein"
/join(<1..345,682..811)
/locus_tag="177013.24"
/note="predicted by genemarkhm"
/codon_start=2
/product="hypothetical protein"
/protein_id="AAP45168.1"
/db_xref="GI:32470642"
/translation="MDPSLRIYPPDGDREFAVDIRGKPERLSRYMYLADPTLOR
VATIRSKAVIVIRKQTDALFRPDICSGDITLSDDELSTTSGITLVLEAYV
FGSLFWETSEYVEALGMPNELIDCWLPELLPEQERVARAGQGTGELNSQI"
/complement(2643..2664)
/rpt_family="AT_rich"
<3067..>7634
/locus_tag="177013.29"
/join(<3067..3304,3388..3488,4038..4246,7049..>7634)
/locus_tag="177013.29"
/product="putative xyloglucan endotransglycosylase-related
protein"
/join(3067..3304,3388..3488,4038..4246,7049..7634)
/locus_tag="177013.29"
/note="similar to xyloglucan endotransglycosylase-related
protein GB:AA018365 GI:1244754 (Arabidopsis thaliana)"
/codon_start=1
/product="putative xyloglucan endotransglycosylase-related
protein"
/protein_id="AAP45169.1"
/db_xref="GI:32470643"
/translation="MDYRVLSVSKSTPFSLLLLLYTPATETTTAAANTTYKAFNL
STTFEBGSPPLFSDFNTERSPDRSPFLLNKSGSGVISTEYNYGFFSASIKLPA
IYTAGIVVAFYTSNADLPEKKNHDELIFLGAVNGQWPRFQTNMGNGSVRGHERY
RMWDPDSKDPQYSILMTPKNIIFYIDETPLREVNRPAMGADFPSPKMSLYATIMDA
SSMANGGKARVDYKVEPATEIKDLVIEGCIIVPTBQIPSTNCTDRSAKLADQYS
ITPERRSKMFRPERIRMYTICYDNLRFPVPEPVCVITYOSRDLFRDSGRLRQMKRG
GSHSHSQTRKRKRPGRSSRRKNVVGASKSGRGSAAAM"
/complement(3312..3349)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="(TA)n"
/complement(6049..6077)
/rpt_family="AT_rich"
/complement(<8645..>11610)
/locus_tag="177013.33"
/complement(join(<8645..8953,9033..9183,9272..9509,
9590..9800,9895..10091,10581..>11610))
/locus_tag="177013.33"
/product="putative receptor protein kinase"
/complement(join(8645..8953,9033..9183,9272..9509,
9590..9800,9895..10091,10581..11610))
/locus_tag="177013.33"
/note="similar to receptor protein kinase GB:AAC23542
GI:836954 (Ipomoea trifida)"
/codon_start=1
/product="putative receptor protein kinase"
```

```
/protein_id="AAP45176.1"
/db_xref="GI:32470650"
/translation="MKRGDVLNHSQVLDSEGRKFLGFFSIPTQNTKTYLGIMVADPV
FKTLMIANPMTPLNHSGLTLTDSGTALRTSGGKTVNLTATPLTSGILARLDSGN
FVVDERTNRRTMNSPDPHPSCLLPKGLGNNLTTRQWNTLTSLVSSAVAPARFTL
SLEAIQAPQIVVSRKEEVITSGAMNNQGPPLPSRDSATTTQYNLNLVSGIDGMF
FOFQKATGSPSELELFSGDIAIADGSIYRKNFCVGYGDDCVSSQLEPCKDDG
KFEQKRDGFDLISGTTTSSYDNASISIGDQCKMEGSCVGFPTLNSNGCLISNG
KFLPRVDSGGRKEEHIRMNADSFNNRTLSGEVREVDQIKIGFGLIMATNV
FSSDNKLAGGGFGPVYKGGPDRGEVAKRLSRSGGLAEKNEILLIAVORNLV
RYLGCCHGBDKMLIYEMMKSLDPLFDPERKLLDMORFELITGGIAGGLLYLHK
YSRKRVITHRLKASNVLDENMKPLDPLGARIFKQNETAYTRRVYGTGWAPER
AMEGAFISKDVSEFVLMLEILSGRNASIQQNRPLNLGIAMELMEKSGGSELKO
PDLEDLDTBQFLRVIHVGLICVQEGATPRMSDIVSMLCNGSMSPILAKQPAFFTG
RDEIYSSSNKTQCSINDCSITVIEAR"
/complement(<12526..>15441)
/locus_tag="177013.32"
/complement(join(<12526..12834,12979..13066,13157..13394,
13479..13689,13770..13966,14062..14130,14268..>15441))
/locus_tag="177013.32"
/product="putative receptor protein kinase"
/complement(join(12526..12834,12979..13066,13157..13394,
13479..13689,13770..13966,14062..14130,14268..15441))
/locus_tag="177013.32"
/note="similar to receptor protein kinase GB:AAC23542
GI:836954 (Ipomoea trifida)"
/codon_start=1
/product="putative receptor protein kinase"
/protein_id="AAP45167.1"
/db_xref="GI:32470641"
/translation="WKSLSNIFLLITLFPESHCTTNLSVAATISLREDELNHSQ
VLDSGGRFKLGFPISIQNNYNYGIYVADDPQKMLIANPNPLNLSGLTLITDT
GLTKITSGKTVNLTPLPLTRSLIAALQSGNVLADDETQNLTLMOFPHPTVLP
GMKLVNLTTRQWNTLTSLSSYIPASGAFLLSLSIDQAFOLYIRRGEEVYISGM
RNSFPLLTLNHSNNRYOYNLNIPECKKQDQPEKQSDPLFDRSKNSVYNAST
DSRYVALYNEFCYTESQDQCVSNQLEPCKKQDQPEKQSDPLFDRSKNSVYNA
SLGQCMRCEWCHSCVGFPTTSTGTCLINNGEEFVDSGNTVAKTYLVSSNSNA
IVPMLISGFIYSIVRRKLOAEKREBEYIRLTLSDSNDNMKSGKGRREVQDLK
IFRGFPLAATNNSSSENKLEGGFGVYKPKPDGSEVAVKRLSRSGQGLVFRKE
LILIAKQVNLVAVLGCJHDEKMLIYEMMKSLDPLFDPERKLLDMORXVEI
LEGAGQVLYHKVSRVIRHDLKASNVLDENMKPLDPLGARILFQNETEAVVA
RVGFTGYMAPERPMEGAFISKDVSEFGLIMLEIMELMEKSGGLKDPALGLDLD
TKLIRQYHVLGCLVQEGATPRMSDIVSMLGNSMPLTPKQPAFFTGNETESH
AGIRARQYVNDSCITVIEAR"
/complement(17040..17075)
/rpt_family="AT_rich"
<17424..>19717
/locus_tag="177013.25"
/join(<17424..17782,18415..>19717)
/locus_tag="177013.25"
/product="hypothetical protein"
/join(17424..17782,18415..19717)
/locus_tag="177013.25"
/note="predicted by fgenesh"
/codon_start=1
/product="hypothetical protein"
/protein_id="AAP45173.1"
/db_xref="GI:32470647"
/translation="MEENTYMESTSTRRPSVDEEDDISKOYVHKYGMERHDDHEE
DYRSGYGGDDQEMKPTKILYVGMWLYTMSRCSEFHTVLIPIYFPLISQTLWPOOPOL
GIVKANAGLGGORRELELYEMLTRRNMLACTRESALEWISIMTILGILIAAPVLGFL
SIHLIDYGYOOLIAASTAIGLFCPLAGFFKTRWIPPYIAALVAAANTVSSCHAH
LGMWNRJLVGSPIRKQSPDRKAVASWLSHSTAAQGLGAALMSAFYHMLRKSDST
SLMWVSIISGLINFIQWNLVATSRPONDLTNSAPKTHVSIIFKYPHAGSLAGV
PLSFTTMCITFTAGVLISGIDLCIPNNILYIMLTYPFLPVSILPHFPOGLRADA
VKQDLGFLITSAIVSGFPYRHRNNMKVHIFETAIOTRATGILHAGVLTMDGSP
SGKGAQSVMSWTRALGACGAPALASTSPONTIMSGVAFCAAILKILLIPGNISN
FGGAKAAGVSDSERGSPVPGLDIGVLEKEPVEVQEEVKQI"
/complement(20398..20420)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="(21006..21044)
/complement(21081..21103)
```

```
repeat_region      /rpe_family="AT-rich"
                    complement(21321..21365)
repeat_region      /rpe_family="AT-rich"
                    complement(21865..21893)
gene               /rpe_family="AT-rich"
                    complement(<23096..>25535)
mRNA               /locus_tag="177013.26"
                    complement(join(<23096..23164,23544..23662,23792..23959,
                    24672..24782,24905..24979,25082..25535))
CDS                /locus_tag="177013.26"
                    /product="hypothetical protein"
                    complement(join(23096..23164,23544..23662,23792..23959,
                    24672..24782,24905..24979,25082..25535))
                    /notes="predicted by genemark-ESM"
                    /codon_start=1

Alignment Scores:
Pred. No.:         9.8e-276      Length:      163635
Score:             3642.00       Matches:     746
Percent Similarity: 76.76%      Conservative: 93
Best Local Similarity: 68.25%   Mismatches: 141
Query Match:       71.04%       Indels:     115
DB:                8            Gaps:       9

US-10-647-268-2 (1-988) x AY303171 (1-163635)

QY      1      MetAlaGluAlaPheLeuGlnValLeuLeuAspLeuThrCysPheIleGlnGly 20
DB      76388  ATGGCTGAAGCTTCTTCCTCAAGTTCTGCTAGATATCTCACTTTTTCATCCAAAGGGA 76447
QY      21      LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThr 40
DB      76448  CTTGGATTGGTTTGGTTTGCAGAAAGAGTTTAAAACTTTCAGAGTATGTTTCAATG 76507
QY      41      IleGlnAlaValLeuGluAspAlaGlnIleuLeuLeuLeuLeuLeuLeuLeu 60
DB      76508  ATCCAGCTGCTGTAAGATGCTCAAGAAAGCACTGAAGTACAAAGCAATAAAGAAC 76567
QY      61      TrpLeuGlnIleLeuAspAlaAlaAlaIleuLeuLeuLeuLeuLeuLeuLeu 80
DB      76568  TGGTTACAGAAATCAATGTTGCTGCATATGAAAGTTGATGACATCTTGATGACGTAAA 76627
QY      81      ThrGluAlaProIleArgGlnIleuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
DB      76628  ACTGAGCA---GCAAGATTCAAGCAGGCTGATTGGGCGCTTATCATCCACGACCATC 76684
QY      101     ThrPheArgHisIleGlyLeuArgMetLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB      76685  ACTTCTGTTACAGAGTGGGAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 76744
QY      121     AlaAlaGluArgIleLeuPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
DB      76745  GCAGAGGAACGAGAGAAATTTTCATTAGTAAAGATTATAGAGACCAAGCTGCTAGA 76804
QY      141     ArgGlnThr----- 143
DB      76805  CGGCAAC-AGGTGCTCATCTTAATTTTAAAAACAATTAAGTATTACAATTCAG 76863
QY      143     ----- 143
DB      76864  AGAAACGAAGAAATTATATTCATTTTATTTTGGCAATTATCAAGTCATTTGTGTT 76923
QY      143     ----- 143
DB      76924  TTAAGCTAGGGAGATTCAAAATATTTTCTTAATCTTAATGTGTGTCATCATCA 76983
QY      143     ----- 143
DB      76984  GCATGATTTTCTCAATCCTTCACTTCACTCCCTCTACTGTGCAAAATATCTTCTAT 77043
QY      144     -----GlyPheVal 146
                    |||||
```

```
DB      77044  TTCTGTGACTCCTAATGAGCTTGAATGTAAACAATCTTGTGGAGCAGGTTTGT 77103
QY      147     LeuAsnGluProGlnValIleGlyArgAspLeuGluLeuAspGluIleValIleLeu 166
DB      77104  TTAACGAGCCAAAAGTTTATGAAAAGAAAAGAGAGATGACATGTGTAATCTTG 77163
QY      167     IleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGly 186
DB      77164  ATAAACAATGTAGTATTCCAAAGAGTTCCAGTACTCCCAATCTTGATGGGGGA 77223
QY      187     LeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGlnIleGlnHisPhe 206
DB      77224  CTAGAAAGAGAGCTCTAGCCCAATGCTCTCAATGATCAAGAAATTAACGACATTC 77283
QY      207     HisProValIleThrIleCysValSerGluAspPheAsnGluLeuLeuLeuLeu 226
DB      77284  AATCTAAAGATATGGGTTTGTCTCAGATATTTATGAGAAAGGTTATTAAGCA 77343
QY      227     IleValGluSerIleGluGluLeuSerLeuGlyMetAspLeuAlaProLeuGln 246
DB      77344  ATTGAGATCTTATGAAAGAAAGTCACTGGGTGACATGAGCTTGCTCCCTCAGAA 77403
QY      247     LysLeuArgAspLeuLeuAsnGlyLeuLeuLeuLeuValLeuAspAspValTrpAsn 266
DB      77404  AAGCTTCAGAGTTGTTGAATGAAAGAAAGATCTTCTTGTGTTGGATGATGTTGGAT 77463
QY      267     GluAspGlnAspIleTrpAlaLeuLeuArgGlnValLeuLeuValGluValAlaSer 286
DB      77464  GAAAGTCAAGAAAGTGGATTAATCTTAAGCAGATTTGAAGATTTGAGCTAGTGCT 77523
QY      287     SerValLeuThrThrThrArgLeuGluLeuValGlySerIleMetGlyThrLeuGln 306
DB      77524  TCAATTCATTAATCTACGCTCGCTTGAAGAAATGGATCAATTAAGGAACTTGGACA 77583
QY      307     TyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArgAla 326
DB      77584  TATCAGTTATCAAAATTTGTCCAAGAGATTTGTTGTTTCACCAACGTCGCAATT 77643
QY      327     GlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyValGluIleValIle 346
DB      77644  TGCCACCAACCGAAACAAAGCTTAATCTTAAGAAATCGAAGAGAAATGTGAAGAA 77703
QY      347     CysGlyGlyValProLeuAlaAlaIleThrLeuGlyGlyIleLeuArgPheLeuArg 366
DB      77704  TGTGGGGTGTCCTCTAGAGCCAAACTTTGAGGCTTTTACGCTTCAAGAGGA 77763
QY      367     GluArgGlnTrpGluHisValArgAspSerGluIleTrpIleuProGlnGluGlnSer 386
DB      77764  GAAAGTAAATGGAAACATGTGAGAGATGTGAGATTTGAATTTTACCTCAAGATCAAAAT 77823
QY      387     SerIleLeuProAlaLeuArgLeuSerThrHisLeuProLeuAspLeuArgGlnCys 406
DB      77824  TCTGTTTGGCTGCTGAGGCTGATATCATCATCTTCCACTTGATTTAAGCAAAAT 77883
QY      407     PheThrIleCysAlaValPheProLeuAspThrGluMetGluLeuGlyAsnLeuIleSer 426
DB      77884  TTTCATATTCGCGAGTATTCCTCAAGAGCACCAAAATAGAAAGAAATATCTATGCT 77943
QY      427     LeuTrpMetAlaHisGlyPheIleLeuSerIleuLeuLeuGluLeuGluAsnValIle 446
DB      77944  CTCTGATGGCACACAGTTTCTTTATCAAAAGGAACATGAGAGCTGAGAGATGTGGGC 78003
QY      447     AsnGluValTrpAsnGluLeuIleuLeuArgSerPhePheGlnGluIleGluValIle 466
DB      78004  AATGAAATGAAATGAATTAATCTAGAGCTTTTTCCAAGAGATTAAGTTAAATCT 78063
QY      467     GlyGlnThrIlePheLeuMetHisAspLeuIleHisAspLeuAlaThrSerLeuPhe 486
DB      78064  GGTAAACTTATTTCAAGATGATCATCTCATGATTTGGCTACATCATATGTTTCA 78123
QY      487     AlaSerThrSerSerSerAsnIleArgGluLeu----- 497
DB      78124  GCAAGCGCATCAACAGAAAGTATCCGCAATTAATGTAAAGATGATGATATGATG 78183
```

```

QY 498 ---IleValGluAsnThrIleHisMetSerIleGlyPheThrIleValValSerSer 516
Db 78184 TTCATTGTAACAATTATTAAGATATGATGTCATGTTGTTCTCCGAAGTGTGCTTCT 78243
QY 517 TyrSerLeuSerHisIleGluIlePheValSerLeuArgValIleAsnLeuSerAspIle 536
Db 78244 TACTCTCCTTGGCTTTAAAGGTTTGC-TGCTTAAAGGTCCTTAATCTAAGTAACCTCA
QY 537 LysLeuLeuGlnLeuProSerSerIleGlyAspLeuValHisIleArgThrLeuAsnLeu 556
Db 78303 GAATTGTGAACGTTACCGTCTTCGTTGAAGATCTAGAACATTTAAGATACCTGACCTG 78362
QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
Db 78363 TCTGTGTAAT---AAATTGTAGTCTTCCAAAGAGTTGTGCAGCTTCAAAATCTGCAG 78419
QY 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysLysLeuProLysGlnThrSerIleLeu 596
Db 78420 ACTCTGTGATCTATATTAATTTGCCAGTCACCTTCTGTGTCGCAACAAACAAGTAAGCTT 78479
QY 597 GlySerLeuArgAsnLeuLeuAspGlyCysThrGlyLeuThrCysMetProProArg 616
Db 78480 TGTAGTCTCCGGAATCTTGATCTGATCAGT---CCATTGACTCTTATGCCACCAAGA 78536
QY 617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLys 636
Db 78537 ATAGGATTTGTCACATGCGCTTAAGACACTAGTTACTTGTGTAGGC---GAGAGGAAA 78593
QY 637 SerCysGlnLeuGlyGlyLeuArgAsnLeuAsnLeuThrGlySerIleGlnIleThrHis 656
Db 78594 GGTATATCAACTGGTGAACCTACGAATTTAAACCTCCGTGTCGCAATTTCCATCACACAT 78653
QY 657 LeuGlnArgValLysAsnAspMetAspAlaLysGlnValAsnLeuSerAlaLysGlnAsn 676
Db 78654 CTTAGAGAGTGAAGAAACGAATATGAGCAAAAGCAATTTATTCGCAAAAGCAAT 78713
QY 677 LeuHisSerLeuSerMetLysThrAspAspAspGluArgProArgIleTyrGlnSerGln 696
Db 78714 CTACACTCTTTAAGCATAGTGGGAT-----AGACCAACAGATATGATCCGAA 78764
QY 697 LysValGluValLeuGlnAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
Db 78765 GAACTTAAAGTGTGAAGCCCTCAACCATCCCATCTGAAATATTATTGAATCAAT 78824
QY 717 GlyPheArgGlyIleArgLeuProAspProMetAsnHisSerValLeuLysAsnValVal 736
Db 78825 GACTTCTGTGATTCTGTCTCCGACTGAGATGATCACTCAGTTTGAATAATGTTGTC 78884
QY 737 SerIleGlnIleIleSerCysLysAsnCysSerCysLeuProProPheGlyLysLeuPro 756
Db 78885 TCTATTCTAATTACCGGTGTGAAGAACTGCTGCTGCTTACCACTTTGGTGAAGCTGCT 78944
QY 757 CysLeuLysSerLeuGlnLeuThrArgGlySerAlaGluValGlyIleVal---AspSer 775
Db 78945 TGTCTAGAAGTCTGAGATTCAAGATGGGCTCTGTGAGGGTGGAGTTGTTGAAGATTCT 79004
QY 776 GlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIleArgGlnPheGly 795
Db 79005 GGATTTCCCGAACAAGAAAGATTTCCATCTCCGAGAAAACCTCATATATAGTGGCTTTTGT 79064
QY 796 AsnLeuLysGlyLeuLeuLysGlyGlyGlyGlnGlnCysProValLeuGlnGlyIle 815
Db 79065 AATCTGAAGGATTCAGAGAAATGAGAGAGAAAGCAATCCCGCTGCTTGAAGAGATG 79124
QY 816 GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLeuVal 835
Db 79125 AAGATTTCGAGATTCCTATGTTGTTTTCGCAACCTTCTCTCTGTCACAAATTTAGAA 79184
QY 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
Db 79185 ATTTGGGGGAG---GCAGATGCAAGAGTTTGAGCTCCATATCTAATCTCAGACACTCTT 79241

```

```

QY 856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGlnLysMetPheLys 875
Db 79242 ACATCCCTCAAAAATTTTCAGTAAACACACAGTCACTTCACTAGAAAGATGTTCAAA 79301
QY 876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGlnLeuPro 895
Db 79302 AGCTTCGAAAATCTCAAAATACCTTGAAGTCTCTTACTTGAAGATCTCAAGACCTGCT 79361
QY 896 ThrSerLeuAlaSerLeuAsnAlaLeuLysHisIleGlnIleHisSerCysTyrAlaLeu 915
Db 79362 ACCAGCTGGCTATCTCAATTAATTTGAAGTGTGATATTCCTTATTTGAGCACTA 79421
QY 916 GluSerLeuProGlnGlnGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThr 935
Db 79422 GAGAGTCTCCCGGAGAAAGGCTGGAAGTTTATCTTCACTACACAGATTATTTGGTCAA 79481
QY 936 TyrCysGlnLysLeuGlnCysLeuProGlnGlyLeuGlnHisIleLeuThrAlaLeuThrAsn 955
Db 79482 CACTGTAAACATGCTAAATATGTTTACAGAGGATTCAGACCTTAACACCTCAAGT 79541
QY 956 LeuSerValGluPheCysProThrLeuAlaLysArgCysGlnLysGlyIleGlyLysAsp 975
Db 79542 TTTAAAAATTCGGGATGTCCAAACTGATCAAGCGTGTGAGAAAGGAATRGAGAAAGAC 79601
QY 976 TrpTyrLysIleAlaHisIleProArgValPheIleTyr 988
Db 79602 TGGCAAAAATTTCTCATCTTCACTTCACTGTAATATATAT 79640

RESULT 8
AX814113
LOCUS AX814113 3592 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 36 from Patent EP1334979.
ACCESSION AX814113
VERSION AX814113.1 GI:39103415
KEYWORDS
SOURCE
ORGANISM
Solanium bulbocastanum
Solanium bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanium.
REFERENCE
1 van der Vossen, E.A. and Allefs, J.J.
Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
Patent: EP 1334979-A 36 13-AUG-2003;
Kwee-en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1..3592
location/qualifiers
/organism="Solanium bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
misc_feature
1..3591
/note="Rpl-d1b including intron sequence (position
428-1106)"
ORIGIN
Alignment Scores:
Pred. No.: 9.5e-278 Length: 3592
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: 6 Gaps: 9
US-10-647-268-2 (1-988) x AX814113 (1-3592)
QY 1 MetAlaGlnAlaPheLeuGlnValIleLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 1 ATGGCTGAGCTTCAATTCAGATTCTGCTAGACATCTCACTTCTTCTTCAAAAGGGGAAA 60
QY 21 LeuGlyLeuIleLeuGlyPheLysAspGlnPheGlnLysLeuGlnSerThrPheThrThr 40
Db 61 CTGTATTTGCTTTTGGGTTTCAAGATGATTCGAAAGGCTTTCACAGCATGTTTCTTAA 120

```


QY 41 ILeGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaLeuGlnAsn 60
 DB 121 ATTCAAGCCGCTCTGGAAGATGCTCAGGAGAAAGCACTCAACACAGCCCTGGAATAAT 180
 QY 61 TTPLeuGlnLysLeuAsnAlaAlaAlaTyrGlnAlaAspAspLysLeuAspGlnCysLys 80
 DB 181 TGGTTGCAAAAACCAATGCTGCTACATATGAGTCGATCGATCTGGATGAATATATAA 240
 QY 81 ThrGlnAlaProLeuArgGlnLysLeuAsnLysTyrGlnCysTyrHisProAsnValIle 100
 DB 241 ACCAAGGCC---ACAAGATTCTCCAGCTGATATATGCGCTTATTCATCCAAAGTTATC 297
 QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlnLysLeuAspValIle 120
 DB 298 CCTTCCGTCACAAAGTCGGGAAAAGATGAGACCAAGATGAAAAAACTTAAGGCATT 357
 QY 121 AlaAlaGlnLysArgLysPheHisLeuAspGlnLysArgHisIleGlnLysGlnValAlaThr 140
 DB 358 GCTGAGAAAGAAAGAAATTTTCATTGCGAAGAAAAAATTGTAGAGACAAAGCTGTAGA 417
 QY 141 ArgGlnThrGly----- 144
 DB 418 CGGAAACAGGACTCATCTTAAATTAGATATACAAACAATAAGTTATATTCATTTT 477
 QY 144 ----- 144
 DB 478 TGGCAATTATCAATTGCAAAAAGGTTAAATATACATCATGTCCTATCGTAATAGTGA 537
 QY 144 ----- 144
 DB 538 TATATACCTCGTGTACTTTCGATCGATATACTTGTCAATCTGGCAAGCTCAGAA 597
 QY 144 ----- 144
 DB 598 TCAAAATATCCACCCCACTTTTAATACTCGATATCTTAGAAATCCACTGTCTACT 657
 QY 144 ----- 144
 DB 658 CATCCACTACCCATTCCTCTTGCTTGATTTCTTTCTTACCTATTAACCTGGAACT 717
 QY 144 ----- 144
 DB 718 CGATCCGTTTGTCTTTCTTAACAAGAGCTCAGAGAAAAGGTTTCTTATCTG 777
 QY 144 ----- 144
 DB 778 TTCTCTGTGTGCTGCACTTGGGTCTTAATCCCATTAATAAAGGGCATGTATATCCA 837
 QY 144 ----- 144
 DB 838 ACGACGGTAGCCTTCTCTGACAGCTGACTGAATTTGTCTTAACAAAGAAAAAAGA 897
 QY 144 ----- 144
 DB 898 TTAGACATGTTTTCTTGTGATGATTAGGCTGATTTCTTTCAGAGTGAATAGAGG 957
 QY 144 ----- 144
 DB 958 GATATATTGGACAAAGTAGAATGGATATATTTAAAGTATTCGTATGAGACAGAG 1017
 QY 144 ----- 144
 DB 1018 TATATGTGCGAAATATCTCTATTTTTCTGTGTCTCTTAATGAGTTGAATATAA 1077
 QY 145 -----Phe-ValLeuAsnGlnProGlnValTyrGln 154
 DB 1078 TATTCATGATGACATTTGCTGACCAAGTTCTGTATTAACGAAACGAGTTTATGG 1137
 QY 154 YArgAspLysGlnLysAspGlnIleValLysIleLeuLysLeuAsnValSerAsnAlaGln 174
 DB 1138 AAGAGCAAAAGAAAGATGAGATGAGAAATCTTAATAAACAATGTATGATGCCCA 1197

QY 174 nThrLeuProValLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaGln 194
 DB 1198 ACACCTTTTCAGTCTCTCCCAATACTGTGTATGGGGGATTGGAAGAAACGACTCTTGCCA 1257
 QY 194 nMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrrPheCysVal 214
 DB 1258 AATGCTTCAAGTACAGAGAGTACTAGCATTTCTCATTCCAAAATATGATTTGTGT 1317
 QY 214 LserGlnAspPheAsnGlnLysArgLeuIleLysGlnIleValGlnSerIleGlnLys 234
 DB 1318 CTGGAGATATTTGATGAGAAGGTTAATTAAGCAATTTGTAATCTTAAGAGAG 1377
 QY 234 sSer---LeuGlyGlyMetAspLeuAlaProLeuGlnLysLeuArgAspLeuAsn 253
 DB 1378 GCCACTACTTGTGAGATGAGTACTGTGCTCACTCAAAAAGAGCTTCAGAGATTCGAA 1437
 QY 253 nGlyLysLysTyrLeuLeuValLeuAspAspValTrrAsnGlnAspGlnAspLysTrrAl 273
 DB 1438 TGGAAAAAGATCTGTTGCTTGAATGATGTTGGAATGAAGATCAACAGAAAGTGGC 1497
 QY 273 aLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrTrx 293
 DB 1498 TAATTTAAGCAAGCTCTTGAAGTTGAGCAAGTGTGCTTCTTATCACTACTCG 1557
 QY 293 GLeuGlnLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLysSerAsnLeuSe 313
 DB 1558 TCTTGAAGAGTGTGATCAATTAATGGAACATTCGAAACATGCAATCTGCAATCTGTC 1617
 QY 313 rGlnGlnAspCysTrrPheLeuPheMetGlnArgAlaPheGlyHisGlnGlnLysIleAs 333
 DB 1618 TCAAGAAATGTTGTTGTTGTTTCATGCAACGTCGATTTGGACCAACAAAGAAATAA 1677
 QY 333 nLeuAsnLeuValAlaIleGlyLysGlnIleValLysCysGlyGlyValProLeuAl 353
 DB 1678 TCCAAACCTTTGCGCAATCGAAGAGATTGGAAGAAAGTGTGTGCTTCTGAC 1737
 QY 353 aAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlnGlnArgGlnTrrGlnHisVal 373
 DB 1738 AGCCAAAACCTTGGAGGTATTTTGTGCTTCAAGAGAAAGAAAGACATGGGAACATGT 1797
 QY 373 LArgAspSerGlnLysTrrPheLysLeuProGlnGlnGlnSerSerIleLeuProAlaLeuArg 393
 DB 1798 GAGGACAGTCCGATTTGGAATTTGCTCAAGATGAAAGTTCATTTGCTGCTGCTGAG 1857
 QY 393 GLeuSerTyrHisIleLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPh 413
 DB 1858 GCTTAGTTACCATCACTTCACTTGAATTTGAACAATGCTTGTGCTATGTGGGTGT 1917
 QY 413 eProLysAspThrGlnMetGlnLysGlyAsnLeuLysSerLeuTrrPheAlaHisGlyPh 433
 DB 1918 CCCAAAGATGCCAAATAGGAAAGAAAGCTATATCTCTCTGATGCGCATGCTT 1977
 QY 433 eIleLeuSerLysGlyAsnLeuGlnLeuGlnValGlyAsnGlnValTrrAsnGlnLe 453
 DB 1978 TCTTTATCAAAAGAAACATGAGCTAGAGATGTGGCGATGAGTATGAGAAAGATT 2037
 QY 453 uTyrLeuArgSerPhePheGlnGlnIleGlnValLysSerGlyGlnThrTyrPheLysMe 473
 DB 2038 ATACTTGAAGTCTTTTTCAGAGATGAAAGTTAAAGATGTAAACCTTAATTCAGAT 2097
 QY 473 tHisAspLeuLysHisAspLeuAlaThrSerLeuPheSerAlaSerHisSerSerAs 493
 DB 2098 GCATGATCTCATCATGATTTGGCAACATCTCTGTTTCGCAAAACATCAACAGCA 2157
 QY 493 nIleArgGlnIleIleValGlnAsnTyrIleHisMetMetSerIleGlyPheThrLysVal 513
 DB 2158 TATCCGTAATATAATTAACACAGTTACACACATATATCTTCATTTGCGCGAAGT 2217
 QY 513 LValSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLe 533
 DB 2218 GGTGTTTTTTTAACTCTTCCCTGGAAAAAGTTATCTGTTAAGATGCTTAATCT 2277
 QY 533 uSerAspLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyr 553

```

Db      2278 AGGATTCGACATTATTAAGTTACCATCTTCATGTGAGATCTAGATCAATTTAAGATA 2337
Qy      553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysGlyLeuG 573
Db      2338 CTTGAACCTGTATGAC--AGTGGCATGCTAGTCTTCCAAAGCGTTATGCAAGCTTCA 2394
Qy      573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProGlyGluTh 593
Db      2395 AATCTGCAAACTCTTGATCTACATATGTCACCAAGCTTGTGTGTTGCCCCAAAAGAAC 2454
Qy      593 rSerLeuLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrglyLeuThrCysMe 613
Db      2455 AAGTAACTGTGTAGTCTCCGAAATCTTTACTGATGTAGCCAGTCATGACCTTGAT 2514
Qy      613 tProProArgIleGlySerLeuThrCysLeuLeuThrLeuSerArgPheValIleGly 633
Db      2515 GCCACCAAGATAGATCATTCAGATGCTTAAGACTTAGGTCAATTTGTTGGA-- 2572
Qy      633 eGlnLeuLysSerCysGlnLeuGlyGluLeuArgAsnLeuLeuLeuTyrglySerIleG 653
Db      2573 -AGGAGAAAGGTTATCAACTTGTGTAAGTACGAAACCTTAATCTCTATGCTCAATTA 2631
Qy      653 uIleThrHisLeuGluArgValIleAsnAspMetAspAlaIleGlyIleAsnLeuSer 673
Db      2632 AATCTCGCATCTTGAGAGAGATGATGATAGAGACCAAGCAATTTATCTGC 2691
Qy      673 alyGlnAsnLeuHisSerLeuSerMetLeuThrAspAspArgIleArgProArgIleTy 693
Db      2692 AAAAGGATCTGCAATCTTTAAGCATAGTTGG--AATAATCTTGAGCCACATATATA 2748
Qy      693 rGluSerGluLysValIleGluAlaLeuLysProHisSerAsnLeuThrCysLe 713
Db      2749 TGAATCAGAGAAGATTAAAGTCTTGAAGCCCTCAACACACTCAATCTGACTTCTT 2808
Qy      713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValLeu 733
Db      2809 AAAATCATATGCTTCAGAGATCATCTCCAGAGTGATGATCACTCAGTATGAA 2868
Qy      733 sAsnValIleSerIleGluIleIleSerCysAlaAsnCysSerCysLeuProProPhe 753
Db      2869 AAATATGTCTCTATCTTAATTAAGCACTTCAAGAACTGCTCATCTTCAACCCCTTGG 2928
Qy      753 yGluLeuProCysLeuLysSerLeuGluLeuTrpArgIleSerAlaGluValIleGly 773
Db      2929 TGATCTGCTTGTCTAGAAAGCTTAGATTACATCGGGGGTCTGGCGATGTGGATATCT 2988
Qy      773 lAsp-----SerGlyPheProThrArgArgPheProSerIle 786
Db      2989 TGAAGAGATGATATTGATGTTCAATCTGGAATCCCAAGAAATTAAGTTCATCCTT 3048
Qy      786 uArgIleLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeuLeuLysGluGly 806
Db      3049 GAGGAAATCTTATATATAGGACTTGTGTAAGGATTTGCTGAAAAAGAAAGAGAGA 3108
Qy      806 uGluGlnCysProValLeuGluGluIleGluIleLysCysCysProMetPheValIle 826
Db      3109 AGAGCAATCTCTGTGCTTGAAGAGATGATTAATTCACAGAGTCCCTTTTTCG-- 3160
Qy      826 oThrLeuSerSerValLysLysLeuValIleSerGlyAspLysSerAspAlaIleGly 846
Db      3161 -ACCTTTCT----- 3169
Qy      846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgIleAsnLysGlu 866
Db      3170 -----TCTATCTTAGGCTCTTACTTCCCTCAGAAATTCCTATAAAGGTAGC 3219
Qy      866 pAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysIleValLeuAsn 886
Db      3220 TACTTCATTTCCAGAGAGATGTTCAAAAACCTTGCAATCTCAAAATCTTGACAAATCT 3279
Qy      886 rPheTyrrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLys 906

```

```

Db      3280 TCGGTGCATAATATCTCAAGAGCTGCTTACCAGCTGCTAGTCTGAATGCTTTGAAGA 3339
Qy      906 sLeuGluIleHisSerCysTyrrAlaLeuGluSerLeuProGluGluValLysGlyLe 926
Db      3340 TCTAAAATTCATTTGTGTTCGCACTTAGAGAGTCTCCCTGAGAAAGGCTCGAAGTTT 3399
Qy      926 uIleSerLeuThrGlnLeuSerIleThrTyrrCysGluMetLeuGlnCysLeuProGlu 946
Db      3400 ATCTCACTCAGACAGATTATTGTGGAACACTGAACATGCTTAATGTTAACCGAGGG 3459
Qy      946 yLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAla 966
Db      3460 ATTACACACCTTAACAACCTCAGACAGTCTTAATAATGGGGATGTCACACTGATCA 3519
Qy      966 sArgCysGluLysGlyIleGlyGluAspTrpTyrrLysIleAlaHisIleProArgVal 986
Db      3520 GCGGTGTAGAGAGGAATAGAGAAAGACTGCGCAAAAATTTCTCAATCTCTAATGGA 3579
Qy      986 eIleTyrr 988
Db      3580 TATATAT 3586

RESULT 9
AX816332
LOCUS AX816332 3592 bp DNA linear PAT 09-DEC-2003
DEFINITION Sequence 49 from Patent WO03066675.
ACCESSION AX816332
VERSION AX816332.1 GI:39646823
KEYWORDS
SOURCE
ORGANISM Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyle;
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
1 Allefs,J.J. and van der Vossen,E.A.
AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
TITLE in solanaceae
JOURNAL Patent: WO 03066675-A 49 14-AUG-2003;
Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1..3592 Location/Qualifiers
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
1..3591
/note="#Roi-bib including intron sequence (position 428-1106)#"

ORIGIN
Alignment Scores:
Pred. No.: 9.56-278 Length: 3592
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: Gaps: 9

US-10-647-268-2 (1-988) x AX816332 (1-3592)
Qy      1 MetaIaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGly 20
Db      1 ATGGCTGAGGCTTCATTCAGATCTCTGACACATCTCACTTCTTCTTCCAAAGGGGAA 60
Qy      21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnInsertThrPheThr 40
Db      61 CTTGATATGCTTTTCGGTTTCAAGATGAGTTCCAAAGGCTTTCAAGCATGTTTCTACA 120
Qy      41 lIleGlnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsn 60
Db      121 ATTCAAGCGCTCTTGAAGAGTCTCAGAGAGAGCAATCTCAACAAGAGCCCTTGAAAT 180
Qy      61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrrGluAlaAspAspIleLeuAspGluCys 80

```

Db	181	TTGTTTGGAAAAACCTCAATGCTGCTACTACATATGAAAGTCAGTACACTTGGATGAAATATTA	240	Db	1258	AATGGCTTCAATGACACAGAGGATTACTGAGCATTTCCATTCCAAAATATATGATTTGGT	131
Qy	81	ThrlGlu1aPro1leArg1nLys1yAsn1yTrc1yCy8TrhisProsnVal1le	100	Qy	214	1serGluAspPheAsnGlnLysArgLeu1leLysGlu1leVal1GluSer1leGluGlu	234
Db	241	ACCAAGGCC---ACAAAGTTCTCCCACTGCAATATGGCCGTTATCATCCAAAGGTTATC	297	Db	1318	CTCGAAGATTTTGTAGAGAGAGGTTAATTAAGCCAAATTTGTAGATCTATTAAGGAAG	1377
Qy	101	ThrPheArgHisLys1leGlyLysArgMetLysLys1leMetGlnLysLeuAspVal1le	120	Qy	234	Asr---LeuGlyGlyMetAspLeu1aProLeuGlnLysLysLysLeuAspLeuAsp	253
Db	298	CTTTTCCCTCCAAAGGTCGGGAAAAAGATGACCAAGATGTGAAAAAATCTAAAGGCCAAAT	357	Db	1378	GCCACCTATCTGGAGATGAGATGGCTGCTCACCCTCAAAAAGAGCTTCAGAGCTTCTAA	1437
Qy	121	Ala1laGluArg1leLysPheHisLeuAspGluArgThr1leGlnArgGlnVal1aThr	140	Qy	253	nGlyLysLysLysLeuValLeuAspAspVal1TPraAsnGluAspGlnAspLys1TPA1	273
Db	358	GCTGAGGAAAAAGAAATTTTCATTTCACGAAAAAATTTGTAGAGAGACAAGCTGTTAGA	417	Db	1438	TGGAAAAAGATCTTCCTGCTCTGTAGATGATGTTTGGATGAAATCAACAGAACTGGGC	1497
Qy	141	Arg1nThrGly-----	144	Qy	273	AlysLeuArgGlnValLeuLysVal1Gly1aSerGly1aSerVal1leuThr1ThrAr	293
Db	418	CGGGAACAGGTACTCACTCTTAATTAGTATTAACAACAATAAGTTATATTCATTTTTT	477	Db	1498	TAATTTAAGACAGCTCTTGAAAGGTTGAGCAAGAGTGCTGTCTTCTTAACACATACG	1557
Qy	144	-----	144	Qy	293	gLeuGlnLysVal1GlySer1leMetGly1ThrLeuGlnProLys1ArgLysLeuSerAsnLys	313
Db	478	TGGCAATTATCAAAATTCAGAAAAAGGTTAAATATCTATGTCCTATCGTAAATAGTGA	537	Db	1558	TCCTGAAAAAGTTGGATCAATTAATGGGAAACATTCGAAACCATATGAACTGTCAACTGTCTC	1617
Qy	144	-----	144	Qy	313	rgLysAspCysTrpLeuLeuPheMetGlnArg1aPheGlyHis1eGlnGluGlu1eAs	333
Db	538	TATATACCTCTCGTTGTACTTTGCGATGTGAATATCTGTCAAAATCTGGCAAGCTCAGAA	597	Db	1618	TCAGAGAGATTTGGTGTGTTGTTCAATGCAAGCTGATTTGGACACCAAGAAATATTA	1677
Qy	144	-----	144	Qy	333	nLeuAsnLeuVal1a1leGlyLysGlu1leVal1LysLysCysGlyGlyVal1ProLeu1	353
Db	598	TCAAAATTAACCAACCCCAACTTTAAATATCTCGATTCCTTAGAAATCCACCTGTCTAACT	657	Db	1678	TCCAAACTTTGTGGCAATCGSAAAGSAGATTTGAAAAAAGTGATGGTGCTCTAGC	1737
Qy	144	-----	144	Qy	353	aAlaLysThrLeuGlyGly1leLeuArgPheLysArgGluGluArgGlnTrpGlnHisVal	373
Db	658	CATCCACATCCCAATCCCTTGGCTTTGAATCTTTTCTTACTTAATAACTTGAACACT	717	Db	1738	AGCCAAACCTCTGGAGGTATTTTGTCTTCAAGAGAGAAAGAAAGCAATGGGAAACATG	1797
Qy	144	-----	144	Qy	373	lArgAspSerGlu1leTrpLysLeuProGlnGluGlnSerSer1leuProAlaLeuArg	393
Db	718	CGATCCGTTTTGCTTTTCTTAACAAAGACGCTCAGAAAAAGAGTTTTCTTCTATTCG	777	Db	1798	GAGAGACGTCCGATTTGGAAATTTGCTCTCAAGATGAAATTTATTTGCTGCGCTTAG	1857
Qy	144	-----	144	Qy	393	gLeuSer1yHisHisLeuProLeuAspLeuArgGlnCysPheThr1yCy8AlaVal1aPh	413
Db	778	TTTTCTGTGTGCTGCACTTGGGTCCTTAATCCCATTAATAAACAGGCACTGTTAATCCA	837	Db	1858	GCTTATGTTACATCAACTTCCACTTGATTTGAACAATGCTTTGGGTATTTGGGGTGT	1917
Qy	144	-----	144	Qy	413	eProLysAspThrGlnMetGlnLysGlyLysLeu1leSerLeuTrpMetAlaHisGlyPh	433
Db	838	ACGACGGTAGCCTTCTCGACAGCTGACGTAAATTTGTCTTAACAAAGAAAAAAGA	897	Db	1918	CCCAAGAGATGCCAAATGAAAAAGAAAGCAATCTCTCTGAGAGGCCCATGCTTT	1977
Qy	144	-----	144	Qy	433	e1leLeuSerLysGlyLysLeuGlnLysGlnLysVal1GlyAsnGlnVal1TPraAsnGlu	453
Db	898	TTAGACATGTTTTCTTGTCAATGATTAGCTGAGATTTCTTTCAGAGTGAACATAGGG	957	Db	1978	TCCTTTATCAAAAGAAACATGAGCTTAAGAGATGGGCGATGAAGATGGAAGAAAT	2037
Qy	144	-----	144	Qy	453	uTyLeuArgSerPhePheGlnGlu1leGluVal1LysSerGlyGlnThr1yPheLysMe	473
Db	958	GATATATTGACCAAAAGTGAATGGGTATATATTTAAGATATTTCTGATAGAACAGAG	1017	Db	2038	ATACTGAGGCTCTTTTTCAGAGATTTGAATTTAAAGATGATTAACCTTATTTCAAGAT	2097
Qy	144	-----	144	Qy	473	Ch1AspLeu1leHisAspLeu1aThrSerLeuPheSer1aSer1ySerSerSerAs	493
Db	1018	TATATTGGGAAAAATATCCCTATTTTCTGTTGTCCTCAATGATGATTTGAATGTAATA	1077	Db	2098	GCATGATCTCATCAATGATTTGGCAAACTCTGTTTTCAGCAAAACATCAACAGCAAA	2157
Qy	145	-----Phe-ValLeuAsnGlnProGlnVal1yTrc1	154	Qy	493	n1leArgGln1le1leVal1GluAsnTr1leHisMetMetSer1leGlyPheThrLysVal	513
Db	1078	TATTTCTATGTGACATTTGCTTGACACAGGTTCTGTATTAACCGAACCCCAAGTTTATAG	1137	Db	2158	TATTCGTGAATTAATTAACACAGATTAACACATATGATGTCATATGTTGTGCGCGAAT	2217
Qy	154	YArgAspLysGlnLysArgGln1leVal1Lys1leLeu1leAsnAsnVal1SerAsn1aG1	174	Qy	513	1Val1SerSer1ySerLeuSerHisLeuGlnLysPheVal1SerLeuAspVal1LeuAsnL	533
Db	1138	AAGAGACAAAGAGAAATAGATAGTAAATCTTAATTAACAAATGTTAGTGAATGCCCA	1197	Db	2218	GGTGTTTTATACACCTTCCCCCTTGAAAAAGTTATCTTCGTTAAAGAGTCTTAATCT	2277
Qy	174	nThrLeuProValLeuPro1leLeuGlyMetGlyGlyLeuGlyLysThr1ThrLeu1aG1	194	Qy	553	uSerAsp1leLysLeuLysGlnLeuProSerSer1leGlyAspLeuVal1HisLysArgTy	553
Db	1198	ACACCTTTAGCTCTCCCAATATCTTGGTATGGGGGGATTAGAAAAAACACACTCTTGCCCA	1257	Db	2278	AGGTGATTCGACATTTAAATAAATGTTACATCTTCCATTTGAGATCTAATTAAGATA	2337
Qy	194	mMetVal1PheAsnAspGlnArgVal1leGluHisPheHisProLys1leTrp1leCysVal	214	Db	2338	CTTGAACCTGTATAGG---AGTGAGATGTGTAGTCTTCCAAAGCAGTTATGCAAGCTTCA	2394

```

QY 573 nasnleuglnthrleuasprleuhsieglycysHisSerleucysCysleuprolysgluTh 593
Db 2395 AATCTGCAAACTCTTGATCTAACAATATTGACCAAGCTTGTTGTTGGCAAAAGAAAC 2454
QY 593 rSerlyseuglySerleuArgasnleuLeuaspjlyCysTyrglyLeuThrCyme 613
Db 2455 AAGTAACTTGGTACTCTCCGAAATCTTTTACTGATGGTAGCCAGTCATTGACTGTAT 2514
QY 613 tProProarglilegylSerleuThrCysleuTyThrleuSerArgpHevalValgly11 633
Db 2515 GCCACCAAGATAGGATGATGACATGCGCTTAAGACTTAGGCTCAATTTGTTGGA-- 2572
QY 633 eGlnlyseSerCysglnleuglygluLeuArgasnleuasnleuTyrglySer11eg1 653
Db 2573 -AGGAGAAAGGATTATCAACTTGGTGAACCTAGAAACCTTAATCTCTATGGCTCAATTAA 2631
QY 653 u1leThrHisleugluArgVallyAsnAspMetAspAla1ysglu1aasnleuSer1 673
Db 2632 AATCTCGCATCTTGAGAGAGTGAAGATGATAGGACCAAAAGACCAATTTATCTGCG 2691
QY 673 alygluAsnleuHisSerleuSerMetLysTrpAspAspArg1ua1proArg1leTy 693
Db 2692 AAAAGGATCTGCACTTCTTAAGCATGAGTTGG--AATACTTTGAGACCAATATATA 2748
QY 693 rGluSerGluTyValylGluValleuGlu1a1leuTyProHisSerAsnleuThrCysle 713
Db 2749 TGAATCAGAAAGATTAAAGTCTTGAAAGCCCTCAACACACTCAATCTGACTTCTTT 2808
QY 713 uThr1leArgglyPheArggly1leArgleuProAspTrpMetAsnHisSerValleuTy 733
Db 2809 AAAATCATGAGCTTCAGAGGATCATCTCCAGAGTGATGATGATCACTCAGATTGAA 2868
QY 733 sAsnValylSer1leGlu1le1leSerCysLysAsnGlySerCysleuProPhePheG1 753
Db 2869 AAAATTTGTCCTATCTTAATTTAGCAACTTCAGAAAGCTCAGCTTATCAACCTTTGG 2928
QY 753 yGluLeuProCysleuTySerleuGluLeuThrArggly1ysEra1GluTyVal 773
Db 2929 TGAATCGCTTGTCTAGAAAGCTTAGAGATTACACGCGGGGCTCGGAGATGCGAGTATGT 2988
QY 773 lAsp-----SerGlyPheProThrArgArgArgPheProSerLe 786
Db 2989 TGAAGAGATGATATTGATGTTTCATTTCTGAGATCCCAAGAAATTAAGTTTCATCTT 3048
QY 786 uArgLysleuasn1leArggluPheglYasnleuTyglYleuTyLysgluTygl 806
Db 3049 GAGAAACTTATATATGCGGACTTTGAGTCTGAAAGATTTGCGAAAAAGAAAGAGA 3108
QY 806 uGluGlnCysProValleuGluGlu1leGlu1leTySerCysPProMetPheVal1lePr 826
Db 3109 AGACAAATTCCTCTGCTTGAAGATGATTAATTCACAGAGCCCTTTTCG----- 3160
QY 826 oThrleuSerSerVallyLysleuValylSerGlyAspLysSerAspAla1leGlyPh 846
Db 3161 -ACCTTTCT----- 3169
QY 846 eSerSer1leSerAsnleuMetAla1leuThrSerleuGln1leArgTyAsnTySgluas 866
Db 3170 -----TCATATCTTAGGCGCTCTTACTTCCCTCAGAAATTTGCTATAATTAAGTAGC 3219
QY 866 pAlaSerleuProGluGluMetPheLysSerleuAlaasnleuTyTyrlleuAsn1leSe 886
Db 3220 TACTTCATTCGCCAAGAGATGTTCAAAAACCTTGCAAAATCTCAAAATCTTGACAATCTC 3279
QY 886 rPheTyThrAsnleuTySgluLeuProThrSerleuAlaSerleuAsnAla1leuTySH 906
Db 3280 TCGGTGCAATATATCTCAAAAGAGCTGCTACCAAGCTTGCTAGTCTGAAATGCTTTGAAAG 3339
QY 906 sLeuGlu1leHisSerCysTyrala1leuGluSerleuProGluGluTyVallySglyle 926
Db 3340 TCTAAAAATTCATATTGTGTGCGCATAGAGAGTCTCCCTGAGGAAGGCGTGGAGGTTT 3399

```

```

QY 926 u1leSerleuThrGlnleuSer1leThrTyrcysGluuMetleuGlnCysleuProGluG1 946
Db 3400 ATCTTCACTCAAGAGTATTATTGTGAAACACTGTAAACATGTTAAATGTTTACAGAGGG 3459
QY 946 yLeuGlnHisleuThrAla1leuThrAsnleuSerValyluPheCysProThrleuVally 966
Db 3460 ATTGACGACCTTACAACACCTCACAAGTTTAAATTCGGGGAGTGCACAACTGATCA 3519
QY 966 sArgCysGluTyglYleGlyGluAspTrpTyTyrlleAla1leHis1leProArgVal1Ph 986
Db 3520 GCGGTGTGAGAAAGGAAATAGGAGAAAGACTGCGACAAAATTTCTCAATTCCTAATGTGAA 3579
QY 986 e1leTyR 988
Db 3580 TATATAT 3586

RESULT 10
AX816333
LOCUS AX816333
DEFINITION Sequence 50 from Patent WO03066675.
ACCESSION AX816333
VERSION AX816333.1 GI:39646824
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Allefs,J.J. and van der Vossen,E.A.
AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
TITLE in solanaceae
JOURNAL Patent: WO 03066675-A 50 14-AUG-2003;
Kweek- en Researchbedrijf Agrico B.V. (NL)
FEATURES
location/Qualifiers
source
1. 5191
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: sequence of 5.2
kb Sca I genomic DNA fragment of S. bulbocastanum BAC SP8
4 present in pRC2-d1b"

ORIGIN
Alignment Scores:
Pred. No.: 1.58e-277 Length: 5191
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
Gaps: 9
US-10-647-268-2 (1-988) x AX816333 (1-5191)

QY 1 MetAlaGluAlaPheleuGlnValleuLeuAspAsnleuThrCysPhe1leGlnTyglu 20
Db 1191 ATGGCTGAAGCTTTCATTCAGATTCGCTAGAACATCTCACTTCTTCCCAAGGGGAA 1250
QY 21 leuGlyLeu1leleuGlyPheLysAspGluPheGluTySgluSer1leThrPheThrThr 40
Db 1251 CTGTATTGCTTTTTCGTTTTCAGATGAGTTCCAAAGGCTTTTCAAGCAGTTTTCACA 1310
QY 41 l1eGlnAlaValleuGluAspAlaGlnTySglu1leuTySAspTySAspTySAspTySAsp 60
Db 1311 ATTCAAGCGCTCTTGAAGATGCTCAGAGAACCACTCAACAAAGCCTTAGAAAT 1370
QY 61 TrpLeuGlnTySleuAsnAla1a1a1a1TyrgluAlaAspAsp1leleuAspGluTySlys 80
Db 1371 TGGTGTCAAAACTCAATGCTGCTACATATGAAAGTGAATGATGATGATGATGATGATGATGAT 1430
QY 81 ThrGluAlaPro1leArgGlnTySAsnTySAspTySAspTySAspTySAspTySAspTySAsp 100
Db 1431 ACCAAGGCC--ACMAATTTCCCACTGCAATATAGCGCTTATCATCTCAAGAGTTATC 1487
QY 101 ThrPheArgHisLys1leGlyLysArgMetLysLys1leMetGluTySleuAspVal1le 120

```



```

Qy      613  tProPArgllleglyserleuThrCysleuylserthleuSerArgpheValValGly1 633
Db      3705  GCGCCACGAGATGAGATGATGACATGCTTAAGCTCTAGGTCAATTGTTGTTGGA-- 3762
Qy      633  eGlnlylserserCysglnleuGlygluleuArgsnleuasnleuTyrglyserilegl 653
Db      3763  -AGGAGAGAAAGATTATCAACTTGGTGAACCTGAAACCTTAATCTCTATGGCTCAATTAA 3821
Qy      653  uileThriAleuGluValValAsnAspMetCaspAlaValsgluAlaenleuSerAl 673
Db      3822  AATCTCGCATCTTGAGACATGAGAAATGATAGACCCAAAGAGCAATTAATTCGTC 3881
Qy      673  alyeGluasnleuHisserleuSerMetLysTriAspAspAspGluAcgProArgileTy 693
Db      3882  AAAAGGGAATCTGCACTCTTAAGCATAGTTGG--AATAACTTGGACCAATATATA 3938
Qy      693  rGluSerGluLysValGluValleuGluAlaleuLysProHisserAsnleuThrCysle 713
Db      3939  TGAATCAAGAAAGATTAAAGTCTGAAGCCCTCAACCACTCATCTGACTTCTTT 3998
Qy      713  uThriLeArgGlyPheArgGlyLleArgleuProAspTriMetAsnHisserValleuLy 733
Db      3999  AAAAATCTATGCTTCAGAGAAATCCATCTCCAGAGTGAATCACTCAGATTGAA 4058
Qy      733  sAsnValValserilegluileleserCysLysAsnCysSerCysleuProProPheG1 753
Db      4059  AAAATATGCTCTATTCTTAATTAAGCACTTCAGAAACCTGCTCACTTCAACCCCTTGG 4118
Qy      753  yGluLeuProCysleuLysSerleuGluLeuTriPArglyleSerAlaGluValGluTyVa 773
Db      4119  TGAATGCTCTGTCTAGAAAGCTAGATTACACAGGGGCTCGGAGATGAGATAGT 4178
Qy      773  lAsp-----SerGlyPheProThrArgArgArgPheProSerle 786
Db      4179  TGAAGAACTGAGATTAATGATGTTCAATTCGATTCGCCCAAGAAATTAAGTTCCATCTT 4238
Qy      786  uArgLysleuAsnileArgGluPheGlyAsnleuLysGlyleuLysGlyGluGly1 806
Db      4239  GAGGAAACTGATATATATATGAGACTTTGATGCTGAAGATGCTGAAAAAGAGAGGA 4298
Qy      806  uGluGlnCysProValleuGluGluileGluileLysCysCysProMetPheValilePr 826
Db      4299  AGAGGAATTCCTGTGCTTGAAGAGATATATTAACAGAGTCCCTTTTCG----- 4350
Qy      826  oThrlleuSerValLysLysleuValValserGlyAspLysSerAspAlaileGlyPh 846
Db      4351  -ACCTTTCT----- 4359
Qy      846  eSerSerileSerAsnleuMetAlaleuThrSerleuGlnileArgTyAsnLysGluAs 866
Db      4410  TACTTCATTCACAGAGATGTTCAAAAACCTTCAATATCTCAATATCTTGACAAATCTC 4469
Qy      866  rPheTyPheAsnleuLysGluLeuProThrserleuAlaserleuAsnAlaleuLysHi 906
Db      4470  TCGGTGCAATATCTCAAAAGAGCTGCTTACAGAGCTTGCTGAAATGCTTTGAAAAG 4529
Qy      906  sLeuGluileHisserCysTyPAlaleuGluSerleuProGluGluValValysGlyLe 926
Db      4530  TCTAATTAATCAATTGTGTGGCAGCTAGAGAGTCTCCCTGAGAGAGGCTGGAAGGTTT 4589
Qy      926  uileSerleuThrGluLeuSerileThrTyCysGluMetleuGlnCysleuProGluG1 946
Db      4590  ATCTTCATCTCAGAGATTAATTGTTGAACACTGTAACATGCTAAATGTTTAAACAGAGG 4649
Qy      946  yLeuGlnHisleuThrAlaleuThrAsnleuSerValGluPheCysProThrleuAlaly 966
Db      4650  AATGAGAGCACTTAACAACCTTCAACAAGTTTAAAAATTCGGGGAGTGTCCAAACTGATCA 4709

```

```

Qy      966  sArgCysGluLysGlyileGlyGluAspTriTyLysileAlaHisileProArgValPh 986
Db      4710  GCGGTGTGAGAGAGGAGATGAGAGAAAGCTGGCAAAATTTCTCATTTCTTAATGCAA 4769
Qy      986  eileTyP 988
Db      4770  TATATAT 4776

RESULT 11
AY336128
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.6824
/organism="Solanum bulbocastanum"
/mol_type="genomic DNA"
/db_xref="taxon:147425"
/chromosome="8"
/map="RB"
<1..>3592
/locus_tag="CB3A14.5"
join(<1..427,1107..>3592)
/locus_tag="CB3A14.5"
/product="putative disease resistant protein RGA2"
join(1..427,1107..3592)
/locus_tag="CB3A14.5"
/note="partial sequence is present in GenBank Accession Number AY03170; similar to phaseolus vulgaris NBS LRR resistance-like protein B11 in GenBank Accession Number AAK61316"
/codon_start=1
/product="putative disease resistant protein RGA2"
/protein_id="AAP6601.1"
/db_xref="GI:32693281"
/translation="MAEAFIOVLNDNTSEFLKGLVLLFGPDFORLISNFSYTIQAV
LEDAOEKIOINNKPLEMLOKLNATYEVNDLIDYKATRFQSESGRYHPKIYPR
HAYGRKRDQWYKTKALAEERKNPHELEKIVERAVARREGSVLTERPOVGRDQXDE
IVKLLINNSDAQHLSTVPLTGNGELKTTLAQVNPDRQYTERFHSKINTCYSEEDD
EKRLLIKAVISIEGRPLIGENDLAPLOKQLDELNGRYLLVDVNNEDQKRAIR
AIVKVGASGAVLTTTRLEKVGSIIMGLOPELISNLSQEDWLFMORARFQHOEINP
NLVAIGKEIYKSGGVPLAAKTGGILICFREBEAMRHVDSPIYMLPODESSILPAL
RLSYHOIPLDKOCFAVCAPPKDAKMEKELISLMAHGLFSKGMNEEDVGEVW
KELYIRSFQPIREYKQDKTYPKAMDLDHDLATSLPSANTSSNIRELINKSYTHMGI
GEFAVIRFVYTLPLEKFTSLKVLNLGSTRKLPSSIGDVLHLYLALYSGMGLSK
OLCLOMLQTLDDYCYRKLCCLPETSKLSLRNLLDGSSQLTOMPRIKGLTCLKT
LGQFVVRKAKGYOLGELGNLNYGSIKISHLERVONDKDAKEANLSAKGNLSLSMS
NNFGPHLYESEBEVLEALKPESVLTSLKTYGFGGILPEMWNHSLVKNIVSLISNF
RNSCCLPRGDLPCLESLLEHWSADVBEVDIVDHSFGPTIRFPSLRKLDIMP
GSLKGLIKREGEQFPYLEKMTIHCEFPVLTSSVLRALTSIRICVNVVATSSPPEMK
NLANLVLTIVTSRCKNLKELPTSLASINAAKSLQOLCAGLESLEBEGLBGSLSTELF
VERCNMLKCLPEGLQHLTTLTSLIKIRGCPOLIKRCEKGIQALDEHMKIIPVNIYI"

```

```
misc_feature 1..3136
              /locus_tag="CB3A14.5"
              /note="corresponds to sequence in BAC CB3A14 in GenBank"
              accession_number AY031170"
misc_difference 3137..6824
```

ORIGIN

Alignment Scores:	
Pred. No.:	2.3e-277
Score:	3538.50
Percent Similarity:	68.03%
Best Local Similarity:	61.65%
Query Match:	70.97%
DB:	8
Length:	6822
Matches:	754
Conservative:	78
Mismatches:	129
Indels:	262
Gaps:	9

US-10-647-268-2 (1-988) X AY336128 (1-6824)

Qy	1	MetAlaGlnAlaPheLeuInValIleuLeuAPanLeuThrCyPheIleGlnGly	20
Qy	1	ATGGCTGAAGCTTTTCAATTCAGTCTCGTACATCTCACCTTCTCTCAAGGGGA	60
Qy	21	LeuGlyLeuIleLeuGlyPheIysAspGlnPheGlnIysLeuGlnSerThrPheThrThr	40
Db	61	CTGTGTCTCTTTCCGTTTTCAAGTGAAGTTCCAAAGGCTTTCAGCATGTTTTTACA	120
Qy	41	IleGlnAlaValIleuGlnIubAplAeGlnIysIysGlnIleuIysAspIysAlaIleGlnAsn	60
Db	121	ATTCMAAGCGTCTGTGAAGATGCTCAGGAAAGCACTCAACMAAGCTCTGAAGAAAT	180
Qy	61	TrpLeuGlnIlyLeuAsnAlaAlaIaIyGlnAlaAspAspIleLeuAspGluCyIysIys	80
Db	181	TGGTTCCAAAACACTCAATGCTGCTACATATGAAGTCAGTACATCTTGGAATATATAA	240
Qy	81	ThrGlnAlaProIleArgIlnIlyIysAsnIlyIyGlyCyIyThrIAspAsnValIle	100
Db	241	ACCAAGGCC---ACAAGATTCCTCCAGTCGTGAATATGGCCGTTATCATCCAAAGTTATC	299
Qy	101	ThrPheArgHisIlyIleGlyIysArgMetIyIysIleMetGlnIyIysLeuAspValIle	120
Db	298	CCTTTCCGTACACAGGCTCGGAAAAGGATGAGCAAGATGAAGAAAACTAAAGGCATTT	357
Qy	121	AlaAlaGlnArgIleIysPheHisIleuAspGlnIyArgThrIleGlnArgIlnValAlaThr	140
Db	358	GCTGAGGAAAAGAAAGATTTTCAATTTTGACGAAAAAATTTGTAGAGACAGCTGTAGA	417
Qy	141	ArgGlnThrGly-----	144
Db	418	CGGGAACACGATCTCATCTTAAATTAGATTACAAACAATAAGTTATATTCAATTTTTT	477
Qy	144	-----	144
Db	478	TGGCAATTATGAATTCAGAAAAAGGTTAAATATATCATCATGCTATGTAATAGTGA	537
Qy	144	-----	144
Db	538	AATATATCTCTCGTTGTACTTTCGATCTGAATATATCTTGCAAAATCGGCAAGCTCAGAA	597
Qy	144	-----	144
Db	598	TCAAAATTACACCCCAACTTTTAATATACGATATCTTTAGAAATTCACCTGCTAACT	657
Qy	144	-----	144
Db	658	CATCACTACCATTCCTCTTGCTTTGAATCTTTCTTTACCTATAAAGTGAAACACT	717
Qy	144	-----	144
Db	718	CGATCCGTTTGTCTTTCTTAAACAAGACGCTCAGAGAAAAGGTTTTCTTCTAATTCG	777

OY	144	----	144
Db	778	TTTCTGTGTGCTGCACCTTGGGTTCCTTAATCCCACTTAAAAAGAGGCATGTTAATCCCA	837
OY	144	----	144
Db	838	ACGACGGTAGGCTTTCTGACAGCGTGACTGTAAATTTTGTCTAACAAAGAAAAAAGAA	897
OY	144	----	144
Db	898	TTAGACATGTTTTCTTGTTCATGATTAGGCTGGATTTCCTTCAGGTGACATAGGG	957
OY	144	----	144
Db	958	GATATATTGACCAAAAGTAGAATGGTATATTATTTAAAGTATTTCTGATAGACAGAG	1011
OY	144	----	144
Db	1018	TATATTTGGCAAAATATCTCTATTTTCTGTGTCTCTATAGAGTTGAATGTAA	107
OY	145	-----Phe-ValLeuAsnGluProGlnValTyrGlu	154
Db	1078	TATTCATGTGCACATGCTTGACACAGGTTCTGTATTAACCGAACCAGAGTTTATAG	113
OY	154	YArgAspIyrsGluIyrsAspGluIleValIyrsIleuIleAsnAnValSerAsnIleGlu	174
Db	1138	AAGAGACAAAGAAAGAAAGATGAGTAAAGAAAACTCTAATTAACAATGTTAGTAGGCCCA	119
OY	174	nThleuProValIleuProIleLeuGluMetGluYglYleuGluIyrsThrThleuIleGlu	194
Db	1198	ACACCTTTCAGTCTCTCCCAATACCTTGATGAGGGGGAATTAGAAAAACGACTTGGCCA	125
OY	194	nMetValPheAsnAspGlnArgValIleGluHisPheHisProIyrsIleTyrIleCysVal	214
Db	1258	AATGTCCTTCATGACACGAGAGTTACTGACCATTTCCATTCAAAATATGATTTGTGT	131
OY	214	IleSerGluAspPheAsnGluIyrsArgIleIleIyrsGluIleValGluSerIleGluGluIy	234
Db	1318	CTCGAAGATTTTATGAGAAAGAGTTATATAAGGCAATTGTAGATCTATTTGAAGGAAG	137
OY	234	sSer-----LeuGluYglMetAspIleuValProLeuGlnIyrsIyrsLeuAspIleuLeuAs	253
Db	1378	GCCACTACCTTGATGATGATGACCTTGCTCCACTTCAAAAGAAAGCTTCAGAGAGTCTGAA	143
OY	253	nGluIyrsIyrsIyrsLeuIyrsValIleuAspAspValTyrAsnGluAspIleuAspIyrsIle	273
Db	1438	TGGAAAAAGATACCTGCTGTCTTANAGATGTTTGGATGAAGATCAACAGAAATGGGC	149
OY	273	AluYleuAspGlnValIleuIyrsValIyrsIleValSerGluYalSerValLeuThrThrThr	293
Db	1498	TAAATTTAAGACACGTCCTTGAAGGTTTGGAGCAAGTGTCCTTCTGTTCACACATACG	155
OY	293	gLeuGluIyrsValIyrsIleMetGluYthrLeuGluProIyrsGluLeuSerAspIleuSe	313
Db	1558	TCTTGAAGAAAGTTGATCAATTTATGGGAACATTCACACATATGAACGTCAAACTGTGC	161
OY	313	rGlnGluAspCysTyrPheIyrsPheMetGlnArgAlaPheGluHisGlnGluIyrsIleAs	333
Db	1618	TCAAGAAAGATTGTTGGTGTGTTGTTCAATCCACGTCGCTTGGACACCAAGAAATATA	167
OY	333	nLeuAsnIleuValAlaIleGluIyrsGluIleValIyrsCysGluIyrsIleProLeuAl	353
Db	1678	TCCAAACCTTGTGGCAATCCGAAAGAGAGATTGTAAAAAAAGTGGTGTGTGCTCTAGC	173
OY	353	AlaIleIyrsThrLeuGluYglIyrsIleLeuAspPheIyrsArgGluIyrsGluIyrsIyrsIle	373
Db	1738	AGCCAAACCTTGGAGGTATTTTGTGCTTCAAGAGAAAGAAAGACATGGAGAACATG	179
OY	373	IArgAspSerGluIleTyrIyrsIleuProGlnGluIyrsSerIleuProAlaLeuArg	393
Db	1798	GAGAGACAGTCCGATTTGGATTTGGCTCTCAAGATGAAGAAAGTTCTATTCGTGCTCCCTAG	185
OY	393	gLeuSerTyrHisIleuProIleuAspIleuArgGlnCysPheThrTyrCysAlaValAlaPh	413

Db 1858 GCTTAGTACCATCAACTTCGATTTGAAACAATGCTTTGGCATGTGCGGTCTT 1917
Qy 413 eProlyAspThrGluMetGluValysAsnLeuIleSerLeuThrPheMetAlaHisGlyPhe 433
Db 1918 CCCAAAGAGATGCCAAAAGGAAAAAGAAAGCTATCTCTCTGGAGTGGCGCATGGTTT 1977
Qy 433 eileSerSerGlyAsnLeuGluValysAsnValGlyAsnGluValTTPAsnGluLe 453
Db 1978 TCTTTTATCAAAAAGAAACATGAGCTAGAGATGTGGCCATGAAAGTATGGAAGAATT 2037
Qy 453 uTyrlLeuArgSerPhePheGlnGluIleGluValysSerGlyGlnThrTyrlPheVal 473
Db 2038 ATACTGTAGGCTCTTTTCCAAAGAGATGGAAGTTAAAGTGTAAACCTTATTTCAAGAT 2097
Qy 473 tHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSer 493
Db 2098 GCATGATCTCATTCATGATGATTTGGCAACATCTCTGTTTCACCAACACATCAAGCAGCA 2157
Qy 493 nileArgGluIleIleValGlyAsnTyrlleHisMetSerIleGlyPheThrVal 513
Db 2158 TATCCGGAATTAATAACACAGTTACACATATGATGTCATGTTGTTTCGCCGAAGT 2217
Qy 513 lValSerSerTyrlSerLeuSerHisIleuGlnLysPheValSerLeuArgValIleuAsnLe 533
Db 2218 GGTGTTTTTTTACACTCTTCCCCCTGGAAAAGTTTATCTCGTTAAGATGCTTAATCT 2277
Qy 533 uSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAsnLeuValHisIleuArgTy 553
Db 2278 AGGTGATTCGACATTTATATATGATTAACCATCTTCATTTGAGATCTAGATCACTTTAAAGTA 2337
Qy 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuG1 573
Db 2338 CTGAACTGTATGCG--AGTGCATCGTAGTCTTCCAAAGCATTAATGCAAGCTTCA 2394
Qy 573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysLysLeuProLysGluTh 593
Db 2395 AAATCTGCAAACTCTTGATCTTACAAATATTTGCAACCAAGCTTGTGTTGCCAAAAGAAAC 2454
Qy 593 rSerLysLeuGlnLysSerLeuArgAsnLeuLeuAspGlyCysTyrlGlyLeuThrCysMe 613
Db 2455 AAGTAACCTTGATGTCGCCAAATCTTTTACTGATGTAGCCACGATTCATGACTTGAT 2514
Qy 613 tProProArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheValIleGlyI1 633
Db 2515 GCCACCAAGATAGGATCATTTGACATGCCCTTAAGACTTAAGCTCAATTGTGTGGA-- 2572
Qy 633 eGlnLysLysSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrlGlySerIleG1 653
Db 2573 -AGGAAGAAAGSTTATCAACTTGGTGAACCTAGAAACCTAATCTCTATGGCTCAATTAA 2631
Qy 653 uileThrHisIleuGluValGlyValysAsnAspMetCaspAlaLysGluAlaAsnLeuSerAl 673
Db 2632 AATCTCGCATTTTGAGAGATGGAAGAAATGATTAAGACCCAAAAGAGCAATTTATCTGC 2691
Qy 673 alyGlyAsnLeuHisSerLeuSerMetLysTriAspAspAspGluArgProArgIleTy 693
Db 2692 AAAAGGGAATCTGACTTTTAAAGCATAGTTGG--AATAACTTGGACCAATATATA 2748
Qy 693 rGlySerGluLysValGluValIleuGluAlaLeuLysAspProHisSerAsnLeuThrCysLe 713
Db 2749 TGAATCAAGAAAGATTAAAGTCTGAAGCCCTCAAAACACACTCCATCTGACTTCTTT 2808
Qy 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTriMetAsnHisSerValIleuLys 733
Db 2809 AAAAATCATATGCTTCAGAGAAATCCATCTCCAGAGGATGATGATCACTCAGATTAA 2868
Qy 733 sAsnValIleSerIleGluIleIleSerCysLysAsnCysSerCysLysProProPheG1 753
Db 2869 AAATATTTCTCTATTTCTAATTAGCAACTTCAGAAAGCTGCTATGCTTAACACCTTTGG 2928
Qy 753 yGluLeuProCysLeuLysSerLeuGluLeuTriArgLysSerAlaGluValGluTyrlVa 773

Db 2929 TGATTCGCTTGTCTAGAAAAGTCTAGAGTTACACTGGGCGGTCTGCGGATGTGAGTATGT 2988
Qy 773 lAsp-----SerGlyPheProThrArgArgArgPheProSerIle 786
Db 2989 TGAAGAAAGTGAATTTGATGTTCATTTCTGATTTCCCAAGAAATTAAGTTTCCATCCTT 3048
Qy 786 uArgLysLeuAsnIleArgGlnPheGlyAsnLeuLysGlyLysLeuLysGlyGluG1 806
Db 3049 GAGAAACTTGATATGAGACTTTGGTAGCTGAAGATGCTGAAAAAGGAAGAGAGA 3108
Qy 806 uGluGlnCysProValIleuGluGluIleGluIleLysCysCysProMetPheValIlePr 826
Db 3109 AGACCAATTCCTCTGTGTTGAAGATGATTAATTCACGAGTGCCTTTTCTG----- 3160
Qy 826 oThrLeuSerSerValLysLysLeuValIleSerGlyAspLysSerAspAlaIleGlyPhe 846
Db 3161 -ACCTTTCT----- 3169
Qy 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTyrlAsnLysGluAs 866
Db 3170 -----TCTAATCTTAGGCGCTTAACTTCCCTCAGAAATTTGCTATATAATAAGTAGC 3219
Qy 866 pAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrlLeuAsnIleSe 886
Db 3220 TACTTCAATTCACAGAAAGATGTTCAAAAACCTTGCAAAATCTCAAAATCTTGACAAATCTC 3279
Qy 886 rPheTyrlPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHis 906
Db 3280 TCGGTGCAATTAATTTCAAAAGCTGCTTACCAAGCTTGGCTAGTGTGAATGCTTTGAAAAG 3339
Qy 906 sLeuGluIleHisSerCysTyrlAlaLeuGluSerLeuProGluGluValLysGlyLe 926
Db 3340 TCTAAAAATTCAAATGATGTTGCGCAGCTAGAGAGTCCCTGAGGAGAGGCTGGAAGGTTT 3399
Qy 926 uileSerLeuThrGlnLeuSerIleThrTyrlCysGluMetLeuGlnCysLeuProGluG1 946
Db 3400 ATCTTCACTCACAGATTAATTTGTGAACACTGTAACATGCTAAATGTTAACAGAGGG 3459
Qy 946 yLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLys 966
Db 3460 ATTGACAGACCTTAACAACCTCACAAGTTTAAATTCGGGAGAGTCCACAGATCA 3519
Qy 966 sArgCysGluLysGlyIleGlyGluAspTyrlLysIleAlaHisIleProArgValPhe 986
Db 3520 GCGGTGTGAGAAAGGAATGAGAGAAAGACTGGCAAAAATTTCTCAATTCATATGTGA 3579
Qy 986 eileTyrl 988
Db 3580 TATATAT 3586

RESULT 12
AX814114 7349 bp DNA linear PAT 05-DEC-2003
LOCUS AX814114
DEFINITION Sequence 37 from Patent EP1334979.
ACCESSION AX814114
VERSION AX814114.1 GI:39103416
KEYWORDS
SOURCE
ORGANISM
Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 van der Vossen, E.A. and Allefs, J.J.
Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
Patent: EP 1334979-A 37 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
FEATURES
source
1..7349
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"

ORIGIN

/note="BAC SPB4-Genomic Fragment"

Alignment Scores:

Pred. No.:	2,55e-277	Length:	7349
Score:	3638.50	Matches:	754
Percent Similarity:	68.03%	Conservative:	78
Best Local Similarity:	70.97%	Mismatches:	129
Query Match:	6	Indels:	262
DB:	6	Gaps:	9

US-10-647-268-2 (1-988) x AX814114 (1-7349)

```
QY      1  MetAlaGluAlaPheLeuGluValLeuLeuAspLeuThrCysPheIleGlnIleGlu 20
DB      2648 ATGGGTGAAGCTTTCATTCAGACTTCTGCTAGACATCTCATTCTTCTCAAGGGA 2707
QY      21  LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThrThr 40
DB      2708 CTTGATTTGCTTTTGGTTTCAAGATGAGTTCCAAAGCTTTCAAAGCATGTTTCTACA 2767
QY      41  IleGlnIleValIleuGluAspAlaGlnIleuLeuLeuAspIleAspIleAlaIleGlu 60
DB      2768 ATTCAGCCGCTCTTGAAGATGCTCAGAGAACTCAACAAAGCTCTAGAAAAT 2827
QY      61  TrpLeuGlnIleLeuAsnAlaAlaIleTyrGluIleAspAspIleLeuAspGluCysIle 80
DB      2828 TGGTTGCAAAAATCTCATGCTGCTACATATGAGTCGATGACATCTTGATGAAATATAA 2887
QY      81  ThrGluAlaProIleArgIleuLeuLeuAsnIleuLeuLeuLeuLeuLeuLeuLeu 100
DB      2888 ACCAAGGCC--ACAAAGATTCCTCCAGCTGATGATGCGCTTATCATCCAAAGTTATC 2944
QY     101  ThrPheArgIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB      2945 CTTTCCCTCCCAAGTCGGAAGGATGAGACCAAGATGAACTAAAGGCAATT 3004
QY     121  AlaAlaGluArgIleLeuPheIleLeuAspGluArgThrIleGluArgIleValAlaThr 140
DB      3005 GCTGAGGAAAGAAAGAAATTTTCATTTCGACGAAAAAATTGTAGAGACAACTGTTGA 3064
QY     141  ArgGlnThrGly----- 144
DB      3065 CGGGAACAGAGTACTCATTAATTAATAGTATACAACTAAGTTATATCATTTT 3124
QY     144  ----- 144
DB      3125 TGGCAATTATCAAAATTCAGAAAAGGTTAAATATACATGTCCTATGTAATAGTGA 3184
QY     144  ----- 144
DB      3185 TATATACCTCTGCTTGTTACTTCGATCTGAATATATCTTGTAATCTGGCAAGCTCAGA 3244
QY     144  ----- 144
DB      3245 TCAATATTACACCCCACTTTTAAATACATGATATCTTTAGAAATCAACCTGTCTACT 3304
QY     144  ----- 144
DB      3305 CATCCACTACCCACTTCCCTTGTGCTTGAATCTTTTCTTTACTATTAACCTTGAACACT 3364
QY     144  ----- 144
DB      3365 CGATCCGTTTGTCTTTCTTTAACAAGACGCTCAGAGAAAAGAGTTTCTTCTATTCTG 3424
QY     144  ----- 144
DB      3425 TTTCTGTGTGTGCTGCACTTGGGCTCTTAATCCATTAAAAACAGGAGATTTATCCCA 3484
QY     144  ----- 144
DB      3485 ACGAGGTAGCCTTCTCTGACAGCTGACTGTAAATTTTGTCTAAACAAAGAAAAAAGA 3544
```

```
QY     144  ----- 144
DB      3545 TTAGACATGTTTTCTTGTCAATGATTAGGCTGGAATTTCTTCAGAGTGAACATAGG 3604
QY     144  ----- 144
DB      3605 GATATATTGACCAAAAGTAGAATGGTATATATTAAAGTATTCTGTAGTAACAGAG 3664
QY     144  ----- 144
DB      3665 TATATTGGCAAAATATCTCTATTCTTGTCTCTCTTAATGAGTTGAATGATATA 3724
QY     145  -----Phe-ValLeuAsnGluProGlnValTyrGlu 154
DB      3725 TATTCTCATGTGACATTGCTTGACACAGGTTCTGTATTAACGAGCCGAGTTTATGG 3784
QY     154  YArgAspIleGluLeuAspGluIleValIleValIleLeuIleAsnIleValIleSerAsnIleGlu 174
DB      3785 AAGAGACAAAGAAAGATGATGTGAATAATCTTAATAACAATGTATGATGCCCA 3844
QY     174  nThrLeuProValLeuProIleLeuGlyMetGlyIleuGlyIleuLeuLeuLeuLeuLeu 194
DB      3845 ACACCTTTCAGTCTCCCAATATCTTGATGAGGAGATGAGAAACGACTCTTGCCCA 3904
QY     194  nMetValPheAsnAspGlnArgValIleGluIlePheIleProIleLeuIleCysVal 214
DB      3905 AATGCTCTCAATGACACAGAGAGTTACAGACATTTCCATTCCAAATATGATTTGTGT 3964
QY     214  IserGluAspPheAsnGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 234
DB      3965 CTCGGAAGATTTTATAGAGAGAGCTTAATTAAGCAATGTATGAACTTATGAAGAG 4024
QY     234  sSer-----LeuGlyIleMetAspLeuAlaProLeuGlnIleuLeuLeuLeuLeuLeu 253
DB      4025 GCCACTCTTGTGTAGATGAGCTTGCTCCACTTCAAAAGAGCTTCGAGGTGCTGAA 4084
QY     253  nGlyLeuLeuLeuLeuLeuValIleuAspAspValTrpAsnGluAspGlnAspIleTrpAl 273
DB      4085 TGGAAAAGATTTGCTGCTGTGTAGATGATTTGGAATGAAATGACAAAGAGTGGC 4144
QY     273  AluLeuArgGlnValLeuLeuValIleGlyAlaIserGlyAlaIserValLeuThrThrThr 293
DB      4145 TAAATTAAAGACACTCTTGAAGGTTGAGAGCAAGGTGCTCTCTTCAACACTACTCG 4204
QY     293  GluGlnIleValGlySerIleMetGlyThrLeuGlnProThrGluLeuSerAsnLeuLeu 313
DB      4205 TCTTGAAGAAGGTGATCAATATATGGAACATTCACACATATATACGTCAAAATCTGTC 4264
QY     313  rGlnIleAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyIleGlnIleuLeuLeu 333
DB      4265 TCAAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4324
QY     333  nLeuAsnLeuValAlaIleGlyIleValIleValIleValIleCysGlyIleValProLeuAl 353
DB      4325 TCCAAACCTTGTGCAATCGGAAGAGATTTGTAAGAAAAAGTGTGTGTGCTCTAGC 4384
QY     353  AlaIleThrLeuGlyIleLeuArgPheLeuArgGluGluArgGlnTrpGluIleValIle 373
DB      4385 AGCCAAACCTTGTGAAGTATTTGTCTTCAAGAGAAAGAAAGAGCAGTGGGAACATGT 4444
QY     373  IArgAspSerGluIleTrpIleuProGlnIleuGlnIleuSerSerIleuProAlaLeuArg 393
DB      4445 GAGAGACAGTCCGATTTGGAATTTGCTCAAGATGAAAGTTCTATTTCTGCTGCTGAG 4504
QY     4505 GCTTAGTACCATCAACTCCACTTGATTTGAACAATGCTTTCGTAATGTGTGCGGCTGT 4564
QY     413  eProIleAspThrGluMetGluLeuGlyAsnLeuIleSerLeuThrPheValAlaIleGly 433
DB      4565 CCAAAAGATGCCAAATATGAAAGAAAGAAAGCTATATCTCTCTGAGTGGGCGCATGGTTT 4624
QY     433  eIleLeuSerIleGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeu 453
```

```

Db 4625 TCTTTATCAAAAGAAACATGAGCTAGAGATGTGGCCATGAAATGGAAGAATT 4684
Qy 463 UTYLEUARGSERPHEPHEGNGUILLGLUVALYSESGLYGINTTYRPHENLYME 473
Db 4685 ATACTTGAAGTCTTTTTCACAGAGATGAAAGTAAAGTAAACCTTTATTCACAT 4744
Qy 473 CHISAPLEULEHISAPLEUALATHRSERUPHESERIALASERTHSERSECSAS 493
Db 4745 GCATATCTCATCCATGATTTGGCAACATCTCTGTTTCAGCAACACATCCAGACGAA 4804
Qy 493 NILEARGLUILLLEVALGLUASNTRYILLEHISMETSERILLEGLYPHEHLYVA 513
Db 4805 TATCCGTAATAATTAATAACACAGATTACACATGATGATCCATGTTGCGCGAAGT 4864
Qy 513 IVALSERSETRYSERLEUSERHISLEUGLINSRHEVALSERLEUARGVALLEUASLE 533
Db 4865 GGTGTTTTTTTACACTCTTCCCTCGTGAAGATTTTATCTGTTAAGAGTGGCTTAATCT 4924
Qy 533 USERASPILEULYSLEULSGINLEUPROSERSEITILEGLYAPLEUVALHISLEUARGTY 553
Db 4925 AGGTGATTCGACATTTAATTAATGATTCATCTTCATGAGATCTAGACATTTAAGATA 4984
Qy 553 RLEUASNLEUSERGTYASNTRYSERILEARGSERLEUPROASNGINLEUCYLYSEUGI 573
Db 4985 CTTGAACTGTATGCG--AGTGCATGCGTATGCTTCCAAAGCAGTTATGCAAGCTTCA 5041
Qy 573 NASNLEUGLINTHRIEUSPHEULHISGLYCYNHISERLEUCYSEULYEPOLYSGUITH 593
Db 5042 AATCTGCAACCTCTTGATCTACATATATGACCAAGCTTTGTTGTTGCGCAAAAGAAC 5101
Qy 593 RSELYSLEUGLISERLEUARGASNLEULEUENUSPGLYCYSTYRGLYLEUTHRCYME 613
Db 5102 AAGTAACTTGAGTGTCCGAAATCTTTTACTGATGAGTACCAAGCATTTGATGAT 5161
Qy 613 CPROPROARGILLEGLYSERLEUTHRCYSEULYTHRIEUSERARGPHEVALVALGLYTI 633
Db 5162 GCCACCAAGAGATGATGATGACATGCGCTTAAGCTTACGCTCAATTTGTTGTA-- 5219
Qy 633 EGLINLYSSERCYSGINLEUGLIGLUUARGASNLEUENUSPGLYRGYISERILEGI 653
Db 5220 -AGAAAGAAAGCTTATCAACTTGGTGAACCTTAATCTCTAGCTCAATTA 5278
Qy 653 UILETHRIHISLEUGLARGVALYVASNAPSPMETASPAIALYSGIUALAENLEUSERAI 673
Db 5279 AATCTCGCATCTTGAGAGATGAAAGATGATAGGACCAAGACCAATTTATCTGCG 5338
Qy 673 ALYGLIUSNLEUHISERLEUSERMETLYSETTPASPHASPAISGLIARGPROARGILETY 693
Db 5339 AAAAGGGAATCTGATCTTTTAACATGATG--AATACTTTGACCAACATATA 5395
Qy 693 RGLISERGLIUSVALIGLUVALLEUGLUALALEUYSERHISERASNLEUTHRCYSE 713
Db 5396 TGAATCGAAGAAAGTTAAAGTCTTGAAGCCCTCAACACATCCATCTGATCTTCTT 5455
Qy 713 UTHRIEARGGLYPHEARGLYILEARGLEUPROASPTTPMEASNHISERVALLEU 733
Db 5456 AAAATATCATGCTTCAGAGAAATCCATCTCCAGAGATGATGATCACTCAGATTGAA 5515
Qy 733 SASNVALVALSERILLEGLIILLERISERCYLYASNSCYSERCYSEULPROPROPHEGI 753
Db 5516 AAAATATTGCTCTATTTCTAATTACCACTTCAAGAAATGCTCAAGCTTCAACACCTTTG 5575
Qy 753 YGLIUSLEUPROCYSEULYSERLEUGLILEUTHRCYSEVALAGLUVALIGIUTRYVA 773
Db 5576 TGATCTGCTTGTCTTAAGAAATCTAGATTAACATCGGGGCTCTCGGATGCGAGTATGT 5635
Qy 773 IASP-----SERGLYPHEPROTHARGIARGPHEPROSERLE 786
Db 5636 TGAAGAAGTGAGATTTGATGTTCACTTCTGATTCGCCCAAGATTAAGTTTCATCTT 5695
Qy 786 UARGLYLEUASNILEARGGLIUSPHEGLYASNLEULYGLYLEUENUSLYSGIUGIYGI 806

```

```

Db 5696 GAGAAACTGATATATGAGACTTTGGTAGCTGAAAGATTTGCTGAAGAAAGAGAGA 5755
Qy 806 UGLUGINCYSERPROVALLEUGLUGUILLGLIILEYCYSEYSEPROMETPHEVALILEPR 826
Db 5756 AGACCAATTCCTGTGTCTTGAAGATGATTAATTCACGAGTCCCTTTTCTG----- 5807
Qy 826 OTHRIEUSERSERVALYLSYSEUVALISERGLYASPLYSERASPAIALILEGIYPH 846
Db 5808 -ACCTTTCT----- 5816
Qy 846 ESERSEITLESERASNLEUETALALEUTHRSERLEUGLILHARGTYRASNLYSGIUS 866
Db 5817 -----TCTATCTTGGGCTCTTACTCTCCCTCAGATTTGCTATATATAAGTAGC 5866
Qy 866 PALASERLEUPROGLIUMETPHELYSERLEUALASNLEULYSTRYLEUASNILESE 886
Db 5867 TACTTCAATCCAGAAAGATGTTCAAAACCTTGCAAACTCAAAATCTTGACAACTTC 5926
Qy 886 RPHETYPHEASNLEULYSGIUSLEUPROTHRSERLEUALASERLEUASNILALEUYSN 906
Db 5927 TCGGTGAATTAATCTCAAGAGCTGCCCTACAGCTTGCTAGTCTGAATGCTTTGAAGA 5986
Qy 906 SLEUGLILHISERCYSTYRALALEUGIUSERLEUPROGLIUGIYVALYSGIYLE 926
Db 5987 TCTAAATTCATTTGTTGCGCCTAGAGAGCTCTCCAGAGAGAGGCGCTGAAGGCTTT 6046
Qy 926 UILESERLEUTHRIEUSERILEUTHRCYRGYSGIUMETLEUGINCYSLEUPROGLI 946
Db 6047 ATCTTCACTACAGAGTATTTGTTGAACCTGATACATCTTAATGTTTCCAGAGGG 6106
Qy 946 YLEUGLILHISLEUTHRALALEUTHASNLEUSERVALIGLUPHESYSEPROTHRIEUAL 966
Db 6107 ATTGCACACCTTAACAACCTCACAAGTTTAAATTCGGGAGTGTCCACACATGATCA 6166
Qy 966 SARGYSGIULYSGIYLEGLYGLIUSPTRYRGLYSLIHALHISLEPROARGIAPH 986
Db 6167 GCGGTGTGAAGAGATGAGAGAGAGAGCTGGCAAAATTTCTCACATTCCTAATGTGA 6226
Qy 986 EILETYR 988
Db 6227 TATTAAT 6233

RESULT 13
AY426259 7349 bp DNA linear PLN 16-DEC-2003
LOCUS Solanum bulbocastanum blight resistance protein RPI gene, complete
DEFINITION
cde
ACCESSION AY426259
VERSION AY426259.1 GI:39636704
KEYWORDS
SOURCE
ORGANISM
Solanum bulbocastanum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 7349)
Van Der Vossen,E., Silkema,A., Hekker Bt,B.L., Gros,J.,
Stevens,P., Muskens,M., Mouters,D., Pereira,A., Stiekema,W. and
Allefs,S.
An ancient R gene from the wild potato species Solanum
bulbocastanum confers broad-spectrum resistance to Phytophthora
infestans in cultivated potato and tomato
Plant J. 36 (6), 867-882 (2003)
14675451
2 (bases 1 to 7349)
van der Vossen,E. and Allefs,S.
Direct Submission
Submitted (30-SEP-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
Location/Qualifiers
1..7349
/organism="Solanum bulbocastanum"
/mol_type="genomic DNA"
FEATURES
Source

```

MRNA
CDS

```
/db_xref="caxon:147425"  
/chromosome="VIII"  
/map="CT88-CT64"  
join(2648..3074,3754..>6239)  
/product="Dlight resistance protein RPI"  
join(2648..3074,3754..6239)  
/note="confers broad-spectrum resistance to Phytophthora  
infestans in potato and tomato"  
/codon_start=1  
/product="Dlight resistance protein RPI"  
/protein_id="AA029069.1"  
/db_xref="gi:39636705"  
/translation="MAEAFIVLIDNLTSPLKGEVLVLFGRFODEFORLSNFTIOAV  
LEDQERQNNKPLEMLQKLAATAYEDDILDEYKTSRQSEYGRYAPKYPFR  
HKQGRMDQWKKLKATAEERKNPLHEKTYERQARVRETQSILTEPQVDRKDE  
IVKILINNSDQHLSPILMGGLGCTTTAQQVNDQRTYEHKSLINCYSEDFD  
EKRLIKAVESIEGRPLGEMDLAPLQKDELLNGKRYLVLDVNMEDQKMNLR  
AVLKVAGASVLTTRPLEKVSIMGTIQPELSLSCEDMLFMORAFQHEINP  
NLVAIGKIVKSGVPLAKTIGILCFKEERAMEHVRDSPIVMDQSSILPAL  
RLSYHQLPLDKQCPAYCAVPKQAKMEKLSLMMAHGFLSKGNMLEDVGEVM  
KEIYRSPROELIYVDGKTYPRMDLIDDLATSLFSANTSSNIREINKSHYTHMSI  
GPAEVFPPTTLPLEKPSLRYLVNIGDSTFNKLPSISIDVHLRLINXGSMSLPK  
QLCKLQNLQTLIDQCTKLCCLPKETSKLSRLNLDGSSQLTCMPRISLCTLKT  
LGEFVYGRKKYQVLEGLNINLYGSIKLSHERVNDKARKANISAKNLSLSMS  
NNGFPIYSESEVKYLEALKPHSNLTSKIFGRGILHPENMNSVLKNIVSILSNF  
RNGSCLPPRGDLPLESLHMGSADEVVEVDIDVSGPTTRRPSLRKLDIMDF  
GSLGILKKEGEBOFVLEMIHCECPRTLSNLRATLSRLCYNKVATSPPEMFK  
NLANDKLTTRCNMKELPYLSLAKSLKIDLCALSLPREGSLGSLTELF  
VEHCNMKCLPEGLQHLTTTSLKIRGCPQLIKRCEKIGIDMWHKISHIPVNIYI"
```

ORIGIN

Alignment Scores:

```
Pred. No.: 2,556-277 Length: 7349  
Score: 3638.50 Matches: 754  
Percent Similarity: 68.03% Conservative: 78  
Best Local Similarity: 61.65% Mismatches: 129  
Query Match: 70.97% Indels: 262  
DB: 8 Gaps: 9
```

US-10-647-268-2 (1-988) x AY426259 (1-7349)

```
1 MetAlaGluAlaPheLeuGlnValLeuLeuApeAenLeuThrCyApeHleGlnGlyGlu 20  
2648 ATGGCTGAAGCTTTCATTCAAGTTCGCTGAGCAATCTCATTCTCTCTCAAGGGGAA 2707  
21 LeuGlyLeuLeuLeuGlyPheLeuApeGluPheGluLeuGlnSerThrPheThrThr 40  
2708 CTTGATTGCTTTGCGTTTTCAGATGAGTCCAAAGGCTTTCAAGCATGTTTCTACA 2767  
41 ILeGlnAlaValLeuGlnApeAlaGlnLeuLeuApeAlaValLeuApeAlaValLeu 60  
2768 ATTCAGCGCGTCTTGAAGATGCTCAGAGAGCAACTCACACAAAGGCTTTAAGAAAT 2827  
61 TrpLeuGlnLeuLeuApeAlaAlaAlaValLeuApeAlaValLeuApeAlaValLeu 80  
2828 TGGCTTCAAAAATCTAATGCTCTCATATGAAAGTCATGATCTTGGATTAATAATAA 2887  
81 ThrGluAlaProIleArgGlnLeuLeuApeAlaValLeuApeAlaValLeuApeAla 100  
2888 ACCAAGGCC---ACAAGATTCTCCAGATCTGAATATGCGCGTTATCATCAAGGTTATC 2944  
101 ThrPheAlaGlnLeuLeuLeuGlyLeuApeAlaValLeuApeAlaValLeuApeAla 120  
2945 CTTTTCCTTCACAAAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3004  
121 AlaAlaGluArgIleLeuApeHleLeuApeGluArgThrIleGluArgGlnValAlaThr 140  
3005 GCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3064  
141 ArgGlnThrGly----- 144  
3065 CGGAGAAACAGGTAACATCTTAATTAAGTATACAAACAATAAGTTATATTCATTTT 3124
```

```
144 ----- 144  
Db 3125 TGGCAATTATCAAAATTGAGAAAAGGTTAAATATATCATGATGCTATGTAATAGTGA 3184  
144 ----- 144  
Db 3185 TATATACCTCTCGTTGTACTTTGCATCTGAATATATACTTGTCAAAATCTGGCAAGCTCAGAA 3244  
144 ----- 144  
Db 3245 TCAAAATATCAACCCCAACTTTTAATATCTGATATCTTTGAAATTCACCTGCTTAATC 3304  
144 ----- 144  
Db 3305 CATCACTACCAACCATTCCTTTGCTTTGAATCTTTTCTTAACATAAATTGGAACACT 3364  
144 ----- 144  
Db 3365 CGATCCGTTTGTCTTTCTTAACAAAGAGCTCAGAGAAAAGAGTTTCTTATTTCTG 3424  
144 ----- 144  
Db 3425 TTTCTCTGTGCTGCACTTGGGCTCTTAATCCATTAAACAGGCAATGTTAATCCCA 3484  
144 ----- 144  
Db 3485 ACGACGTAAGCTTTCCTGACAGCTGATTAATTTTGTCTAACAAAGAAAAAAGA 3544  
144 ----- 144  
Db 3545 TTAGACATGTTTTCCTTGCATGATTAGCTGATTTCTTCAGAGTGAGACATAGGG 3604  
144 ----- 144  
Db 3605 GATATATTGACCAAAAGTAGATGGTATATATTAAAGTATTTCTGATGAAACAGAG 3664  
144 ----- 144  
Db 3665 TATATGTGCGAAATAATCTCTATTTCTGTGCTCTTAATGATGTTGAATGATATA 3724  
145 ----- 145  
Db 3725 TATTTCTCATGTGACATTTGCTTGACACAGGTTCTGTATTAACGAAACGCGAGTTATGG 3784  
154 YArgApeLeuGlnLeuApeGluValLeuAlaValLeuLeuApeAlaValLeuApeAla 174  
3785 AAGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3844  
174 nThrLeuProValLeuProIleLeuGlyMetGlyLeuGlnLeuGlySerThrLeuAla 194  
3845 ACACCTTTCATCTCTCCCAATATCTTGTATGGGGAGTTAGAGAAAAGAGAGAGAGAG 3904  
194 nMetValPheApeApeGlnArgValIleGlnHleApeHleProLeuValLeuPheVal 214  
3905 AATGCTCTTCAATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3964  
214 lSerGlnApePheApeGlnLeuApeGlnLeuApeGlnLeuApeGlnLeuApeGlnLeu 234  
3965 CTGGAGAGATTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4024  
224 sSer---LeuGlyGlyMetApeLeuAlaProLeuGlnLeuApeAlaValLeuApeAla 253  
4025 GCCACTACTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4084  
253 nGlyLeuApeGlnLeuApeAlaValLeuApeApeValIlePheApeGlnApeAlaValLeu 273  
4085 TGGAGAAAAGATATCTTGTCTTATGATGATGTTTGAATGATGATGATGATGATGATG 4144  
273 alyLeuApeGlnValLeuApeValGlyAlaSerGlyAlaSerValLeuThrThrThrThr 293  
4145 TAAATTAAGACAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4204  
293 gLeuGlnLeuValGlySerIleMetGlyThrLeuGlnProTyrGlnLeuSerApeAlaLeu 313
```

Db	4205	TTTGAAGAGTTGGATCATATTATGGGAACATTGGACACATATGAACTGCAAACTGTGC	426
QY	313	rglnlgnlsrpsyrpldeuPhemecfinaarglaPheglyniSGInglunilEas	333
Db	4265	TCAAGAAAGTTCTTGTTGTTCTTTTCATGCAGCTGATTTGGACACCAAGAAATATA	432
QY	333	nleuansleuValaialleglyysglunilevallyseuCySGIygllyvalProleuA	353
Db	4325	TCCAACCTTGTCGCAATTCGGAAGAGAGATGTGTGAAGAAAAAGTGGTGCTCTCTAGC	438
QY	353	aAlaIysrThrlenugllygllylleuadxpPheylarggluniluaraglntprglunihEva	373
Db	4395	AGCCAAACTCTGGAGGATATTTGTCTCAAGAGAGAGAAAGAAAGCATGGAAACATGT	444
QY	373	lArgaspserrguilietrplyleuProglnglunluseSerlileuProAlaleuAr	393
Db	4445	CAGACACAGTCCGATTTGGAAATTTGCTCTCAGATGAATGAATTTATCTTGCTGCGCTGAG	450
QY	393	gleuSerTyrlshisileuProleuAspleuarglncysPheThrTyCyvalaIvalph	413
Db	4505	GCTTATGATACCATCAACTTCCACTTGATTTGAACAATGCTTGGCGATGTCGCGGTGT	456
QY	413	eProlyAsrThrTglumeglnlygllyAsnleuileSerleuTprmeAlahIglyph	433
Db	4565	CCCAAGAGTGCCAAAATGGAAAAAGAAAGCTAATCTCTCTGATAGCGCAGCGTTT	462
QY	433	eileuSerTyrglyAsnleuGllyeuGllyAsnleuAlglyAsnGllyuAlTprAsnGlye	453
Db	4625	TCTTTATTCMAAGAAACATGAGACTAGAGATGTGGCGCATGAAGATAGTGAAGAATT	468
QY	453	uTyrlleuargSerPhepegInglunilleglyuAllySerGlyInthrTyPheIyme	473
Db	4685	ATACTTGAGTCTTTTTCGAAGATTTGAAGTTAAAGTGTAAACTTATTTCAAGAT	474
QY	473	ThIsAsrpleuilehisAsrpleuAlathSerleuPheSerAlaserrThrSerSerS	493
Db	4745	GCATATCTCAACCAATGATGGCAACATCTGTGTTTCAGAAACACATCAAGACAGAA	480
QY	493	nileArgguileleValaIGluAsnTyrllehismetSerlilegIlyPheThTyva	513
Db	4805	TATCCGTAAATATAATAACACAGATTACACACATATGATGTCCATTTGGTTGCCAAAGT	486
QY	513	IvalserSerTySerleuSerhisIleuGlnlyAspheValSerleuArgValleuAsnle	533
Db	4865	GGTGTATTTTTCACACTTCCCCCCTGGAAAAAGTTTATCTGTAAAGATGCTTAATCT	492
QY	533	userAsrpleuIySleuLySglnleuPProserSerlilegIyAsrpleuValhisIleuArgTy	553
Db	4925	AGGTATTTTCGACATTTAATTAATGTTACATCTTCATTTGAGAGATTCATGATTAAGATA	498
QY	553	rIleuAsnleuSerGlyAsnThrSerlileArgSerleuPProAsnGlnleuCySlySleuGl	573
Db	4985	CTTGAACTGTATGTC---AGTGGCATGCGTATGTTTCCAAAGCAGTTATGCAAGCTTCA	504
QY	573	nasnleuGlnThrlleuAsrpleuThsIleGlyCyshisSerleuCySyleuProlySglnTh	593
Db	5042	AAATCTGAAACTCTTGATCTACATTAATGTCGCAAGCTTTGTGTTGCCAAAGAAAC	510
QY	593	rSerIySleuGlySerleuArgAsnleuIleuAsnIyCySlyTyrgIyIleuThrCyme	613
Db	5102	AAGTAAACTTGATATCTCCGAAACTTTTACTTGATGTAGCCAGTCATTTGACTTGAT	516
QY	613	tProPArArglilegIySerleuThrCyaleuIyThrlleuSerArgPheValaIGlyI	633
Db	5162	GCCACCAAGATGGATCATGACATGCTTAAGCTCTAGTCCATTAATGTGTGTGGA--	521
QY	633	eGlnlyAsrSerCySglnleuGlyGlyleuArgAsnleuAsnleuTyrgIySerlilegI	653
Db	5220	AGCAAGAAAGGTTATCAACTTGTGTGAACATGAAACCTTAATCTATGTGCTCAATTAA	527
QY	653	uIleThrThIsleuGluArgValIyAsnAspMetAspAlalySgIuAlaAsnleuSerAl	673

Db	5279	AATCTCGATCTTGAGAGAGTGAAGAAATGATTAAGACCCAAAGAGCAATTTATCTGC	5339
Qy	673	ALysGIuAsnLeuHisSerLeuSerMetLysTrpAspAspGIuArgProArgLysIleTyr	693
Db	5339	AAAAAGGAATCTGCATCTTTAAGCATGAGTTGG---AATAAATTGGACCAATATATATA	5395
Qy	693	RGluSerGIuLysValGIuValLeuGIuValLeuLysProHisSerAsnLeuThrCysLe	713
Db	5396	TGAATCACAAGAAAGTTAAAGTCTGAAGCCCTCAAAACCACTCAATCTGACTTCCTT	5455
Qy	713	uThrIleArgGIuPheArgGIyLileArgLeuProAspTrpMetAsnHisSerValLeuLys	733
Db	5456	AAAAATCTATAGCTTCAGAGAAATCCATCTCCAGAGTGAATGATCACTCAATTTGAA	5515
Qy	733	AsnValValSerIleLeuLileSerCysLysAsnCysSerCysLeuProProPheGI	753
Db	5516	AAATATGTCTCTATTTCTTAATTAGCAACTTCAGAAATGCTCATGCTTACCACTTGG	5576
Qy	753	YGIuLeuProCysLeuLysSerLeuGIuLeuTrpArgLysSerAlaGIuValGIuTyrVa	773
Db	5576	TGATCTGCTCTGTCTGAAGATCTCAAGATTCACTGGGGGCTCTGGGATGTGGAATAGT	5633
Qy	773	LAsp-----SerGIuPheProThrArgArgAspPheProSerLe	786
Db	5636	TGAAGAAATGGATTTGATGATTTGATCTTCATCTTCGATTTCCCAAGAAATAGTTTCCATCTT	5699
Qy	786	uArgLysLeuAsnIleArgGIuPheGIYAsnLeuLysGIYLeuLeuLysGIuGIYGI	806
Db	5696	GAGGAAATCTGATATATATGAGACTTTGGTAGCTGAAAGATTTGCTGAAGAAAGAGAGAGA	5755
Qy	806	uGIuGIuCysProValLeuGIuGIuLileGIuLileLysCysCysProMetPheValIlePr	826
Db	5756	AGAGAAATTTCCCTGTGCTTGAAGAGATGATATATTCACAGAGGCCCTTTTTCG-----	5807
Qy	826	oThrLeuSerSerValLysLysLeuValValSerGIYAspLysSerAspAlaIleGIYPh	846
Db	5808	-ACCTTTCT-----	5816
Qy	846	eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGIuIleArgTyrAsnLysGIuAs	866
Db	5817	-----TCTAATCTTTAGGGCTCTTACTTCCCTCGAATTTGGTATATATAAAGTGC	5866
Qy	866	pAlaSerLeuProGIuGIuMetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSe	886
Db	5867	TACTTCATTTCCCAAGAGATGTTCAAAACCTTGCAATCTCAATCTTGACAAATCTC	5926
Qy	886	rPheTyrPheAsnLeuLysGIuLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHi	906
Db	5927	TGGTGCAATATATCTCAAGAGCTGCTTCCAGCTTGCTGATGCTTGAATGCTTTGAAGAG	5986
Qy	906	sLeuGIuLileHisSerCysTyrAlaLeuGIuSerLeuProGIuGIuValLysGIYLe	926
Db	5987	TCTAAAAATTCAAATTTGGTGGCGACTAGAGAGTCTCCCTGAGGAAGGGCTGGAAGGTTT	6046
Qy	926	uIleSerLeuThrGIuLeuSerIleThrTyrCysGIuMetLeuGIuCysLeuProGIuGI	946
Db	6047	ATCTTCACTCAAGAGATTATTTGTGAACACTGTAAACATGCTTAATTAATTTTAAACAGAGGG	6106
Qy	946	YLeuGIuHisLeuThrAlaLeuThrAsnLeuSerValGIuPheCysProThrIleAsnAlaLys	966
Db	6107	ATTGAGAGCACTTAACAACTTCACAAAGTTTAAAAATTTGGGGAGTGTCCACAACCTGATCA	6166
Qy	966	sArgCysGIuLysGIYLileGIYGIuAspTrpTyrLysIleAlaHisIleProArgValPh	986
Db	6167	GCGGTGTGAAGAGGAATAGGAAGAAGCTGSCACAAATTTCTCAATTTCTTAATGTGAA	6226
Qy	986	eIleTyr 988	
Db	6227	TATATAT 6233	

DEFINITION Sequence 39 from Patent EP1334979.
ACCESSION AX814116
VERSION AX814116.1 GI:39103418
KEYWORDS
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS van der Vossen, E.A. and Alléfs, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
JOURNAL Patent: EP 1334979-A 39 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
location/Qualifiers
FEATURES
Source
1..3971
/organism="Solanum bulbocastanum"
/mol_type="unassigned DNA"
/db_xref="taxon:147425"
misc_feature
1..3971
/note="KGC3-blb"
ORIGIN
Alignment Scores:
Pred. No.: 3,72e-275 Length: 3971
Score: 3606.50 Matches: 763
Percent Similarity: 63.02% Conservative: 77
Best Local Similarity: 57.24% Mismatches: 137
Query Match: 70.34% Indels: 357
DB: Gaps: 9
US-10-647-268-2 (1-988) x AX814116 (1-3971)
QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
DB 1 ATGCTGAAGCTTTCATTCAGTTGTGCTAGACAACTCACCCTTCTCCGAAAGGGGAA 60
QY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThrThr 40
DB 61 CTGTATGCTTTTCGTTTCAGATGAGTCCAAAGGCTTTCAGAGATGTTCTCA 120
QY 41 IleglnAlaValLeuGlnAspAlaGlnIleuLeuAspIleValIleGlnValIle 60
DB 121 ATCCAGCCGCTCTTGAAGATGCTCAGAGAAAGCACTCAAGCAAGACCTCTAGAAAT 180
QY 61 TTPLeuGlnIleLeuAsnAlaAlaAlaTyrgIuAlaAspAspIleLeuAspGluCysLeu 80
DB 181 TGGTTGCAAAACCTAATGCTGCTCATATGAAAGTCAGATGACATCTTGGATGAATATAA 240
QY 81 ThrGluAlaProIleArgGlnIleuLeuAsnIleTyrgIleCysIlePheProAsnValIle 100
DB 241 ACTAAGGCC--ACAAGATTCCTTGCAAGTCTGAAATGGCCGTTTACATCCAAAGGTTATC 297
QY 101 ThrPheArgHileuIleGlyLeuArgMetLeuIleMetGlnIleLeuAspValIle 120
DB 298 CCTTCCCTCAGAGGTTGGGAAAGATGACCAAGATGAAAGAACTGAATCAAT 357
QY 121 AlaAlaGluArgIleuPheHileuAspGluArgThrIleGluArgGlnValAlaThr 140
DB 358 GCTGAGAAACGAAAGAAATTTTCATTGCAAGAAAGATTATAGAGACAAAGCTGCTCA 417
QY 141 ArgGlnThrGlyPhe----- 145
DB 418 CGGGAACAGGATC--TCATCTTAATAGTATTACAACTAGTTATATCATTTGTTT 476
QY 145 ----- 145
DB 477 GGGCAATGATCAATATTATGTAAGGTCAATATCTCATGTAAGTAAATAGTTAA 536
QY 145 ----- 145
DB 537 ATATACCTAGTATATCTATAGTATAGTACAACTACTCCCATATATCTTTGAAACAAAT 596

QY 145 ----- 145
DB 597 ATTCCTTAACGAATATAAGACAGTGAAAGTTCAAGTTCAAAATATCCACCTCAATTT 656
QY 145 ----- 145
DB 657 TAAATCTGATTTCTTTAGAAACCACCTCATCTCCGTTTGTAGATTCTTAAGAAACA 716
QY 145 ----- 145
DB 717 GCTGAGAAAGAGTTTCTTCTGTTCTGTTCTGCTGCATTTGTGCTTAATCCAT 776
QY 145 ----- 145
DB 777 AACCAACAATCAATTAATATATGTTACGATGAGGTAGTCTTTCTACTAGACATG 836
QY 145 ----- 145
DB 837 AACTGAGTAAATTTTGTTTTAAGAAAGAAAGAAATGATTAGGCTGATTTCTTTCA 896
QY 145 ----- 145
DB 897 GAGTGAATATAGGGGATAAAGTTGAGCATAGAGTTCCATCGTTATTTCTTCTTA 956
QY 145 ----- 145
DB 957 AAGTAACAAGTTCACAAAATGATATCAAGGTACGTAATGAAATTTATAGACAGTC 1016
QY 145 ----- 145
DB 1017 TAAACTACAAATATGAAATAGAACTTAATATCAGTACAAATATCATCTTAATATAA 1076
QY 145 ----- 145
DB 1077 GCTACCAATTTAATCATGATATACAGAGAAACCAAAAAATTAGGGGTGAATTTAT 1136
QY 145 ----- 145
DB 1137 GATTCTATGCTTATCATGATGCTTCCCATCAACATCAAGAAATTTGTGCCAAAGTAT 1196
QY 145 ----- 145
DB 1197 AAACGGCGGTATATTTGATGTAAGTAAGAAACAGAGATATCATTTGACTAAAGTA 1256
QY 145 ----- 145
DB 1257 TAACAATAGTATATTTGATCATTTATATGTAACAATTCATGTGTTTGGGAGAAAG 1316
QY 145 ----- 145
DB 1317 GAAGTTCAATGTTTCAATGCTGCTCATCTCATCATATCTCTTTATTTGTGCAAAAC 1376
QY 145 ----- 145
DB 1377 CCTTCTATTTAATCTATTTTCTGCCAGCTCTAATAGCTTGAATGTAACATATTTCTC 1436
QY 146 ----- 146
DB 1437 ATCTGACATTTGTCGACCGAGTTCTGTGTTAATCTGAACCAAGTTTATAGAAAGGAC 1496
QY 147 ----- 147
DB 1497 AAAGAAAAGATGATGATGTAAGAAATCTTATTAACAATGTTATGATGCCCAAAATCTC 1556
QY 1497 ProValLeuProIleLeuGlyMetGlyLeuGlyLeuThrThrLeuAlaGlnMetVal 196
DB 1557 TCAGTCTCCCAATATCTTGTATGAGGGGACTAGAAAGCAACTCTTTCCCAATGGTC 1616
QY 157 ----- 157
DB 1597 PheAsnAspGlnArgValIleGlnIlePheHileuProIleThrPheCysValSerGlu 216
QY 1617 TTCAATATATCAGAGATACAGAGCTTCTATTCCTCAAAATATGATGATTTGGTCTCGAT 1676

QY 217 AspPheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeu 236
 Db 1677 GATTTTGGATGAGAAGAGTGGATTAAGGCAATAGTAGATCTATTGGAAGGAAAGTCCCTC 1736
 QY 237 GlyGlyMetAspLeuAlaProLeuGluLysLysLeuAspLeuLeuAsnGlyLysLys 256
 Db 1737 AGTGCATGAGACTGGCTCCACTTCAMAAAGAACTTCAAGAGTCTGATGAAAGAAAAGA 1796
 QY 257 TyrLeuLeuValLeuAspAspValTTPAsnGluAspGluAspLysTTPAlaLysLeuArg 276
 Db 1797 TACTTCCTGTTGCTTGAATGATTTGGAAATGAAATCAACATAGAGGAGCTAATTATTAAGA 1856
 QY 277 GluValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrArgLeuGluLys 296
 Db 1857 GCAGCTCTGAAGGTGGAGCAAGTGGTGCACTTGTCTTAAGTACTACTAGCTGCTGAAAAG 1916
 QY 297 ValGlySerIleMetGlyThrLeuGluProTyrGluLeuSerAsnLeuSerGluAsp 316
 Db 1917 GTTGATCAATTATGGAAACATTCACACCATATGAAATGTCMAATCTGCTCCAGAGAT 1976
 QY 317 CysTTPLeuLeuPheMetGluArgAlaPheGlyHisGluGluGluIleAsnLeuAsnLeu 336
 Db 1977 TGTGCTTTTGTGTATGATGAGGTGCATTTGGACACCAAGAAATTAATCCAAACCTT 2036
 QY 337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaLysThr 356
 Db 2037 GTGGCAATCGGAAGAGATTTGAAAAAATGTGGTGGTGCCCTGAGCCCAAGCT 2096
 QY 357 LeuGlyGlyIleLeuArgPheLysArgGluGluValGluGluIleValArgAspSer 376
 Db 2097 CTGGAGGTATTTTGGCGCTTCAAGAGAAAGAAAGAAAGATGGAACATGTAGAGACAGT 2156
 QY 377 GluIleTTPLysLeuProGluGluLysSerIleLeuProAlaLeuArgLysSerTyr 396
 Db 2157 CCGATTTGGAAATTTGCCCTCAAGATGAAGTTCTATCTGCGCTGAGCTTAGTTAC 2216
 QY 397 HisHisLeuProLeuAspLeuArgGluCysPheThrTyrCysAlaValPheProLysAsp 416
 Db 2217 CATCATCTTCCACTTGATTTGAGCAATGCTTTGTGTGGTGATTTGCCAAGAC 2276
 QY 417 ThrGluMetGluLysGlyAsnLeuIleSerLeuTTPMetAlaHisGlyPheIleLeuSer 436
 Db 2277 ACCAAATATGGCAAGAAAGAAATCTTATGCTTTTGGAGTGCACAAAGTTCCTTTATCG 2336
 QY 437 LysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTTPAsnGluLeuTyrLysArg 456
 Db 2337 AAAGAAATTTGGAGCTAGAGATGAGATGAATGAAGATGAATTAATTAATCTAGAG 2396
 QY 457 SerPheGluGluIleGluValLysSerGlyGluThrTyrPheLysMetHisAspLeu 476
 Db 2397 TCTTCTTCCAAAGATTTGAAGTTGAATCTGTGTAATCTTATTTCAAGATGCATGACCTC 2456
 QY 477 IleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlu 496
 Db 2457 ATCATGATTTGGCTACATCTCTGTTTTCAGCAACACATCAACAGCAATATTCGGA 2516
 QY 497 IleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSer 516
 Db 2517 ATAAATGCTAATTATGATGATATATGATGATGATGATTTGCTGAAGTGATCTTCT 2576
 QY 517 TyrSerLeuSerHisLeuGluLysPheValSerLeuArgValLeuAsnLeuSerAspIle 536
 Db 2577 TACCTCTCTTCACTTGGCAAAAGTTTGTCTCATTAAGGGGTCTTAATCTTAAGAACTCG 2636
 QY 537 LysLeuLysGluLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu 556
 Db 2637 AACCTAATCAATTATCAATCTTCCATTGGAGATCTAGTACATTAATCACTCGGACTTG 2696
 QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGluLeuCysLysLeuGluAsnLeuGlu 576
 Db 2697 TCTGGCAATTTAGAAATTCGAATCTTCAAAAGAGATTAAGCAGGCTTCAAAATCTGAG 2756
 QY 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysLeuProLysGluThrSerLysLeu 596

Db 2757 ACTCTGATCTACATTTATTTGGACTCTCTTCTTGTGTCACAAACAAACAGTAATCTT 2816
 QY 597 GlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArg 616
 Db 2817 GGTAGTCTCCCAAAATCTTTACTTGAATGGCTGT---TCATTTAGAGTCAACGCCCAAGG 2873
 QY 617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyIleGluLysLys 636
 Db 2874 ATAGAGTTGTTGACATGCTTAAGTCTTAAGTTGCTTTGTTATGGC---AAGAGAAA 2930
 QY 637 SerCysGluLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHis 656
 Db 2931 GGTATATCAACTGGTGAACCTTAATAAACCTTAATCTATAGGCTCAATTCATCACAAA 2990
 QY 657 LeuGluLysValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsn 676
 Db 2991 CTTGACAGAGTGAAGAAAGATAGCGATGCAAAAGAACTTAATTTATCTGCTAAAGCAAT 3050
 QY 677 LeuHisSerLeuSerMetLysTTPAspAspGluArgProArgIleTyrGluSerGlu 696
 Db 3051 CTGCACTCTTTATGCTGAGTGGAGCTTGATGAAACATAGA---TATGATTC--- 3104
 QY 697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
 Db 3105 -----GAACTTCTGAAGCCCTCAAAACACACTCCAACTGAAATATTAGAATCAAT 3158
 QY 717 GlyPheArgGlyIleArgLeuProArgTTPMetAsnHisSerValLeuLysAsnValVal 736
 Db 3159 GGCCTCGAAGAAATCCCTCTCCAGATGGATGAATCAACATTTTGAATAATGTTGTC 3218
 QY 737 SerIleGluIleIleSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuPro 756
 Db 3219 TCTATTAGATTTAGAGTTGTGAATACTGCTATGCTTACCACTTGGTGAAGTGCCT 3278
 QY 757 CysLeuLysSerLeuGluLeuTyrPheArgLysSerAlaGluValGluTyrVal---AspSer 775
 Db 3279 TGTCTGAAGAACTCAGAGTTACACACCGGGTGCAGAGATGGAGATGTTGAAGATTAAT 3338
 QY 776 GlyPheProThrArgPheArgPheProSerLeuArgLysLeuAsnIleArgGluPheGly 795
 Db 3339 GTTCATCTCT---GGAAGTTCCTCACTCTTGAAGAACTGTTATATAGGACTTTACT 3392
 QY 796 AsnLeuLysGlyLeuLeuLysLysGluGlyGluGluGluCysProValLeuGluGluIle 815
 Db 3393 AATCTAAGAGATTTGCTGAAGAAAGAGAAAGAAACAAATCTCCTGCTTGAAGAGATG 3452
 QY 816 GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLysLeuVal 835
 Db 3453 ACATTTTACTGTCGCCCTATGTTGTTATTCGACCCCTTCTCTGCAAGACATTGA 3512
 QY 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
 Db 3513 GTTATTTGCG-----ACAGATGCACAGATTTTGAAGTCCATATCTTAATCTTGAAGGCTCTT 3566
 QY 856 ThrSerLeuGluIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLys 875
 Db 3567 ACTTCCTTGAACATTTGCAATACATAGAAAGCACTTCACTCCCAAGAAAGATTTCA 3626
 QY 876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
 Db 3627 AGCCTTGCAATCTCAAAATCTGATATCTCTTCTTGAAGAAATTCMAAGTTGGCT 3686
 QY 896 ThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeu 915
 Db 3687 ACCAGCTGCTAGTCTCAATGCTTTGAAGAGCTCAAAATTTGAATTTGTAAAGCAGCA 3746
 QY 916 GluSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGluLeuSerIleThr 935
 Db 3747 GAGAGCTCCCAAGAGAAAGGGGTAAGGTTTAATCTTCACTCAACGAGTGTGCTGCACT 3806
 QY 936 TyrCysGluMetLeuGluCysLeuProGluGlyLeuGluHisLeuThrAlaLeuThrAsn 955

QY 157 LysGluLysAspGluIleValLysIleLeuIleAsnValSerAsnAlaGlnThrLeu 176
| | | | |
Db 1497 AAGGAAAGATGAGATGATGAAATCTTAATAACAATGATGAGCCCAAAACTTC 1556
| | | | |
QY 177 ProValLeuProIleLeuGlyMetGlyLeuGlyLysThrThrLeuAlaGlnMetVal 196
| | | | |
Db 1557 TCAGTCTCCCAATCTTGATGAGGGGAGCTAGAGAAAGACAACCTTCCCAATGTGC 1616
| | | | |
QY 197 PheAsnArgGlnArgValIleGluHisPheHisProLysIleTrpIleCysValSerGlu 216
| | | | |
Db 1617 TTCATGATGACAGAGTAAGTACGAGCGTTCTATCCCAAAATATGATTTGGCTCCGAT 1676
| | | | |
QY 217 AspPheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeu 236
| | | | |
Db 1677 GATTTGATGAGAGAGGTTGATTAAGCAATGATGATGATGATGATGATGATGATGAT 1736
| | | | |
QY 237 GlyLysMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLys 256
| | | | |
Db 1737 AGTGCATGAGACTGGCTCCACTTCAAAAGAAAGCTTCAAGAGTTGCTGAATGAAAAAGA 1796
| | | | |
QY 257 TyrLeuLeuValIleAspAspValTrpAsnGluAspGluAspLysTrpAlaLysLeuArg 276
| | | | |
Db 1797 TACTTCTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1856
| | | | |
QY 277 GlnValLeuLysValGlyAlaSerGlyValaSerValLeuThrThrArgLeuGluLys 296
| | | | |
Db 1857 GCAGCTTGAAAGGTTGGAGCAAGTGTGCAATTTGTTCTAATCTAATCTGCTTGAAGA 1916
| | | | |
QY 297 ValGlySerIleMetGlyThrLeuGlnProGlyLeuSerAsnLeuSerGlnGluAsp 316
| | | | |
Db 1917 GTTGATCAATTAATGAGGAACATTCGACCATATGATGATGATGATGATGATGATGATGAT 1976
| | | | |
QY 317 CysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeu 336
| | | | |
Db 1977 TGTGGTTTGTGTCATGACAGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 2036
| | | | |
QY 337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThr 356
| | | | |
Db 2037 GTGCAATTCGAAAGGAGATGTAAGAAATGTGGTGTGCTGCTGAGCCCAAGACT 2096
| | | | |
QY 357 LeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnTrpGluHisValArgAspSer 376
| | | | |
Db 2097 CTGGAGGATATTTGGCGCTTCAGAGAGAAAGAAAGATGAGAAACATGTGAGACACT 2156
| | | | |
QY 377 GluIleTrpLysLeuProGlnGluLysSerIleLeuProAlaLeuArgLeuSerTyr 396
| | | | |
Db 2157 CCGATTGGAATTTGCTCCAGATGAAAGTTCTATTTCTGCTGCTGAGGCTTATGTTAC 2216
| | | | |
QY 397 HisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAsp 416
| | | | |
Db 2217 CATCATCTTCACATGATTTGAGACAATGCTTTGATTTGTGGGATATTCCTCAAGAGAC 2276
| | | | |
QY 417 ThrGluMetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSer 436
| | | | |
Db 2277 ACCAAATGGCAAGAAATCTTATCGCTTTTGGATGAGCACTGATTTCTTTATG 2336
| | | | |
QY 437 LysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArg 456
| | | | |
Db 2337 AAGAGAAATTTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2396
| | | | |
QY 457 SerPheGlnGlnIleGlyValLysSerGlyGlnThrTyrPheLysMetHisAspLeu 476
| | | | |
Db 2397 TCTTCTTCCAGAGATTTGAAGTGAATCTGTAAACTTATTTCAAGATGATGATGATGATGAT 2456
| | | | |
QY 477 IleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlu 496
| | | | |
Db 2457 ATCCATATATTTGGCTACATCTGTGTTTTCAGCAAAACATCAACACATATTTCCGAA 2516
| | | | |
QY 497 IleIleValGluLeuTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSer 516
| | | | |
Db 2517 ATTAATCTAATTAATGATGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2576
| | | | |

QY 517 TyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIle 536
| | | | |
Db 2577 TACTCTCTTCACTCTTGCAAAAGTTTGTCTCATTAAGGGTCTTAATCTTAAGAACTCG 2636
| | | | |
QY 537 LysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu 556
| | | | |
Db 2637 AACCTAATCAATTAACCATCTTCCATGAGAGATCTAATCAATTAAGATACCTGACTTG 2696
| | | | |
QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
| | | | |
Db 2697 TCTGGCAATTTTGAATTCGTAATCTTCCAAAGGATTAAGCAGGCTTCAAAATCTTCAG 2756
| | | | |
QY 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysSerLeuProLysGluTrpSerLysLeu 596
| | | | |
Db 2757 ACTTTGATCTACATTAATTTGAGACTCTTCTTGTGTTGCCAAACAAACAAAGTAACCTT 2816
| | | | |
QY 597 GlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArg 616
| | | | |
Db 2817 GGTAGTCTCCGAATCTTTTAACTTGATGGCTGT---TCATTTGACGTCAACGCCACAAAG 2873
| | | | |
QY 617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLys 636
| | | | |
Db 2874 ATAGGATTTGATGATGCTTAAGTCTTAAGTCTTAAGTCTTGTATGTGC---AAGAGAAA 2930
| | | | |
QY 637 SerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHis 656
| | | | |
Db 2931 GGTATTAATCTTGATGATCAATTAACCTTAATCTGATGCTCAATTTCAATCAACAAA 2990
| | | | |
QY 657 LeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsn 676
| | | | |
Db 2991 CTTCAGCAGATGAAAGAAAGATAGCAGATGCAAAAGAAAGCTAATTAATCTGCTAAAGCAAT 3050
| | | | |
QY 677 LeuHisSerLeuSerMetLysTrpAspAspGluArgProArgIleTyrGluSerGlu 696
| | | | |
Db 3051 TGTGACTTTTATGCTGAGAGTGGACCTTGATGAGAAATATGA---TATGATTC--- 3104
| | | | |
QY 697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
| | | | |
Db 3105 -----GAAGTTCTTGAAGCCCTCAAAACCACTCCCATCTGAATATTTAGAAATCAAT 3158
| | | | |
QY 717 GlyPheArgGlyIleArgLeuProArgTrpMetAsnHisSerValLeuLysAsnValVal 736
| | | | |
Db 3159 GGCCTTCGAGAAATCCGCTCCAGATGGATGAATCAATCAATTTTGAAGAAATGTTGTC 3218
| | | | |
QY 737 SerIleGluIleLeuSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuPro 756
| | | | |
Db 3219 TCTATTGAATTTAGAGTTGTGAAGAACTGCTCATGCTTACCACTTTGGTGAAGCTGCT 3278
| | | | |
QY 757 CysLeuLysSerLeuGluLeuTrpArgGlySerAlaGluValGluTyrVal---AspSer 775
| | | | |
Db 3279 TGTCTAGAAAGTCTAAGTTACACACCGGGGTGAGAGATGAGATGATGATGATGATGATGAT 3338
| | | | |
QY 776 GlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIleArgGluPheGly 795
| | | | |
Db 3339 GTTCATCTC-----GGAAGGTTTCAATCTTGAAGAACTGTTATATGAGCACTTATG 3392
| | | | |
QY 796 AsnLeuLysGlyLeuLeuLysLysGluGlyGluGluGluCysProValLeuGluGluIle 815
| | | | |
Db 3393 AACTTAAGAAATGCTGTAAGAAAGAAAGAAAGAAACAAATTCCTGCTGTAAGAGATG 3452
| | | | |
QY 816 GluIleLysCysProMetPheValIleProThrLeuSerSerValLysLysLeuVal 835
| | | | |
Db 3453 ACATTTTAACTGAGGCCCTATGTTGTTATCCGACCCCTTCTGCTCAAGACATGAA 3512
| | | | |
QY 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
| | | | |
Db 3513 GTTATTTGCG-----ACAGATGCAACAGTTTGAAGGTCCATATCTAATCTTGAAGGCTCTT 3566
| | | | |
QY 856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLys 875
| | | | |
Db 3567 ACTTCCCTTGACATTGACATTAACATTAACATTAACATTAACATTAACATTAACATTAACAT 3626
| | | | |
QY 876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
| | | | |

Accession	Gene	Species	Position (nt)	Sequence	Position (nt)
D8	3627	ACCCCTGGCAAAATCTCAAACTACTGAAATATCTCTTTCTTTAGCAATCTCAAAAGATGGCT	3668	3668
Qy	896	ThrsSerLeuAlaSerLeuAsnAlaLeuYshIshLeuGluIshSerCysTyrAlaLeu	915	915
D8	3687	ACCAAGCCTGGCTAGCTCAATGCTTTGGAAGAGTCTCAAAATTGAAATTTGTAACGCACTA	3746	3746
Qy	916	GlusSerLeuProGluGluGlyValIshGlyLeuIshSerLeuThrGlnLeuSerIshLeu	935	935
D8	3747	GAGAGTCTCCAGAGGAAGGGGTGAAGGTTAACTTACTACCCGAATTGTCTGTCACT	3806	3806
Qy	936	TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnIshLeuThrAlaLeuThrAsn	955	955
D8	3807	AACGTGTATGATGCTAAATGTTTACCAGGAGGATGGACGACCTTAACAGCCCTCACAACT	3866	3866
Qy	956	LeuSerValGluPheCysProThrLeuAlaIshArgCysGluYshGlyIshGlyGluAsp	975	975
D8	3867	TTAAACAATTACTCAATGCTCAATAGTATTCAAGCGGTGTGAGAGAGGAATGGAGAAAGAC	3926	3926
Qy	976	ThrTyrIshValIshAlaIshIshLeuProArgValPheIshTyr	988	988
D8	3927	TGGACAAATTTGCTACATTCATATTTGACTCTCATAT	3965	3965

Search completed: April 17, 2005, 03:01:42Z
Job time : 9559 BECS

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 20:33:57 ; Search time 1086 Seconds

(without alignments)
5385.547 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFGLVLDNLTCFIQGE.....EKIGEDMYKIAHPRVFIY 988

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 segs, 2359870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_plus.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10647266/runat_15042005_154719_26465/app_query.fasta_1.1159
-DB=N_Geneseq_16Dec04 -QMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPTCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blisum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=plco -NOEM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647268_QCGN_1_1_708 @runat_15042005_154719_26465 -NCPUB=6 -ICPU=3
-NO MMAP -LARGESOURERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:

1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001as:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5127	100.0	3193	12	ADK98516
2	5028.5	98.1	3595	12	ADK98518
3	5028.5	98.1	5028	12	ADK98524
4	4475	87.3	3347	12	ADK98520
5	3766.5	73.5	2913	10	ADK17759

6	3766.5	73.5	2913	12	ADH51531	Adh51531 S bulboca
7	3648	71.2	3260	10	ADP17762	Adf17762 S bulboca
8	3648	71.2	3260	10	ADH51534	Adh51534 S bulboca
9	3638.5	71.0	3592	10	ADP17760	Adf17760 Solanum b
10	3638.5	71.0	3592	12	ADH51532	Adh51532 S bulboca
11	3638.5	71.0	5191	12	ADH51533	Adh51533 S bulboca
12	3638.5	70.3	7349	10	ADP17761	Adf17761 Solanum b
13	3606.5	70.3	3971	10	ADP17763	Adf17763 S bulboca
14	3606.5	70.3	3971	12	ADH51535	Adh51535 S bulboca
15	3400	66.3	3899	10	ADP17764	Adf17764 S bulboca
16	3400	66.3	3899	12	ADH51536	Adh51536 S bulboca
17	3342	65.2	3222	12	ADK98522	Adk98522 S bulboca
18	1346.5	26.3	3879	8	ADA69439	Ada69439 Rice gene
19	1323	25.8	4149	8	ADA70126	Ada70126 Rice gene
20	1244	24.3	3801	3	AA59332	AA59332 Nucleotid
21	1244	24.3	6658	2	AAT79882	Aat79882 Tomato im
22	1235	24.1	4465	2	AAT42135	Aat42135 I2C-2 gen
23	1198	23.4	4948	2	AAT42134	Aat42134 I2C-1 gen
24	1028.5	20.1	4208	2	AAV44188	AAV44188 Lettuce r
25	1028.5	20.1	4208	6	ABK67786	ABK67786 Lettuce p
26	1008.5	19.7	4163	6	ABK67828	ABK67828 Lettuce p
27	1007.5	19.7	4163	2	AAV44230	AAV44230 Lettuce r
28	966.5	18.9	2353	2	AAV44189	AAV44189 Lettuce r
29	966.5	18.9	2353	6	ABK67787	ABK67787 Lettuce p
30	941	18.4	3852	2	AAZ20602	AAZ20602 Zea mays
31	937	18.3	3833	2	AAZ20601	AAZ20601 Zea mays
32	937	18.3	4390	2	AAZ20597	AAZ20597 Zea mays
33	937	18.3	5948	2	AAZ20596	AAZ20596 Zea mays
34	910	17.7	5763	2	AAZ20606	AAZ20606 Zea mays
35	908	17.7	5540	8	ADA71374	Ada71374 Rice gene
36	905.5	17.7	3855	2	AAZ20598	AAZ20598 Zea mays
37	904	17.6	5910	2	AAV66798	AAV66798 Rice bact
38	902	17.6	3853	2	AAZ20603	AAZ20603 Zea mays
39	901	17.6	3837	2	AAZ20600	AAZ20600 Zea mays
40	890	17.4	3879	2	AAZ20599	AAZ20599 Zea mays
41	852.5	16.6	4557	8	ADA71375	Ada71375 Rice gene
42	842	16.4	8206	2	AAZ20605	AAZ20605 Zea mays
43	821.5	16.0	4001	10	AA154262	AA154262 Movable g
44	782.5	15.3	2988	8	ADA71057	Ada71057 Rice gene
45	763.5	14.9	2559	6	AB213950	AB213950 Arabidops

ALIGNMENTS

RESULT 1
ID ADK98516 standard; cDNA; 3193 BP.
AC ADK98516;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX S Bulbocastanum Sbul1 cDNA sequence SegID1.
DE
XX plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
KM conferring pathogen resistance; Sbul1; gene; ss.
XX
XX Solanum bulbocastanum.
XX
XX Key Location/Qualifiers
FH 52..3018
FT CDS
FT
FT
FT
XX
XX W02004020594-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027045.
XX
XX 29-AUG-2002; 2002US-0407100P.
XX 20-AUG-2003; 2003US-00647268.
PR

/*tag= a

/product= "S Bulbocastanum Sbul1 protein"

XX (USDA) US SEC OF AGRIC.
 PA (DRYC-) DRY CREEK LAB.
 XX
 PI Osumi T, Belknap WR, Rockhold DR, Macree MM;
 XX WPI; 2004-239179/22.
 DR P-PSDB; ADK98517.
 XX
 PT New isolated Solanum bulbocastanum late blight resistance nucleic acid
 PT molecule encoding a plant disease resistance polypeptide, useful for
 XX conferring pathogen resistance to Phytophthora infestans in plants.
 PS
 XX Claim 1; SEQ ID NO 1; 103pp; English.
 CC This invention relates to a novel isolated nucleic acid molecule encoding
 CC a plant disease resistance polypeptide. The preferred plant is a
 CC solanaceous plant that is potato. The resistance is to late blight
 CC disease, caused by the fungus Phytophthora infestans. The invention is
 CC useful for conferring pathogen resistance in plants using a Solanum
 CC bulbocastanum late blight resistance gene. The present sequence is the S
 CC bulbocastanum cDNA sequence of the invention.
 SQ Sequence 3193 BP; 1031 A; 543 C; 671 G; 948 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3193
 Score: 5127.00 Matches: 988
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 12 Indels: 0
 Gaps: 0
 US-10-647-268-2 (1-988) x ADK98516 (1-3193)

Db 592 ATACTGGTATGGGGGCACTAGAAAGACACTCTTGCCCAATGCTTCATGATCAG 651
 QY ArgValIleGIuHISpHeHISpRoLYsIleTrpIleCYsValISerGIuAspPheASnGIu 220
 Db 652 AGAGTAATGAGCATTTCCATCCCAAAATATGATTTGTCTCGGAAGATTTTAAATGAG 711
 QY 221 LysArgLeuIleLYSGIuIleValGIuSerIleGIuGIuLYSserLeuGIYGIuMetAsp 240
 Db 712 AAGAGTTGATMAAGAAATTTGTAGAAATCTATTMAAGAAAGTCACTGGTGCGATGAC 771
 QY 241 LeuAlaProLeuGIuLYSLeuArgAspLeuLeuSNGIuLYSLeuValIle 260
 Db 772 TTGGCTCCACTTCAAAAGAACTTCGGGACTTGCCTGAATGGAAAAAATTTCTGCTC 831
 QY 261 LeuAspAspValITPAsnGIuAspGIuAspLYSTrpAlaLYSLeuArgGIuValIleLYS 280
 Db 832 TTAATATGATGTTTGGATGAAAGATCAAGATTAAGGGCTTAAGTAAACAAGCTTTGAG 891
 QY 281 ValGIuAlaSerGIuAlaSerValIleuThrThrArgLeuGIuLYSValGIYSerIle 300
 Db 892 GTTGAAGCAAGTGGCGCTTCTGTTTACCACTACCTGCTTGAAAAGGTTGGATCAATT 951
 QY 301 MetGIYThrLeuGIuProTYrGIuLeuSerAsnLeuSerGIuGIuAspCYSTPLeuLeu 320
 Db 952 ATGGGAACATTTGCACACCATATGAAATTTGCTCAATTTGCTCAAGAAATTTGGTTGTTG 1011
 QY 321 PheMetGIuArgAlaPheGIuHISGIuGIuIleAsnLeuAsnLeuValAlaIleGIY 340
 Db 1012 TTCAATGCAAGTGCATTTGGGACCAAGAAATTAATCTTGTGGCTATCCGGA 1071
 QY 341 LysGIuIleValIYSLYSLeuGIYValIleProLeuAlaAlaLYSThrLeuGIYGIYIle 360
 Db 1072 AAGGAATTTGTAAAAAATGTGGTGCTGCTTACAGCTTAAACTCTTGAAGGATATT 1131
 QY 361 LeuArgPheLYSArgGIuArgGIuArgINTPGLuHISValArgAspSerGIuIleTrpLYS 380
 Db 1132 TTGCGCTTTAAGAGAAGAAAGACAGTGGGAACATGTGAGATGTGAGATTGGAA 1191
 QY 381 LeuProGIuGIuGIuSerIleLeuProAlaLeuArgLeuSerTYrHISLeuPro 400
 Db 1192 TTCCCTCAAGAAAGAAATGCTTATTCGCTGCTTACAGCTTAAAGTAACTTTCCTTCA 1251
 QY 401 LeuAspLeuArgGIuLYSLeuThrTYrCYsAlaValaPheProLYSAspThrGIuMetGIu 420
 Db 1252 CTTGATTTGAGCAAACTGCTTACATATGTGCAAGTATCCCAAGGATACCAAAAGGAA 1311
 QY 421 LysGIYAsnLeuIleSerLeuTrpMetAlaHISGIYpHeIleuSerLYSGLYAsnLeu 440
 Db 1312 AAGGAAATCTATATCTCTCTGGATGGACATGTGTTTATTTATCGAAAGGAAACTTG 1371
 QY 441 GIuLeuGIuAsnValaGIYAsnGIuValITPAsnGIuLeuTYrLeuArgSerPhePheGIu 460
 Db 1372 GAGCTTGAAGAAATGTAGGTAATGAATGAATGAATTAATCTTGGGCTTTCTTCCAA 1431
 QY 461 GIuIleGIuValIYSerGIYGIuThrTYrPheLYSMeTHISAspLeuIleHISAspLeu 480
 Db 1432 GAGATTTGAAGTTAAATCTGTCAAACTTATTTCAAGATCAAGATCTCATGATCTCG 1491
 QY 481 AlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGIuIleIleValaGIu 500
 Db 1492 GCAACATCTCTATTTTGGCAAGCACATCAACACCAAAATATTCGAAATAATTTGTAGAA 1551
 QY 501 AsnTYrIleHISMeMetSerIleGIYpHeThrLYSValIleSerSerTYrSerLeuSer 520
 Db 1552 AATTACATACATATGATGTCCATTTGTTCACTAAAGTGATCTTTTACTCTCTTCC 1611
 QY 521 HISLeuGIuLYSPheValaSerLeuArgValaLeuAsnLeuSerAspIleLYSLeuLYSGIu 540
 Db 1612 CACTTGGAGAAATTTGTCTGTTGAGGGTCTTATCTTAAGGACATMAAACTTAAGCAG 1671
 QY 541 LeuProSerSerIleGIYAspLeuValaHISLeuArgTYrLeuAsnLeuSerGIYAsnThr 560
 Db 1672 TTACCGCTTTCATTTGAGATCTATGATCAATTAAGATACCTAAACTTGTCTGGCAATACT 1731

QY 561 SerLeuArgSerLeuProAsnGlnLeuCysIleuLeuGlnAsnLeuGlnThrLeuAspLeu 580
 DB 1732 AGTATGCTGATGCTCTCCAAACCAAGTATGCAAGCTTCAAAATCTGCACACTGATGCTTA 1791
 QY 581 HisGlyCysHisSerLeuCysSerLeuProIleuThrSerLeuGlySerLeuArg 600
 DB 1792 CATGGCTGCTCAATTCATTGTTGTTGCCAAAGAAACAGCAAACTGGTAGTCTTGA 1851
 QY 601 AsnLeuLeuLeuAspGlyCysIleuThrCysMetProProArgIleGlySerLeu 620
 DB 1852 AATCTTTAATTGATGTTGCTATGATGATGCTGTATGCAACCAAGATAGGATCTTGG 1911
 QY 621 ThrCysLeuLeuThrLeuSerArgPheValValGlyIleGlnIleuLeuSerCysGlnLeu 640
 DB 1912 ACATGCTTAAAGACTTAAAGTAGTATGTTGGTGGGAATTCAGAAAGAAAGTTGTCACCTT 1971
 QY 641 GlyIleuLeuArgAsnLeuAsnLeuThrGlySerIleGlnIleThrHisLeuGlnArgVal 660
 DB 1972 GGTGAATTAACGAAACCTGATCTGATGCTCAATGTAATCAGCATCTTGAGAGAGTGTG 2031
 QY 661 LysAsnAspMetAspAlaLeuGlyIleAlaAsnLeuSerAlaIleGlyAsnLeuHisSerLeu 680
 DB 2032 AAGAATGATATGATGCAAAAGAACCAATTATCTGCAAAAGAAATCTGCATCTCTTA 2091
 QY 681 SerMetLeuTPAspAspAspGluArgProArgIleTyrgIuSerGlnIleValGluVal 700
 DB 2092 AGCATGAATGAGATGACATGATGATGCTCACTATATATGATATGCAAAAGTTGAAATGTG 2151
 QY 701 LeuGlnAlaLeuLeuProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
 DB 2152 CTGGAAGCTCTCAAAACCAACACTCCAACTGACTGTTTAAACATCAGGGGCTTCAGAGGA 2211
 QY 721 IleArgLeuProArgTPMetAsnHisSerValLeuLeuValAsnValValSerIleGlnIle 740
 DB 2212 ATCCGCTCTCCAGACTGATGATGATCAGCTTGTGAAATATGTTGCTCTAATTGAAATTC 2271
 QY 741 IleSerCysIleAsnCysSerCysLeuProProPheGlyIleuProCysLeuIleuSer 760
 DB 2272 ATCAAGTTCAAAACACTGCTCACTGCTTACCACTTGTGAGCTGCTGTCTTAAAGAT 2331
 QY 761 LeuGlnLeuLeuTPArgGlySerAlaGluValGluTyValAspSerGlyPheProThrArg 780
 DB 2332 CTAGAGTTGTGGAGGGGCTCTCGGAGATGAGATGTTGATTCCTGATTCCTTCAAGA 2391
 QY 781 ArgArgPheProSerLeuArgIleLeuAsnIleArgGluPheGlyAsnLeuGlySerLeu 800
 DB 2392 AGAAGTTTCCATCTCTGAGAAACTTAATATACCGCAATTTGGTAAATCTGAAAGATTTG 2451
 QY 801 LeuIleuLeuGluGluGluGluGlnCysProValLeuGluGluIleGluIleLeuGlyCys 820
 DB 2452 CTGAAAAAGGAAGGAAGAGCAATGCCCTGTGCTTGAAGATATGAATTAAGTTTGC 2511
 QY 821 PrometPheValIleProThrLeuSerSerValIleuLeuValValSerGlyAspIle 840
 DB 2512 CCTATGTTTGTATTCACACCTTCTCTCTGCAAGAAATGGTAGTATGGGGACAAG 2571
 QY 841 SerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIle 860
 DB 2572 TCAGATGCATATAGTTTCACTTCACTATCTAATCTCATGGCTCTTACCTCCCAAAAT 2631
 QY 861 ArgTyValAsnLeuGluAspAlaSerLeuProGluGluMetCysPheLeuSerLeuAlaAsnLeu 880
 DB 2632 CGCTATTAACAAGAGATGCTTCACTCCCAAGAGAGATGTTCAAAAGCTTGCACAAATCTC 2691
 QY 881 LysTyValAsnIleSerPheTyPheAsnLeuLeuGluLeuProThrSerLeuAlaSer 900
 DB 2692 AAATATCTGAATATCTCTTTTACTTCACTTAAGAGCTGCCCTACAGCTGCTAGT 2751
 QY 901 LeuAsnAlaLeuLeuHisLeuGluIleHisSerCysTyValAlaLeuGluSerLeuProGlu 920
 DB 2752 CTCATGCTTGAAGACATCTGGAATTCATAGTTGTATGACAGTGAAGTCTCCCGAG 2811

QY 921 GlnGlyValIleuGlyLeuIleSerLeuThrGlnLeuSerIleuThrTyrgIleuLeu 940
 DB 2812 GAAGGTGGAAAGGTTTAAATTTCACTACACAGTTATCCATATACATGTAATGCTA 2871
 QY 941 GlnCysLeuProGluGluGluGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPhe 960
 DB 2872 CAATGTTTACCGGAGGATTTGACAGCACCCTTAACAGCTCTCAAAATTAATCAGTTGAGTTT 2931
 QY 961 CysProThrLeuAlaIleArgCysGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 980
 DB 2932 TGTCCAACTGCGCCCAAGCGGTGTGAGAGGGAATGAGAGAACTGTACAAATTTGCT 2991
 QY 981 HisIleProArgValPheIleTyrg 988
 DB 2992 CACATTCCTGCTGTGTTTATTTAT 3015
 DB
 RESULT 2
 ADK98518
 ID ADK98518 standard; DNA; 3595 BP.
 XX
 AC ADK98518;
 DT 03-JUN-2004 (first entry)
 XX
 DE S Bulbocastanum Sbul1 gene genomic DNA sequence SeqID3.
 XX
 KW plant disease resistance polypeptide; solanaceous plant; potato;
 KW late blight disease; fungus; Phytophthora infestans;
 XX conferring pathogen resistance; Sbul1; gene; de.
 OS Solanum bulbocastanum.
 XX
 PH Key Location/Qualifiers
 FT CDS 57..3432
 FT /*tag= a
 FT /product= "S Bulbocastanum Sbul1 protein"
 FT intron 488..899
 FT /*tag= b
 FT
 PM WO2004020594-A2.
 XX
 XX 11-MAR-2004.
 PD
 XX
 PE 28-AUG-2003; 2003WO-US027045.
 XX
 PR 29-AUG-2002; 2002US-0407100P.
 PR 20-AUG-2003; 2003US-00647268.
 XX
 XX (USDA) US SEC OF AGRIC.
 PA (DRYC-) DRY CREEK LAB.
 PA
 XX Osumi T, Belknap WR, Rockhold DR, Maccree MM;
 PI WPI; 2004-239179/22.
 DR P-PSDB; ADK98519.
 DR
 XX
 PT New isolated Solanum bulbocastanum late blight resistance nucleic acid
 PT molecule encoding a plant disease resistance polypeptide, useful for
 PT conferring pathogen resistance to phytophthora infestans in plants.
 XX
 XX Claim 1; SEQ ID NO 3; 103pp; English.
 PS
 CC This invention relates to a novel isolated nucleic acid molecule encoding
 CC a plant disease resistance polypeptide. The preferred plant is a
 CC solanaceous plant that is potato. The resistance is to late blight
 CC disease, caused by the fungus Phytophthora infestans. The invention is
 CC useful for conferring pathogen resistance in plants using a Solanum
 CC bulbocastanum late blight resistance gene. The present sequence is the S
 CC bulbocastanum gene sequence of the invention.
 XX
 SO Sequence 3595 BP; 1139 A; 614 C; 737 G; 1105 T; 0 U; 0 Other;
 Alignment Scores:

Pred. No.: 0 Length: 3595
 Score: 5028.50 Matches: 987
 Percent Similarity: 87.66% Conservative: 0
 Best Local Similarity: 87.66% Mismatches: 1
 Query Match: 98.08% Indels: 138
 DB: 12 Gaps: 1
 US-10-647-268-2 (1-988) x ADK98518 (1-3595)

1 MetAlaGluAlaPheLeuGluValLeuLeuAspAsnLeuThrCysPheIleGlnGlyIu 20
 57 ATGGCTGAAAGCTTCTTCAAGTCTGTAGACAACTGACTGTTTCATCCAGGGGAA 116
 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuLeuGlnSerThrPheThr 40
 117 CTGGATTCATCTTGGTTTAAGATGAGTTCGAAAGACCTTCAAAGCAGCTTTACTA 176
 41 IleglnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsn 60
 177 ATCCAGAGCTGCTGAGAGATGCTCAGAAAGCAATTGAAAGACAGGCAATTGAAAT 236
 61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrgLysAlaAspAspIleLeuAspGluCysLys 80
 237 TGGTTGCAGAACTCAATGCTGCTGCAITAGAGCTGATGACATCTTGACCAATGTAA 296
 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrgLysCysTyrgLysProAsnValIle 100
 297 ACTGAGGCACCAATTAGACAGAAAGAACAAAATGGGTGTATCATCCAAACGTTATC 356
 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
 357 ACTTTTCGCAACAATGGGAAAAGATGAAAAAAGATTATGAGAAACTGATGTAAAT 416
 121 AlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
 417 GCAGGGGAACGAATTAAATTCAATTGATGAAAGACTATAGAGACCAAGTTCCTACA 476
 141 ArgGlnThr----- 143
 477 CGCCAAACAGGTGCTCATCTTAGATATTTTCTGAAAAAAGAGCTTATATCATCAAT 536
 143 ----- 143
 537 CATGTGTTTGGGAATTCGTCTAATCTAAATGTTGCTCAAGCTTAAGTAGATAAGT 596
 143 ----- 143
 597 GAATCCAGCTTGGATTATTATTAATCTATTAGCTAAATCTGTTTAGTGAAGTTTAAAT 656
 143 ----- 143
 657 ATATTAACCTCAGATTAATCATAGCTTAATCATAGATTAGATAGGCCCCCAAGCTTAA 716
 143 ----- 143
 717 ATGACAGATAAACCAGAGTTGTTTAGCTTCTTAATAATTAAATTAACAATGATTAATATG 776
 143 ----- 143
 777 ATTCAAAAAGTGAATTTTAAATTTGAATATTTTCGCTGCTTCAAGCTTATCAT 836
 143 ----- 143
 837 GTCTTTTACTGTGCAAAATTTCTAATTGATTTTGTGCTGATCTTACCGAGCTTGGGCC 896
 144 -GlyPheValLeuAsnGluProGlnValTyrgLysArgAspLysGluLysAspGluIle 163
 897 AGGTTTGTGTTTGAATTAACAACAAGTTTATGAGAGACAAAGAAAAGACAGATAGT 956
 163 IlyPheIleuLysAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGln 183
 957 GAAATTCCTGATTAACAATGTATGCAATGCCCCAAACACTTCCAGTCTCCCAATATCTGG 1016

183 YMetGlyGlyLeuGlnGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIle 203
 1017 TATGGGGGAGCTTAGGAAAGACGACTTGTGCCAAATGGCTTTCATATGACAGAGTAAT 1076
 203 eGluHisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGluLysArgLe 223
 1077 TGAGCATTTCCATCCCAAAATATGATGATTTGTGCTCCGAAAGATTTTATATGAAAGAGGTT 1136
 223 uIleLysGluIleValGluSerIleGluGluLysSerLeuGlyGlyMetAspLeuAlaPr 243
 1137 GATAAAGGAATTTGAGATCTATTTGAAGAAAGATCTAGTGGTGCATGAGACTGGCTCC 1196
 243 OLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrlLeuValLeuAspAs 263
 1197 ACTTCAAAGAGCTTGCGACCTTGCAATGCAAAAAAATATTGCTCGCTTAGATGA 1256
 263 PValTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysValGlyAl 283
 1257 TGTTCGATGATGATCAAGATTAAGTGGGCTAAGTTAAGCAAGTCTTGAAGGTTGAGC 1316
 283 AserGlyAlaSerValLeuThrThrThrArgLeuGluLysValGlySerIleMetGlyTh 303
 1317 AAGTGGGCTTGTGTTTAACTACTCTGCTTGAAGAGTTGATCAATATATGGGAC 1376
 303 rLeuGlnProTyrgLysLeuSerAsnLeuSerGlnLysAspCysTrpLeuPheMetGln 323
 1377 ATTCACACATATGAAATTTGCTCAAGAAATTTGTTGGTTGTTTCATGCA 1436
 323 nArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLysGluI 343
 1437 ACGTCATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGCTATCCGAAAGGAGAT 1496
 343 eValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPh 363
 1497 TGTGAAAAAATGTGTGTGTGCTCTGACAGCTTAAACTTTGGAGATTTTGGCGTT 1556
 363 eLysArgGluGluArgGlnTrpGluHisValArgAspSerGluIleTrpLysLeuProGln 383
 1557 TAAAGAGAGAAAGAACAGTGGGAACATGTGAGATGATGAGATTTGGAAATTTGCTCA 1616
 383 nGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrlHisIleLeuProLeuAspLe 403
 1617 AGAAGAAAGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676
 403 uArgGlnCysPheThrTyrgLysAlaValPheProLysAspThrGluMetGluLysGlyAs 423
 1677 GAGACAAATGCTTTACATATTTGTGCAATATCCCAAGAGATCCGAATGGAAGAGGAAA 1736
 423 nLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGlyAsnLeuGluLeuGln 443
 1737 TCTAATCTCTCTGATGAGCAGATGTTTATTTATCGAAAGAACTTGGAGCTTGA 1796
 443 uAsnValGlyAsnGluValTrpAsnGluLeuTyrlLeuArgSerPhePheGlnGluIleGln 463
 1797 GAATGTAGATTAAGATGAGATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1856
 463 uValLysSerGlyGlnThrTyrgLysMetHisAspLeuIleHisAspLeuAlaThrSe 483
 1857 AGTTAATCTGGTCAAACTTATTTCAAGATGATGATCTCATTCATGATCTGGCAACATC 1916
 483 rLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrl 503
 1917 TCTAATTTGGCAAGCAATCAAGCAGCAATATCCAGAAATTAATTTGTAAGAAATTTACAT 1976
 503 eHisMetSerIleGlyPheThrLysValValSerSerTyrlSerLeuSerHisLeuGln 523
 1977 ACTATGATGCTCATTTGTTTCACTTAAGTGTATCTTTTCTCTTTTCCCACTTGCA 2036
 523 nLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLysGlnLeuProSe 543
 2037 GAAAGTTGTCTGTGAGGGGTCTTAATCTAAGTACATTAATAAATTAAGACATTAACCGTC 2096
 543 rSerIleGlyAspLeuValHisLeuArgTyrlLeuAsnLeuSerGlyAsnThrSerIleAr 563

```

Db      2097 TTCCATTGAGAGTCTAGTACATTAACTTAACCTTGTCTGGCAATACATGATTCG 2156
Qy      553 GSErLeuProaenGlnuCyblyLeuGlnaenleuGlnhThrLeuAapleuHleGlyCy 583
Db      2157 TAGTCTTCCAAACCGATTATGACACCTTCAAAATCTGACAGCTTGTGATCTAATGAGGCTG 2216
Qy      583 sHleuSerLeuCyblyeProlyeGluThrSerlyLeuGlySerLeuAArgaenleu 603
Db      2217 TCATTCACTTTGTTGTTGGCCAAAAGAAACAAAGCAACTTGGTATCTTCCAAATCTTT 2276
Qy      603 uLeuAapGlyCyblyrGlyLeuThrCyblyeProProaGlyleGlySerLeuThrCyblye 623
Db      2277 ACTTGATGGTTCATGATGATTCATCTTGATGCCCAAGAGATGAGATCTTGACATGCTC 2336
Qy      623 uLyethrLeuSerAaGpheValValGlylleglulyslySerCyblyeGlnuGlylule 643
Db      2337 TAAAGCTCTAAGTATGATTGTGTGGGAATTCAGAAAGAAAGTTGTCAACTTGTGTAAT 2396
Qy      643 uArgaenleuAenleuTyrglySerlleglulethrHlsleuGluAArgVallyeAaAs 663
Db      2397 ACGAAACCTGATCTCTATGCTCAATTGAAATCGCATCTTGAGAGATGAGAAATGCA 2456
Qy      663 pMeaAapAlayGlyuAlaAenleuSerAlayGlyuAenleuHlsSerLeuSerMetly 683
Db      2457 TATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGCATGAA 2516
Qy      683 sTrpAapAapAapGlyuAArgProaGlyleTyrglySerGlyuLyValGlyValleuGluAl 703
Db      2517 ATGGGATACAGATGAAACGTCCACGTATATGAAATCAAGAAAGTGAAGGCTTGAAGC 2576
Qy      703 aLeuLyAProHlsSerAenleuThrCyblyeThrlleArgGlyPheaGlylleArgle 723
Db      2577 TCTCAACCAACACTCCATCTGACTTGTTTAAACATCGAGGCTTCAAGAGATCCGCT 2636
Qy      723 uProAapTrpMeaAaenHlsSerValleuLyAaenValyserlleglulieSerCy 743
Db      2637 CCCAGACTGATGATGATCACTGATTTGAAAATGTTGCTCTATGAAATCATCATGTTG 2696
Qy      743 bLyAaenCySerCyblyeProProaGlyluleuProCyblyeLybSerLeuGlyule 763
Db      2697 CAAAAACCTGCTCATGCTTACCAACCTTGTGTGAGCTGCTTGTCAAAAAGCTGACAT 2756
Qy      763 uTrpAArglySerAlayGlyuAlayGlyuValyAapSerGlyPheaProAaArgAaPh 783
Db      2757 ATGGAGGGGGTCTGGGAGATGAGATGATGATTTCTGGATTCCTTACAGAGAGAGTT 2816
Qy      783 eProSerLeuAArglyLeuAenleuAArglyuPheGlyAaenleuLyGlyLeuLeuLyly 803
Db      2817 TCCATCTCTGAGAAACCTTAATATACGGGAATTTGATATCTGAAAGAGATTTGCTGAAA 2876
Qy      803 sGluGlylGluGluGlnCyblyProValleuGluGluGlylleglulieLyCyblyeProMetPh 823
Db      2877 GGAAGGAAAGAGCAATGCCCTGTCTTGAAGAGATTAAGATTAATGTGGCCCTATGTT 2936
Qy      823 eValleuProHrLeuSerSerVallyeLyblyeValyseryAaPlyblyeSerAaAl 843
Db      2937 TGTATTCCAACCCCTTCTCTGTAAGAAATGTGATGTGGGAGCAAGTCAAGATGC 2996
Qy      843 aileGlyPheSerSerleuSerAaenleuMeAlaLeuThrSerLeuGlnleuArgTyAs 863
Db      2997 AATAGGTTTCAAGTTCCATATCTAATCTCATGCTTTACTTCCCTCAAAATTCGTAATA 3056
Qy      863 nLyGlyuAapAlaSerLeuProGluGluMeCPheLySerLeuAlaAenleuLyTyLe 883
Db      3057 CAAGAAAGATGCTTCACTCCAGAAAGAGATGTTCAAAAGCCCTTGAAGATTCCAAAATAC 3116
Qy      883 uAaenleuSerPheTyrrPheaenleuLyGlyuAenleuProHrSerleuAlaSerLeuAaAl 903
Db      3117 GAATATCTCTTTTACTTAATCTTAAGAGAGCTGCTTCCAGCCCTAGTCTCAATGC 3176
Qy      903 aLeuLyHlslyeGluGlylHlsSerCyblyrAlaLeuGlyuSerLeuProGluGlylVa 923

```

```

Db      3177 TTTAAGACATCTGAAATTCATAGTTGATGCACTAGAGAGTCTCCCGAGAGAGTGT 3236
Qy      923 llyeGlyLeuHlsSerLeuThrGlnleuSerlleglulethrTyrcyGlyleuGlnCyblye 943
Db      3237 GAAAGGTTAATTTCACTACACAGTTATTCATATACATACGTGATAAAGCTAACAATGTT 3296
Qy      943 uProGluGlyLeuGlnHlsleuThrAlaLeuThrAaenleuSerValGlyuPheCybProth 963
Db      3297 ACCGAGGAGATTGCAGCACCTTACAGCCCTCACAATTTATCAGTTGTTGCTCAAC 3356
Qy      963 rLeuAlaLyAArgCyblyGlyuGlylleglulyslyAapTrpTyrrlyValHlslePr 983
Db      3357 ACTGGCCAAAGCGGTGTGAGAAAGGAATAGAGAAAGACTGTGACAAATGTCTCAATTC 3416
Qy      983 oArgValPheleTyrr 988
Db      3417 TCGTGTGTTTATTTAT 3432

RESULT 3
ADK98524
ID ADK98524 standard; DNA; 5028 BP.
XX
AC ADK98524;
XX
DT 03-JUN-2004 (first entry)
XX
DE S Bulbocastanum Sbul protein-related chimeric transgene Segid9.
XX
KW plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
XX conferring pathogen resistance; gene; ds; transgenic; Ubi 3 promoter.
XX
OS Solanum bulbocastanum.
XX
CH Chimeric.
XX
Key Location/Qualifiers
FH 1029..4404
FT CDS
FT /*tag= a
FT /product= "S Bulbocastanum Sbul1 protein"
FT intron
FT 1460..1871
FT /*tag= b
PN
PN WO2004020594-A2.
PD
PD 11-MAR-2004.
XX
PF 28-AUG-2003; 2003WO-US027045.
XX
PR 29-AUG-2002; 2002US-0407100P.
PR 20-AUG-2003; 2003US-00647268.
XX
PA (USDA ) US SEC OF AGRIC.
PA (DRYC-) DRY CREEK LAB.
PI
PI Osumi T, Belknap WR, Rockhold DR, Maccree MW;
XX
XX WPI: 2004-239179/22.
XX
XX P-PSDB; ADK98525.
XX
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX molecule encoding a plant disease resistance polypeptide, useful for
XX conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Claim 1; SEQ ID NO 9; 103bp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum
XX bulbocastanum late blight resistance gene. The present sequence is that
XX of a chimeric transgene (Sbul1 gene with a potato Ubi1 promoter sequence)
XX of the invention.

```

XX Sequence 5028 BP; 1647 A; 847 C; 958 G; 1576 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 5028
Score: 5028.50 Matches: 987
Percent Similarity: 87.66% Conservative: 0
Best Local Similarity: 87.66% Mismatches: 1
Query Match: 98.08% Indels: 138
DB: 12 Gaps: 1
US-10-647-268-2 (1-988) x ADR98524 (1-5028)
QY 1 MetcIaGluaIaPheLeuGlnValIleuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 1029 ATGGCTGAAGCTTCTCTCAAGTCTGTTAGCAATCTGACTGTTTCAATCCAGAGGGA 1088
QY 21 LeuGlyLeuIleLeuGlyPheLeysAspGluPheGluIleuGlnSerThrPheThrThr 40
Db 1089 CTTGGATTGATCTTGTTTAAAGATGAGTTCGAAAAGCTTCAAAGCAGCTTACTACA 1148
QY 41 IlegIaIaValIleuGluAspAlaGlnIleuLeysAspIleAlaIleGluAsn 60
Db 1149 ATCCAGCTGTCGTAAGAGATGCTCAGAAAGCAATTGAAGCAGCAATTGAAAAT 1208
QY 61 TrpLeuGlnIleLeuAsnAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 80
Db 1209 TGGTTGCAAGAACTCAATGCTGCTGCTCATATGAGCTGATGACTTTGGACGAATGTAA 1268
QY 81 ThrGluAlaProIleArgGlnIleLeysAsnIleuIleuIleuIleuIleuIleuIleuIle 100
Db 1269 ACTGAGGACCAATTGACAGAAAGAAACAATGAGTGTATCATCCAAACGTATAC 1328
QY 101 ThrPheArgHisIleValIleGlyIleuArgMetIleValIleMetGluLeuLeuAspValIle 120
Db 1329 ACTTTTCGTCACAAATTTGGGAAAGAGATGAAAGATTTAGGAAAATCTAGATGTAAT 1388
QY 121 AlaIa 140
Db 1389 GCAGGGAAACGAATTAAAGTTTCATTGATGAAGACATATAGAGACAAAGTTGCTACA 1448
QY 141 ArgGlnThr----- 143
Db 1449 CGCCAAACAGGTGCTCATAGATATTTTCTGAAAAACAGCTTATATCATCAAAAT 1508
QY 143 ----- 143
Db 1509 CATGTGCTTTGGGAATTCGTATATCTAAATGTTCGTCAAGTCTAAGTAGATAAGT 1568
QY 143 ----- 143
Db 1569 GGATCAGCTTTGATTTATTAATCTATTAATCTGTAATCTGTTTAGTGAAGTTTAAACAT 1628
QY 143 ----- 143
Db 1629 ATATAAACCCTCAGATAATCCATAGCTTACTCATAGATTAGAGATGAGCCCCCAAGTCTAA 1688
QY 143 ----- 143
Db 1689 ATGACAGGATAAACCAGAGTTGTTTAGCTCTTATTAATTAACATGATATAATGTGA 1748
QY 143 ----- 143
Db 1749 ATTCAAAAAAGTCATTTTAAATTTGAATATTTCTGCTGCTTCTCAAGCTTATCATAT 1808
QY 143 ----- 143
Db 1809 GTCTTTTACTGTGCAAAATTTCTACTTTGATTTTTCGTAACCTCTACCGAGCTTGAGCC 1868
QY 144 -GlyPheValIleuAsnGluProGlnValIleuIleuIleuIleuIleuIleuIleuIleu 163
Db 1869 AGGTTTGTCTTTTGAATACCAAGATTTAATGAAAGACAAAGAAAAGACAGATAGT 1928

QY 163 IlyeIleuIleuIleuAsnValIleuAsnAlaGlnThrIleuProValIleuProIleuGln 183
Db 1929 GAAAATCTGTATTAACAATGTTTACCAATGACCAACCTTCACATCTCCCAATACATTTGG 1988
QY 183 YMeCglYglYeuGlyIleuThrThrIleuAlaGlnMetValPheAsnAspGlnArgValIle 203
Db 1989 TATGGGGGGAATTAGAAAGAGACTCTTGCCCAATGTCTTCAATGATCAGAGATGAT 2048
QY 203 eGluHisPheHisProIleValIleGlyValIleGlyValIleGlyValIleGlyValIleGly 223
Db 2049 TGAGCATTTTCCATCCCAAAATATGATATTTGTCTCGGAAGATTTTAATGAAAGAGCTT 2108
QY 223 uIleGlnIleuIleuValGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 243
Db 2109 GATTAAGGAATTTGATGATCTTATTTGAAGAAAGATCTTGAGGCAATGAGCTTGCTCC 2168
QY 243 OleuGlnIleuLeuArgAspLeuLeuAsnGlyIleuIleuIleuIleuIleuIleuIleuIle 263
Db 2169 ACTTCAAAAGAACTTCGGGACTTGCTGAAATGMAAAAAAATATTGCTCGCTTAGATGA 2228
QY 263 pValITrpAsnGluAspGlnAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 283
Db 2229 TGTTTGAAATGAAATGATCAAGATTAAGTGGCTTAAGTCAAGTCTTGAAGGTTGAGC 2288
QY 283 aSerGlyAlaSerValIleuThrThrThrArgLeuGluIleuValGlySerIleMetGlyThr 303
Db 2289 AAGTGGCGCTTCTGTTTAAACCACTACTGCTTGAAGAGTTGATCAATTTGGGAC 2348
QY 303 rLeuGlnProIleuIleuSerAsnLeuSerGlnIleuAspCysTrpLeuLeuPheMetGln 323
Db 2349 ATTGCAACCAATGAAATTTGCAAAATTTGCTCAAGAAAGATTTGTTGTTGTTGATCAGCA 2408
QY 323 nArgAlaPheGlyHisGlnGlnGlnIleuAsnLeuValAlaIleGlyIleuGlyIleuGly 343
Db 2409 ACGTCAATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGCTGCTATGCGAAAGAGAT 2468
QY 343 eValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 363
Db 2469 TGTGAAAAAATGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2528
QY 363 eIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 383
Db 2529 TAAAGAGAAAGAAAGACAGTGGGAAACATGGAAGATGGAAGATTTGGCTCA 2588
QY 383 nGluGlnSerSerIleuProAlaLeuArgLeuSerIleuHisIleuProIleuIleuIleu 403
Db 2589 AGAAGAAAGTTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2648
QY 403 uArgGlnCysPheThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 423
Db 2649 GAGCAATGCTTACATATTTGTCAGATTTCCCAAGGAATACCGAAATGGAAAAAGGAAA 2708
QY 423 nIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 443
Db 2709 TCTAATCTCTCTGAGATGACATGCTTTTATTTATGAAAGAAACTTGGAGCTTAA 2768
QY 443 uAsnValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 463
Db 2769 GAATGATGAGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2828
QY 463 uValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 483
Db 2829 AGTTAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGATGATGATGAT 2888
QY 483 rIleuPheSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 503
Db 2889 TCTAATTTGGGCAAGCAATCAAGCAGCAATATCCCAAGAAATATTTGTAAGAAATTAACAT 2948
QY 503 eHisMetSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 523
Db 2949 ACHATATGATGCTCATTTGTTTCACTTAAAGTGTATCTTCTTCTTCTTCTTCTTCTTCTT 3008
QY 523 nIleuPheValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 543

Db 3009 GAAGTTTCTCGTGGAGGTCCTTAATCTAAGTACATAAACTTAAGCAGTACCGTC 3068
 Qy 543 rSer11eGlyAspLeuVal1H1sleuAArgTyrLeuAsnLeuSerGlyAsnThrSer11eAr 563
 Db 3069 TTCCATTCGGAATCTAGTACATTTAAATTAAGTAACTTAAGTCTGCAATTAATGATTCG 3128
 Qy 563 gSerLeuProAsnGlnLeuCybLeuGlnAsnLeuGlnThrLeuAspLeuH1sGlyCy 583
 Db 3129 TAGCTTCCTCAACCAAGTATTCAGAGCTTCAAATTCGAGACTCTGTATCTACATGCGTCG 3168
 Qy 583 sH1sSerLeuCybLeuProGlyLeuThrSer11eGlyLeuGlnLeuGlnLeuLeu 603
 Db 3189 TCATTCACCTTGTGTTGTCAGAAAAGAAACAAGCAACTGTGAGTCTTCGAAATCTTTT 3248
 Qy 603 uLeuAspGlyCybTyrGlyLeuThrCyMetProProArg11eGlySerLeuThrCyLe 623
 Db 3249 ACTTGATGGTTCATAGGATTCATGATGCAACCAAGATAGGATCTTTGACATGCGCT 3308
 Qy 623 uLysThrLeuSerArgPheVal1Val1Gly11eGlnLysLysSerCybGlnLeuGlyLeu 643
 Db 3309 TTAAGCTTAAGTACATTTGTTGGTGGAAATTCAGAAAGAAAGTTGTCAACTTGGTGAAT 3368
 Qy 643 uArgAsnLeuAsnLeuTyrGlySer11eGln11eThr11sleuGlnuArgVal1LysAsnAs 663
 Db 3369 ACGAAACCTGATCTCTATGGCTCAATTGAATACGCAATCGCATCTTGAGAGATGAAGATGA 3428
 Qy 663 pMetAspAlaLysGlyuAlaAsnLeuSerAlaLysGlyuAsnLeuH1sSerLeuMetLys 683
 Db 3429 TATGGATGCAGAAAGCAATTTATTCGCAAAAGAAATCTGCAATCTTTAAGATGAA 3488
 Qy 683 sTrpAspAspAspGluArgProArg11eTyrGlnSerGlnLysVal1GluVal1LeuGlnAl 703
 Db 3489 ATGGAGATGACATGACATCCATCGATATATGATGATCAAGAAAGTTGAAGTCTTGAAAGC 3548
 Qy 703 aLeuLysProH1sSerAsnLeuThrCybLeuThr11eArgGlyPheArgGly11eArgLe 723
 Db 3549 TCTCAACCAACATCCATCTGACTTGTTTAAACATCAAGGCGCTCAAGGAATCCGCT 3608
 Qy 723 uProAspTrpMetAsnH1sSerVal1LeuLysAsnVal1AspSer11eGln11eLysSerCy 743
 Db 3609 CCCAGACTGATGATCACTCACTGATTTGAAAAATGTTCTCTATTTGAATCATCATGATG 3668
 Qy 743 sLysAsnCybSerCybLeuProProPheGlyGlnLeuProCybLeuLysSerLeuGlnLe 763
 Db 3669 CAAATACTGCTCACTGCTTACCACTTGTGAGCTGCTTGTCTTAAAAAGTCTAGAGTT 3728
 Qy 763 uTrpArgGlySerAlaGlnuVal1GluTyrVal1AspSerGlyPheProThrArgArgArgPh 783
 Db 3729 ATGAGAGGGGCTCTGCGGAAGTGAAGTATGTTCTGATTTCCCTACAAAGAAAGGTT 3788
 Qy 783 eProSerLeuArgLysLeuAsn11eArgGlnPheGlyAsnLeuLysGlyLeuLeuLysLys 803
 Db 3789 TCCATCTCTGAGAAAACTTAATATATACGCAATTTGATATCTGAAGGATTCGTAAGAAA 3848
 Qy 803 sGlnGlyGlnGlnGlnCybProVal1LeuGlnGln11eGln11eLysCybCybProMetPh 823
 Db 3849 GGAAGGAGAAAGCAATGCCCTGCTTGAAGAGATGAAGATTAATTTGCCCTATGTT 3908
 Qy 823 eVal11eProThrLeuSerSerVal1LysLysLeuVal1AspSerGlyAspLysSerAspAl 843
 Db 3909 TGTATTCCTCAACCTCTTCTCTGTCAGAAATTTGTTATTTAGTGGGCAAGTCAAGATGC 3968
 Qy 843 a11eGlyPheSerSer11eSerAsnLeuMetAlaLeuThrSerLeuGln11eArgTyrAs 863
 Db 3969 AATAGGTTTCAGTTCATATCTAATCTCATGCTTCTTCCCTCCAAATTCGCTATAAA 4028
 Qy 863 nLysGlnuAspAlaSerLeuProGlnuMetPheLysSerLeu11aAsnLeuLysTyrLe 883
 Db 4029 CAAAGAAATGCTTCACTCCAGAAAGATGTTCAAAGCCCTGCAAAATTCCAAAATACTT 4088
 Qy 883 uAsn11eSerPheTyrPheAsnLeuLysGlnuLeuProThrSerLeuAlaSerLeuAsnAl 903

Db 4089 GAATATCTCTTTTACTTCATCTTAAAGAGCTCCCTACAGCCTGCTACTTCATGTC 4148
 Qy 903 aLeuLysH1sLeuGln11eH1sSerCybTyrAlaLeuGlnuSerLeuProGlnuGlyVal 923
 Db 4149 TTTAAGCATCTGAAATTCATATGTTTATGCTATGAGAGTCTCCCGAGAAAGTCT 4208
 Qy 923 LysGlyLeuL1sSerLeuThrGlnLeuSer11eThrTyrCybGlnuMetLeuGlnCyLe 943
 Db 4209 GAAAGTTTATTTCACTCAACAGATTATCCATATACATGTAAGTGAATGCTACAAATGTTT 4268
 Qy 943 uProGlnGlyLeuGlnH1sleuThrAlaLeuThrAsnLeuSerVal1GlnPheCybProth 963
 Db 4269 ACCGAGAGATTCGACGACCTTAACAGCCCTCAAAATTTATCAGTTTGTTCACAC 4328
 Qy 963 rLeuAlaLysArgCybGlnuLysGly11eGlyLysAspTrpTyr11eAlaH1s11ePr 983
 Db 4329 ACTGGCCAGCGGCTGTAGAGAGGAAATAGAGAAAGACTGTGTACAAATTTGCTCACATTC 4388
 Qy 983 cArgValPhe11eTyr 988
 Db 4389 TCGTGTGTTATTTAT 4404
 RESULT 4
 ID ADK98520 standard; DNA; 3347 BP.
 XX ADK98520;
 AC ADK98520;
 XX 03-JUN-2004 (first entry)
 DT
 XX
 DE S Bulbocastanum Sbul2 gene sequence SeqID5.
 XX
 KW plant disease resistance polypeptide; solanaceous plant; potato;
 KW late blight disease; fungus; Phytophthora infestans;
 KW conferring pathogen resistance; Sbul2; gene; ds.
 OS Solanum bulbocastanum.
 XX
 FH Key Location/Qualifiers
 FT CDS 57..3344
 FT /*tag= a
 FT /product= "S Bulbocastanum Sbul2 protein"
 FT 510..788
 FT intron /*tag= b
 XX
 XX WO2004020594-A2.
 XX
 XX 11-MAR-2004.
 XX
 XX PD
 XX 28-AUG-2003; 2003WO-US027045.
 XX
 XX PF
 XX 29-AUG-2002; 2002US-0407100P.
 XX PR 20-AUG-2003; 2003US-00647268.
 XX
 XX PA (USDA) US SEC OF AGRIC.
 XX (DRYC-) DRY CREEK LAB.
 XX
 XX PA
 XX Osumi T, Belknap WR, Rockhold DR, Maccree MM;
 XX
 XX PI
 XX WPI; 2004-239179/22.
 XX DR P-PSDB; ADK98521.
 XX
 XX PT New isolated Solanum bulbocastanum late blight resistance nucleic acid
 XX molecule encoding a plant disease resistance polypeptide, useful for
 XX conferring pathogen resistance to Phytophthora infestans in plants.
 XX
 XX PS Example; SEQ ID NO 5; 103bp; English.
 XX
 CC This invention relates to a novel isolated nucleic acid molecule encoding
 CC a plant disease resistance polypeptide. The preferred plant is a
 CC solanaceous plant that is potato. The resistance is to late blight
 CC disease, caused by the fungus Phytophthora infestans. The invention is
 CC useful for conferring pathogen resistance in plants using a Solanum

CC buldocastanum late blight resistance gene. The present sequence is the S
CC buldocastanum Sbul 2 gene sequence which was used in the exemplification
CC of the invention.

XX Sequence 3347 BP; 1070 A; 577 C; 693 G; 1007 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3347
Score:	4475.00	Matches:	883
Percent Similarity:	83.94%	Conservative:	37
Best Local Similarity:	80.57%	Mismatches:	66
Query Match:	87.28%	Indels:	110
DB:	12	Gaps:	2

US-10-647-268-2 (1-988) x ADK98520 (1-3347)

```
OY 1 MetAlaGluAlaPheLeuGlnValLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 57 ATGGCTGAAGCTTCTTCCTCAAGTTCTGTAGACATCTGACTTGTTCATCCAAAGGGA 116
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGlyLeuGlnSerThrPheThrThr 40
Db 117 GTGGATTGATTTCTGGTTTAAAGATGAGTTGCAAAAGCTTCAAAAGCACATTTACTACA 176
OY 41 ILeuGlnAlaValLeuGlnAspAlaGlnLysGlnLeuLysAspLysAlaIleGlnLysn 60
Db 177 ATCCAAAGCTGGCTCTGAAGATGCTCAGAAAGCAATTTGAAGGACAAAGCATAGAAAT 236
OY 61 TTPLeuGlnLysLeuAsnAlaAlaAlaIleArgGluAlaAspAspIleLeuAspGluCysLys 80
Db 237 TGGTTGCGAAACCTCAATGCTGCTGTATATGAAAGCTGACGACATCTTGCAAGAAATGTAAA 296
OY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
Db 297 ACTGAGGACCAATTTAGACAGAAAGAACAAATTTGGGTCTTATCATCCAAAGCTTATC 356
OY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlnLysLeuAspValIle 120
Db 357 GCTTTCCTGCACAAAGATTGGGAAAAAGATGAAAAAATTTATGGAATCTGATGTATT 416
OY 121 AlaAlaGluArgIleLysPheHisLeuAspGluLysThrIleGlnLysGlnValAlaThr 140
Db 417 GCAGGGGAAACGAATTAAGTTTCATTTGGCTGAAAGACTACAGAGACAAAGTTGTCTACA 476
OY 141 ArgGlnThr----- 143
Db 477 CGCCAAACAGGTGCTCATCTTAGATATTTTCTAAAAAACAAGCTTATATCATGAATTT 536
OY 143 ----- 143
Db 537 CATGTGCTTTGGGATTTTCTTAATCTAAATGTTGCTCAAGCTTAAGTAAAGTGG 596
OY 143 ----- 143
Db 597 ATCCAAATTTGGATATATTAATATTAATTAATCTAAATTTGTTTCTGAAATTTTAAACAGAT 656
OY 143 ----- 143
Db 657 AAAGCTGAGTTGTTTAAACATTATAAATTAAACAATGATTAATAATGGAATTCAAAAA 716
OY 143 ----- 143
Db 717 GTGCATTATGTCGTGCTCTCTCAAGCTTATCATGTCTCTTTATTTGCAAAATTTCTTC 776
OY 144 ----- 144
Db 777 TTGCTTTTTCGCTGACTCTCTACTGAGCTTGGACCAAGTTTGTGTTTAAATGAACCAAA 836
OY 152 ValTyrGlyArgAspLysGlnLysAspGluIleValLysIleLeuIleAsnValSer 171
Db 837 GTTATGAGAGAGACAAAGAAAGATGAGATGTAAGAAATCCGATTAATCAATTTGTTAGC 896
OY 172 AsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyLeuGlyLysThrThr 191
```

```
Db 897 GATGCCCAACACATTTCAATCTCCCAATTAATCTGGTATGGGGGATTAAGAAACACACA 956
OY 192 LeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrp 211
Db 957 CTTGCCCAATATGCTTCAATGATCAGAGATATTAAGCATTTTCTTCCAAAATATGG 1016
OY 212 IleCysValSerGlnAspPheAsnGlnLysArgLeuIleLysGluIleValGlnSerIle 231
Db 1017 ATTTGTCTTCGAAAGATTTTAAATGAGAAAGAGTTGATTAAGAAATTTGATGATCTATT 1076
OY 232 GlnGlnLysSerLeuGlnGlyMetAspLeuAlaProLeuGlnLysLysLeuAspAspLeu 251
Db 1077 GAAGAAAAGTCACCTTGTCACATGAGACTTGCTCCACTTCAAAAGAACTTTCAGGACTTG 1136
OY 252 LeuAsnGlnLysLysTyrLeuLeuValLeuAspAspValTrpAsnGlnLysAspLys 271
Db 1137 CTGAATGCAAAAAAATTTTGTCTTGTAGATGATTTTGAATGAAGATCAAGATTAAG 1196
OY 272 TrpAlaLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThr 291
Db 1197 TGGGCTAAGTTACGAGAAAGTTGAAGTTGAGCAAGTGCTCTTATCTTAACTAACACT 1256
OY 292 ThrArgLeuGlnLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLeuSerAsn 311
Db 1257 ACTGCTTTGAAAAGCTTGAGATCAATTAATGCAAACTTTGACCAATTAATGATTTGTTCAAC 1316
OY 312 LeuSerGlnGlnLysAspTyrTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGln 331
Db 1317 TTGTGTCAAAAGATGCTGCTGGTTGGTTGTTTCATCAACGTCATTTGGGACCAAGAAAGAA 1376
OY 332 IleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLysCysGlnGlyValPro 351
Db 1377 ATTAATATTAATCTTTGGCTTATCGAAAGAGATTTGTAAGAAAGATGGTGATGGCT 1436
OY 352 LeuAlaAlaLysThrLeuGlnGlyIleLeuArgPheLysArgGlnLysArgGlnTrpGln 371
Db 1437 CTAGCAGCTTAAACTCTTGAGGATATTTGGCATTCACAGACACAAAGAACAGCTGGGAA 1496
OY 372 HisValArgAspSerGlnIleTrpLysLeuProGlnGlnLysSerIleLeuProAla 391
Db 1497 CATGTAGAGATGTGATGATTTGGAAATTTGCCCAAGAAAGTTCATTTGCCGGGCC 1556
OY 392 LeuArgLeuSerTyrHisLysLeuProLeuAspLeuArgLysPheThrTyrCysAla 411
Db 1557 CTGAACCTTAGTACATCATCTTCCACTTGATTTAGACAAATGCTTTTCATATTTGCA 1616
OY 412 ValPheProLysAspThrGlnMetGlnLysGlyAsnLeuIleSerLeuTrpMetAlaHis 431
Db 1617 GATATCCCAAGAGATACCAAAATGAAAGAAATCTAATCTCTCTGATGGACAT 1676
OY 432 GlyPheIleLeuSerLysGlyAsnLeuGlnLysAsnValGlyAsnGlnValTrpAsn 451
Db 1677 GGTTCCTTTTACGAAAGAACTTGAGCTTGAAGATGAGTATTAAGATATGGAAT 1736
OY 452 GlnLeuTyrLeuArgSerPhePheGlnGlnIleGlnValLysSerGlyGlnThrTyrPhe 471
Db 1737 GAATTAATCTTGAAGCTTCTTCTTCCAAAGATTTGAAGTTACATATGATAAATCTATTTTC 1796
OY 472 LysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSer 491
Db 1797 AAGATCATGATCTCATCATGATTTGGCTACATCTCTATTTTGGCAAGCCGATCAAGC 1856
OY 492 SerAsnIleArgGlnIleIleValGlnAsnTyrIleHisMetMetSerIleGlyPheThr 511
Db 1857 AACAAATATCCGTAAGAAATTAATGTAAGGTTAACCAATATATATGTCGATTTGGCTTGA 1916
OY 512 LysValIleSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeu 531
Db 1917 AAAGTGCTCTTTTACTCTGCTTCTCACTCCAAAAGTTTGCTCGTTAAGGATGCTT 1976
OY 532 AsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeu 551
```

```

Db 1977 AATCTAAGTAACTAGAACTCAGACGATTCCATCTTCACATTTGGGATCTAGTACATTTA 2036
Qy ArgTyrLeuAenLeuSerGlyYasnThrSerIleArgSerLeuProAenGlnLeuCysIlys 571
Db 2037 AGATACCTTAACCTTGTCTGACAAATAATAGAAATTCCTAGCTTCCAGACAGTATGCAAG 2096
Qy 572 LeuGlnAenLeuGlnThrLeuAenLeuHISGlyCysHISerLeuCysLeuProIlys 591
Db 2097 CTTCAAAATCTGCAGACCTTGTATCTACGTTGTCTGACAGACTTCTGTGTTGGCAAAA 2156
Qy 592 GlnThrSerIlybLeuGlySerLeuAenLeuLeuAenAenGlyCysArgIlyLeuThr 611
Db 2157 GAAAACACCAACTTGTAGTCTCCGAAATCTTTACTGATCGTTGCCATGAGATGACT 2216
Qy 612 CysMetProProArgIleGlySerLeuThrCysLeuIysThrLeuSerArgPheValVal 631
Db 2217 TGTATGCCACCAAGATAGATCATTTGATCCCTTAAAGACTTGAATCGCTTTCCAATG 2276
Qy 632 GlyIleGlnIlybSerCysGlnLeuGlyGlnLeuAenLeuAenLeuTyGlySer 651
Db 2277 GGA---AGGAGAGAAAGTCTCAATGTGTAATTACGAAACCTGAATCTGTATGCTCA 2333
Qy 652 IlegIuIleThrHISLeuGlnArgValIlybAenAenMetAenPalaIlyGlnAenLeu 671
Db 2334 ATTCAATCACCGCATCTTGAGAGATGAAAGATGATGATGAAAGAAAGCCCAATTTA 2393
Qy 672 SerAlaIlybGlnAenLeuHISerLeuSerMetIlybTPAenAenAenGlnAenProArg 691
Db 2394 TCTTCAAAAGAAATCTGATCTTTAAAGATGATGAGATGAGAAAGATGAAAGCTCAAT 2453
Qy 692 IleyrGlnSerGlnIlybValGlnValIleuGlnAenLeuIysProHISerAenLeuThr 711
Db 2454 AGATATGATACGAGAGATGTTGAAGTGTGAGAGCTCAAAACCACTCCATCTGACT 2513
Qy 712 CysLeuThrIleArgGlyPheArgGlyIleArgLeuProArgTPMetAenHISerVal 731
Db 2514 TGTTTAACAAATTAATGGCTTCAGAGAAATCCGCTCCACAGCTGATGAATCACTCACTT 2573
Qy 732 LeuIysAenValIleSerIlegIuIleIleSerCysIysAenCysSerCysLeuProPro 751
Db 2574 TTGAAAAATGTGTCTCTTGAATTCAGCCATTCGAAATCTGCTACAGCTTACACCC 2633
Qy 752 PheGlyGlnLeuProCysLeuIysSerLeuGlnLeuIleTPArgGlySerAlaGlnValGln 771
Db 2634 TTTGGTGAAGTCCCTGTCTAATAGTCTACAGTATGAGAGGCTCGCAGAGTGAAG 2693
Qy 772 TyrValAenPserGlyPheProThrArgArgPheProSerLeuArgIlybLeuAenIle 791
Db 2694 TATATGATTCGTGATTCCTTAAGAAAGAGTTTCCATCTCGAGAAACTTATATA 2753
Qy 792 ArgGlnPheGlyAenLeuIlybGlyLeuLeuIlybGlyGlnGlnCysProVal 811
Db 2754 GGCGAATTTGTAATCTAAGAGATGTGTGAAAGAAAGAAAGAAAGCAATTCCTGTG 2813
Qy 812 LeuGlnGlnIleGlnIleIysCysPserMetPheValIleProThrLeuSerSerVal 831
Db 2814 CTTGAGAGAGATGAGATTAACGTGGCCCTATGTTTGTATTCGACCCCTTCTCTGTC 2873
Qy 832 LysIlybLeuValIleSerGlyAenIlybSerAenPalaIleGlyPheSerSerIleSerAen 851
Db 2874 AACCAATTTGTAATGTGAGAGAGATGAGATGCAATGAGCTTCATCTCATATCTAAT 2933
Qy 852 LeuMetAlaLeuThrSerLeuGlnIleArgIlybAenIlybGlnAenPalaIleSerLeuProGln 871
Db 2934 CTCAGAGGCTTACTTCTCTCAATTAAGCTTAATCTGAAAGCTACTTCCCAAA 2993
Qy 872 GlnMetPheIysSerLeuAlaAenLeuIysTyrLeuAenIleSerPheTyrPheAenLeu 891
Db 2994 GAGATGTTCAAAAGCTTCGAAATCTAATAATCTTGAATATCTATATTCTCAAGATGTC 3053
Qy 892 LysGlnLeuProThrSerLeuAlaSerLeuAenAlaLeuIlybHISerLeuGlnIleHISer 911
Db 3054 AAAGAGCTGCTACCAACCTGGCTGTATGCTTGAAGAAATCTGGAATTTGAAGT 3113

```

```

Qy 912 CysTyrAlaLeuGlnSerLeuProGlnGlnIlybValIysGlyLeuIleSerLeuThrGln 931
Db 3114 TGTATGACATGAGAGATCTCCGAGAGAGTGTGAAAGGTTTAATCTTACCTTACACA 3173
Qy 932 LeuSerIleThrTyrCysGlnMetLeuGlnCysLeuProGlnGlyIlybLeuHISerLeu 951
Db 3174 TTATCCATTAACATCTGCACGATCTCAATGTTTATCGGAGGATTCGACACCTTAACA 3233
Qy 952 AlaLeuThrAenLeuSerValGlnPheCysProThrLeuAlaIlybArgCysGlnIlybGly 971
Db 3234 GCCCTCAAAATTTATCACTTGAAGATGTCAACACTGGCCCAAGCTGTGAGAGAGGA 3293
Qy 972 IlegIyGlnAenTPTyTyrIlybAlaHISerProArgValPheIle 987
Db 3294 ATAGAGAGACTGTGTAACAAATTTGCTCACATCTCTGATGTGTTATC 3341

RESULT 5
ADP17759
ID ADP17759 standard; DNA; 2913 BP.
XX
XX
XX ADP17759;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX DE Solanum bulbocastanum Rpi-b1b DNA sequence.
XX
XX gene, ds; Rpi-b1b; Rpi-b1b gene cluster; growth regulant;
KM oomycete infection; introgression breeding; plant; late blight.
XX
XX Solanum bulbocastanum.
XX
XX OS
XX FH
XX Key 1. .2913
FT CDS /*tag= a
FT /product= "Rpi-b1b protein"
XX
XX
XX EP1334979-A1.
XX
XX PD 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX PF 08-FEB-2002; 2002EP-00075565.
XX
XX PR 08-FEB-2002; 2002EP-00075565.
XX
XX
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
XX
XX PA
XX PI Van Der Vossen BAG, Allefs JHM;
XX
XX DR MPI: 2003-714439/68.
XX
XX DR P-PSDB: ADP17765.
XX
XX
XX PT New resistance gene conferring resistance against an oomycete pathogen,
PT useful for producing plants, especially potatoes and tomatoes, resistant
PT against oomycete pathogens such as Phytophthora infestans.
XX
XX
XX Example 5; SEQ ID NO 35; 86pp; English.
XX
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
XX described as plant growth regulants. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b DNA of
XX the invention.

```

```
XX SQ Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,796-314 Length: 2913
Score: 3766.50 Matches: 753
Percent Similarity: 83.43% Conservative: 78
Best Local Similarity: 75.60% Mismatches: 130
Query Match: 73.46% Indels: 35
DB: 10 Gaps: 8
US-10-647-268-2 (1-988) x ADF17759 (1-2913)
OY 1 MetalagluAlaPheLeuGlnValLeuAspAsnLeuThrCysPheIleGlnIleGlu 20
DB 1 ATGGGTGAAGCTTTCATTCAAGTTCCTAGAGCAATCTCACTTCTTCTCAAGGGAA 60
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThr 40
DB 61 CTGTGATTGCTTTTGGTTTCAAGATGAGTTCAGAGGCTTTCAGCATGTTTCTACA 120
OY 41 IleglnAlaValLeuGlnAspAlaGlnIleGluLeuLeuAspGluAlaIleGln 60
DB 121 ATTCAGCGCTTCCTTGAAGATGCTCAGAGAGCAACTCAACAGCAAGCTCTAGAAAT 180
OY 61 TryLeuGlnIleLeuAsnAlaAlaIleTyrGlnIleAspAspIleLeuAspGluCys 80
DB 181 TGGTTGCAAAAACCTCAATGCTGCTCATATGAGTCGATGACATCTTGGAATATATA 240
OY 81 ThrGluAlaProIleArgGlnIleLeuAsnIleTyrGlyCysTyrHisProAsnVal 100
DB 241 ACCAAGGCC--ACAAAGATTCTCCAGCTGAATGAGCCGTTATCATCCAAAGGTATC 297
OY 101 ThrPheArgHisIleGlyLeuAspMetLeuIleMetGluLeuLeuAspValIle 120
DB 298 CCTTTCCTGCACAAAGTCGAGAAAGATGACCAAGATGAAAGAACTAAAGGCAATT 357
OY 121 AlaAlaGluArgIleLeuPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
DB 358 GCTGAGGAAAGAAAGAAATTTTCATTGTCACGAAAAAATGTAGAGAGCAAGCTGTAGA 417
OY 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValTyrGlyArgAspLeuGluAsp 160
DB 418 CGGAAACAGAGTTCGTATTACCGAACCCGAGGTTATGGAAGAAGCAAGAAAGAT 477
OY 161 GluIleValIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
DB 478 GAGATAGTGAATAATCTTAATAAACAATGTAGATGCCCCAACCTTTCAGTCCCTCCA 537
OY 181 IleLeuGlyMetGlyLeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGln 200
DB 538 ATACTGGGTATGGGGGAGTTAGGAAAAACGACTCTGCGCAAAAGCTTTCATAGACAG 597
OY 201 ArgValIleGluHisPheHisProLeuIleTyrIleCysValSerGluAspPheAsnGlu 220
DB 598 AGAGTTTCTGAGCAATTCATTCCAAAATATGATGTTGTGTCTGGAAGATTTTGAGAG 657
OY 221 LysArgLeuIleLeuGluIleValGlnSerIleGluGluLeuSer---LeuGlyGlyMet 239
DB 658 AAGAGGTAAATAAAGGCAATGTAGAAATCTAATTAAGAGAGGCACTAATGGTGAATG 717
OY 240 AspLeuAlaProLeuGlnIleLeuAspLeuAspLeuLeuAsnGlyLeuLeuLeu 259
DB 718 GACTTGGCTCACTTCAAAAGAACCTTCAGAGATGTCGTAATGAAAAAGATCTTCTT 777
OY 260 ValLeuAspAspValTyrAsnGluAspGluAspLeuTyrAlaIleLeuValLeu 279
DB 778 GTCTTATAGATGATGTTGGAATGAAAGATCAACAGAGGCGCTAATTAAAGAGCAGTCTG 837
OY 280 LysValGlyIleAspGlyAlaSerValLeuThrThrArgLeuGluLeuValGlySer 299
DB 838 AAGGTGGAGCAGAGTGCTTCTGTCTTAAACACTACTGCTTGAAGAGTTGATCA 897
OY 300 IleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnIleAspCysThrLeu 319
DB 898 ATTATGGACATATGCAACCATATGAACTGTCAAAATCTGTCTCAAGAAAGATGTGGTG 957
OY 320 LeuPheMetGlnArgAlaPheGlyHisGlnIleGluIleAsnLeuAsnLeuValAlaIle 339
DB 958 TTGTTTCATGCAACGTGATTTTGACACCAAGAAATAATTCAAACCTGTGGCAATC 1017
OY 340 GlyLeuGluIleValIleLeuLeuGlyValAlaProLeuAlaAlaIleThrLeuGlyGly 359
DB 1018 GAAAAAGAGATTGAAAAAAAGTGGTGCTGTCTTACAGCCCAAACTCTTGAGGT 1077
OY 360 IleLeuArgPheLeuAspGluGluArgIleTyrGlnIleValIleArgAspSerGluIleTyr 379
DB 1078 ATTTTGCTTCAAGAGAGAAAGAAAGCAATGGGAAACATGTGAGAGACAGTCCGATTTGG 1137
OY 380 LysLeuProGlnIleGlnSerSerIleLeuProAlaLeuArgLeuSerTyrHisIleLeu 399
DB 1138 AATTGGCTCAAGATGAAGTTCATATCTGCTGCTGAGGCTTATGATTCATCAACTT 1197
OY 400 ProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMet 419
DB 1198 CCACCTGATTTGAAACATGCTTGGCGATTTGGCGGTGTTCCTCAAGAGATGCCAAATG 1257
OY 420 GluLeuGlyAsnLeuIleSerLeuTyrPheAlaHisGlyPheIleLeuSerIleGlyAsn 439
DB 1258 GAAAAAAGAAAGCAATCTCTCTGATGCGCATGCTTTCTTTATCAAAAAGAAAC 1317
OY 440 LeuGluLeuGlnAsnValIleGluGlnValTyrAsnGluLeuTyrLeuArgSerPhe 459
DB 1318 ATGAGGCTGAGAGATGGGCGATGAGATGAGAAAGAAATTAATATCACTGATCTTTTTC 1377
OY 460 GlnGluIleGluValIleLeuSerGlyGlnThrTyrPheLeuMetHisAspLeuIleHisAsp 479
DB 1378 CAAGAGATTAGATTAAAGATGGTAAATCTTATTTCAAGATGATGATTCATCATGAT 1437
OY 480 LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleVal 499
DB 1438 TTGGCAACATCTCTGTTTACGAAACACATCAAGAGCAATTCGTAATAATAATAA 1497
OY 500 GluAsnTyrIleHisMetMetSerIleGlyPheThrIleValIleSerTyrSerLeu 519
DB 1498 CACAGTTACACACATATGATGATCATATGCTGTTGCGCAAGTGTGTGTTTTCACCTTT 1557
OY 520 SerHisLeuGlnIlePheValSerLeuArgValLeuAsnLeuSerAspIleLeuLeu 539
DB 1558 CCCCCCTGGAAAAAGTTTATCTGTTAAGAGTCTTAATCTAGCTGATGACATTTAAT 1617
OY 540 GlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsn 559
DB 1618 AAGTTACCATCTTCCATTTGAGATCTAGTACATTTAAGATTAATGAACTGTATGTC-- 1674
OY 560 ThrSerIleArgSerLeuProAsnGlnLeuCysGlyLeuGlnAsnLeuGlnThrLeuAsp 579
DB 1675 AGTGGCATGTGTGCTTCCAAAGCAGTTATGCAACCTTCMAAATCTGCMAACTCTTGAT 1734
OY 580 LeuHisGlyCysHisSerLeuCysGlyLeuProGlyGlnThrSerIleLeuGlySerLeu 599
DB 1735 CTACATATTTGCAACCAAGCTTTGTGTGTCGCAAAAGAAACAATGAATCTGTGATGCTC 1794
OY 600 ArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySer 619
DB 1795 CGAAATCTTTTACTTATGATGATGACCGATTCATTTGATGATGCAACAGAGATGATCA 1854
OY 620 LeuThrCysLeuIleThrLeuSerArgPheValValGlyIleGlnIleLeuLeuSerGln 639
DB 1855 TTGACATGCTTAAAGCTCTAGGTCAATTTGTGTGTGA--AGGAAGAAAGGTTATCA 1911
OY 640 LeuGlyGluLeuArgAsnLeuLeuTyrGlySerIleGluIleThrHisLeuGluArg 659
DB 1912 CTGTGGAATGAGAAACCTTAATCTTATGCTCATTAATAATCTCGCATCTTGAGAA 1971
OY 660 ValIleAsnAspMetAspAlaIleGluAlaAsnLeuSerAlaIleGlyGluAsnLeuHisSer 679
```



```

Db      1972 GTGAAGAAATGATPAGACGCAAAAGACATTTATCTGCAAAAGGAAATCTGCATCT 2031
Qy      660 LeuserMeLysTPRAspAspGluArgProArgIleYrGluSerGluValGlu 699
Db      2032 TTACACATGAGTTGG--AAATACCTTTGGACACATATATATGAAATCGAAGAACTTAA 2088
Qy      700 ValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArg 719
Db      2089 GTGCTTGAAGCCCTCAAAACACATCCATCTGATCTTCTTAAATCATATGCTTCA 2148
Qy      720 GlyIleArgLeuProAspTTPMeLanHisSerValLeuLysAsnValValSerIleGlu 739
Db      2149 GGAATCCATCTCCACAGAGTGATGATCATCATGATGAAATAATATGTCTATCTCA 2208
Qy      740 IleIleSerCysLysAsnCysSerCysLeuProPheGlyGluLeuProCysLeuLys 759
Db      2209 ATTGCAACTTCAGAACTGCTCATGCTTACCACTTGTGGATCTGCTGTCTAGAA 2268
Qy      760 SerLeuGluLeuThrArgGlySerIleGluValGluIleValAsp----- 774
Db      2269 AGTCTAGAGTTACACTGGGGGCTCTCGGATGTGAGTATGTTGAAGAAGTGATTTGAT 2328
Qy      775 -----SerGlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIleArg 792
Db      2329 GTTCATCTGATTCCTCCACAAAGATAAGTTTCATCTTGAGGAACCTTGATATATGG 2388
Qy      793 GluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGluGluCysProValLeu 812
Db      2389 GACTTGTGTAGCTGAAAGATGCTGTAAGAAAGAAAGAAAGCAATTCCTGTGTCTT 2448
Qy      813 GluGluIleGluIleLysCysCysProMetPheValIleProThrLeuSerSerValLys 832
Db      2449 GAAGAGATGATATATTCAGAGATGCCCTTTCTG-----ACCTTTCT----- 2490
Qy      833 LysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeu 852
Db      2491 -----TCTAATCTT 2499
Qy      853 MetAlaLeuThrSerLeuGluIleArgTyrAsnLysGluAspAlaSerLeuProGluGlu 872
Db      2500 AGGCTCTTACTTCCCTCAGAAATTTGCTATATTAAGTACTTCTCCAGAAAG 2559
Qy      873 MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
Db      2560 ATGTTCAAAAACCTTGCAATCTCAAAATCTTGACAATCTTCGGTGCATATATCTCAA 2619
Qy      893 GluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCys 912
Db      2620 GAGCTGCTTACAGCTTGGTCTAGTCTGAATGCTTTGAAAAGCTTAAATTCATTTGTGT 2679
Qy      913 TyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGluLeu 932
Db      2680 TGCCGCACTAGAGATCTCCCTCAGAGAAAGGCTGAAAGGTTTATCTTCACTCACAAGTTA 2739
Qy      933 SerIleThrTyrCysGluMetLeuGluCysLeuProGluGluLysLeuGluHisLeuThrAla 952
Db      2740 TTTGTTGAACCTGTAACATCTAAATATGTTTACAGAGGGAATGACACCTTAACACC 2799
Qy      953 LeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIle 972
Db      2800 CTCACAAGTTAAAAAATTCGGGAGATGTCACAACAATGATCAAGCGGTGTGAAGAGGATA 2859
Qy      973 GlyLysAspTTPYrLysIleAlaHisIleProArgValPheIleTyr 988
Db      2860 GGAGAAGACTGGCACAATAATTTCTCACTTCTAATGTGAATATATAT 2907

```

RESULT 6
 ADH51531 standard; DNA; 2913 BP.
 ID ADH51531
 AC ADH51531;

```

DT      25-MAR-2004 (first entry)
DE      XX
XX      S bulbocastanum Rpi-b1b gene SeqId48.
XX      plant disease; oomycete infection; Phytophthora infestans; fungicide;
XX      Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
XX      ds.
OS      Solanum bulbocastanum.
XX      XX
XX      US2003221215-A1.
XX      27-NOV-2003.
XX      07-FEB-2003; 2003US-00360522.
XX      07-FEB-2003; 2003US-00360522.
XX      (KWE-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX      Allele JHM, Van Der Vossen EAG;
XX      WPI; 2004-010903/01.
XX      DR P-PSDB; ADH51537.
XX      PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
XX      for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX      with resistance against oomycete infection.
XX      Claim 6; SEQ ID NO 48; 98bp; English.
XX      CC
XX      CC This invention relates to a novel DNA sequence in the field of plant
XX      CC disease, in particular oomycete infections. The DNA sequence encodes a
XX      CC protein which may provide a plant or its progeny with at least partial
XX      CC resistance against an oomycete infection caused by Phytophthora
XX      CC infestans. The invention may be useful for the development of compounds
XX      CC with a fungicide activity. The DNA sequence of the invention encodes an
XX      CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX      CC cell, protein or binding molecule is useful for providing a plant or its
XX      CC progeny with resistance against an oomycete infection such as late blight
XX      CC (a disease of major importance to production of Solanaceae such as potato
XX      CC and tomato cultivars). The present sequence is that of the S
XX      CC bulbocastanum Rpi-b1b gene of the invention.
XX      SQ
XX      SQ Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;

```

Alignment Scores:
 Pred. No.: 2,79e-314 Length: 2913
 Score: 3766.50 Matches: 753
 Percent Similarity: 83.43% Conservative: 78
 Best Local Similarity: 75.60% Mismatches: 130
 Query Match: 73.46% Indels: 35
 DB: 12 Gaps: 8

```

US-10-647-268-2 (1-988) x ADH51531 (1-2913)
Qy      1 MetAlaGluAlaPheLeuGluValLeuLysAsnLeuThrCysPheIleGluGlu 20
Db      1 ATGGCTGAAGCTTTCATCAAGTTCTGCTAGACATCTCACTTCTTCCCAAGGGGAA 60
Qy      21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGluInsertPheThrThr 40
Db      61 CTGTATATGCTTTTGGGTTTTCAGATGATGATTCCAAGGCTTTCACAGCATGTTTCTACA 120
Qy      41 IleGluAlaValLeuGluAlaPheAlaGluLysGluLeuLysAspLysAlaIleGluAsn 60
Db      121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAAACCACTCAACAAGCCTTAAGAAAT 180
Qy      61 TTPLeuGluLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
Db      181 TGGTTGCAAAAACCTCATATGCTGCTACATATATGAAGTGCATGATGATGATATATA 240
Qy      81 ThrGluAlaProIleArgLysLysLysLysLysLysLysLysLysLysLysLysLys 100

```

D	241	ACCAAGGCC--ACAAGATCTCCAGCTGAATATGCGCGTTATCATCCAAAGGTTATC	297
O	101	ThrpheArGHisLysIleGlyLeaArgMetLysIleMetGlyLysLeuAspValIle	120
D	298	CCTTCCCGTCAAGAGTGGGGAAGATGGAACAAGTATGAAAAAATCTTAAGGCATT	357
O	121	AlaAlaGluValGlyLeuPheHisLeuAspGluArgThrIleGluArgGluValAlaThr	140
D	358	GCTGAGGAAGAAAGAAATTTTCATTGTGCAGAAAAAATTTGAGGACACAAAGCTGTTAGA	417
O	141	ArgGlnThrGlyPheValLeuAsnGluProGlnValTyrGlyArgAspLysGluAsp	160
D	418	CGGGAACAAGGTTCTGTTATTAACGAACCGAGTTTATGGAAGACACAAAGAAAGAT	477
O	161	GluIleValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro	180
D	478	GAGATAGTGAAGAAATCTTAATTAACAATGTTAGTATGCCAACCTTCAAGCTCCCA	537
O	181	IleLeuGlyMetGlyLysIleLeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGln	200
D	538	ATACTGTTGATAGGGGGGATTTGGAAGAAACGACTTTCGCCAAATGGCTTCAATGACCA	597
O	201	ArgValIleGluHisPheHisAspProLysIleTrpIleCysValSerGluAspPheAsnGlu	220
D	598	AGAGTTACTGAGCAATTTCCATTCCAAATATGATTTGTGTCTCGGAAGATTTTGTATGAG	657
O	221	LysArgLeuIleLysGluIleValGlnSerIleGluGluLysSer--LeuGlyGlyMet	239
D	658	AAGAGGTTAATAAAGGCAATGTGAATCTATTGAAGAAAGGCACTACTGTTGGTAGAG	717
O	240	AspLeuAlaProLeuGlnLysLysLeuAspLeuLeuAsnGlyLysIleThrLeuLeu	259
D	718	GACTGGGCTCACTTCAAAAGAACCTTCAGAGAGTTGTGATGGAAGAAAGATACCTTGCT	777
O	260	ValLeuAspAspValITrpaAsnGluAspGluAspLysTrpAlaLysLeuArgGlnValLeu	279
D	778	GCTTAGTAGTATGTTTGGAAATGAAGATCAACAAGTGGCTAATTATTAAGACACAGCTTGG	837
O	280	LysValGlyLysSerGlyLysValLeuThrThrThrArgLeuGluLysValGlySer	299
D	838	AAGGTGGAGCAATGGTGTCTGTCTTCAACCACTACTGCTTGAAGAGTTGGATCA	897
O	300	IleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnLysAspCysTrpLeu	319
D	898	ATTATGGAACTTGCACCAATATGAACCTGTCAAACTGTCTCAAGAAATGTTGGTGG	957
O	320	LeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIle	339
D	958	TTGTTCATGCAAGCTGATTTGGACACACAGAAAGAAATTAATTCAAACCTTGTGGCAATC	1017
O	340	GlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGly	359
D	1018	GGAAGAGAGATTGGAAAAAAGTGGTGTGTGCTCTAGACAGCCAAACTCTTGAAGGT	1077
O	360	IleLeuAspPheLysArgGluGluArgGlnTrpGluHisValArgAspSerGluIleTrp	379
D	1078	ATTTTGTGCTTCAAGAGAGAAAGAGCATGGAGAACATGTAAGACAGCTCCGATTTGG	1137
O	380	LysLeuProGlnGluGlnSerSerIleLeuProAlaLeuArgLeuSerTyrHisIleAsn	399
D	1138	AATTTGCTCAAGATGAAGATTTCTAATTCGGCCGCTGAGGCTTAAGTTACATCAACTT	1197
O	400	ProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMet	419
D	1198	CCACTGTGATTTGAAACATGCTTTGTGCGTATGTGCGGTGTTCCAAAGAGATGCCAAATG	1257
O	420	GluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGlyAsn	439
D	1258	GAAAAAGAAAGATATCTCTCTCGATGGCGCAGTGTTCCTTTATCAAAAGGAAC	1317
O	440	LeuGluLeuGluAsnValGlyAsnGluValITrpaAsnGluLeuTyrLeuArgSerPhe	459
D	1318	ATGAGCTTAAGAGATGTGGCGATGAAGATGAGAAAGAAATTTACTGAGTCTTTTTC	1377
O	460	GlnGluIleGluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAsp	479
D	1378	CAAGATTTGATAGTTAAAGTGTAAACCTTATTTCAAGATCAATCATCATAT	1437
O	480	LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleVal	499
D	1438	TTGGCAACATCTCTGTTTTCAGCAAAACATCAACAGCAATATCCGGAATATTAATAA	1497
O	500	GluAsnTyrIleHisMetMetSerIleGlyPheThrLysValValSerSerTyrSerLeu	519
D	1498	CACAGTTACACATATGATGATGCTATGGTTTCCCGGAAGTGTCTTTTATACACTCTT	1557
O	520	SerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLys	539
D	1558	CCCCCTTGGAAAGATTATCTCGTTTAAGAGCTTAACTTAAGTGATTTGCACATTTAAT	1617
O	540	GlnLeuProSerSerIleGlyAspLeuValHisAlaArgTyrLeuAsnLeuSerGlyAsn	559
D	1618	AAGTTACCATCTTCCATGGAATGATGATCACTTAAGATCTTGAACCTGTATGGC--	1674
O	560	ThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAsp	579
D	1675	AGTGGATGATGATGCTTCCAAAGACAGTTATGCAAGCTTCAAAATCTGCAAACTTGAT	1734
O	580	LeuHisGlyCysHisSerLeuCysCysLeuProLysGluThrSerLysLeuGlySerLeu	599
D	1735	CTACAAATATTTGACCAAGGCTTTGTTGTTGGCCAAAGAAACAACTTAACCTTGATGCTC	1794
O	600	ArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProArgIleGlySer	619
D	1795	CGAAATCTTTACTGATGATGATGCCAGATCACTTGTATGCCACCAAGATAGATCA	1854
O	620	LeuThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLysSerCysGln	639
D	1855	TTGACATGAGCTTAAAGCTCTAGCTCAATTTGTGTGTGA--AGAGAAAGAGTTATCAA	1911
O	640	LeuGlyIleLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleTrpHisLeuGluArg	659
D	1912	CTTGGTGAACCTGAACCTTAATCTTATGTGCTCAATTAACCTGCACTTTGAGAGA	1971
O	660	ValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSer	679
D	1972	GTCAGAAATGAATAGAGACGCAAAAGAACCAATTTATCTGCAAAAGGAATCTGCATTCT	2031
O	680	LeuSerMetLysTrpAspAspAspGluArgProArgIleTyrGlnSerGluLysValGlu	699
D	2032	TTAAGCATAGTTGG--AATTACTTTGACACCAATATATGATGATCAAGAAAGTTAA	2088
O	700	ValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArg	719
D	2089	GTGCTTGAAGCCCTCAAAACCACTCCAACTGCACTCTTTAAAAATCTATGGCTTCAGA	2148
O	720	GlyIleArgLeuProAspTrpMetAsnHisSerValLeuLysAsnValValSerIleGlu	739
D	2149	GGAATTCATCTCCAGAGATGATGAATCACTCAAGATTTGAAAAATTTGTCTATTTCTTA	2208
O	740	IleIleSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuProCysLeuLys	759

```

QY      813  GluGluIleGluIleLeuCyseCyseProMetPheValIleProThrLeuSerSerVallys 832
DB      2449  GAAGAGATGATTAATTCACGAGTGCCTTTCTG-----ACCTTTCT----- 2490
QY      833  LysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeu 852
DB      2491  -----TCTTAATCTT 2499
QY      853  MetAlaLeuThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGlu 872
DB      2500  AGGGCTCTTACTCTCCCTCAGAAATTTGCTATATATAAGTAGCTACTTCAATCCCGAAGAG 2559
QY      873  MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
DB      2560  ATGTTCAAAAACCTTGCAATCTCAAAATCTGACAAATCTCTCGGTGCAATATCTCAA 2619
QY      893  GluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCys 912
DB      2620  GAGCTGCCTACCAAGCTTGCTAGTCTGAATGCTTGAATAATCTAAATCAATGTGT 2679
QY      913  TyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGluLeu 932
DB      2680  TCGGCACCTAGAGAGTCTCCCTGAGGAGAGGCTGGAAGGTTTATCTTCACTCAGAGATTA 2739
QY      933  SerIleThrTyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnHisLeuThrAla 952
DB      2740  TTGTGTGAACACTGTGAATATGCTAAATGTTTACCAAGAGGATTCGACACTTAACACC 2799
QY      953  LeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIle 972
DB      2800  CTCACAGATTAAAAATTCGGGGATGTCTCACACAGATGATCAAGCGGTGGAAGAGGAAATA 2859
QY      973  GlyGluAspTyrTyrLeuIleAlaHisIleProArgValPheIleTyr 988
DB      2860  GGAAGAGACTGGCACAAATTTCTCACATCTTAATGTAATATATAT 2907

RESULT 7
ADF17762
ID  ADF17762 standard; DNA; 3260 BP.
XX
AC  ADF17762;
XX
DT  12-FEB-2004 (first entry)
XX
DE  S_bulbocastanum RGCI-b1b coding DNA containing an intronic sequence.
XX
KW  gene; ds; RGCI-b1b; Rpi-b1b gene cluster; growth regulator;
KM  oomycete infection; introgression breeding; plant; late blight.
XX
OS  Solanum bulbocastanum.
XX
FH  Key
FT  CDS
FT  1..3260
FT  /tag= a
FT  /product= "RGCI-b1b protein"
FT  /note= "this coding sequence contains one intron"
FT  /transl_except= (pos: 709..710, aa: Gly)
FT  intron
FT  428..708
FT  /tag= b
FT  /number= 1
XX
PN  EP1334979-A1.
XX
PD  13-AUG-2003.
XX
PE  08-FEB-2002; 2002EP-00075565.
XX
PR  08-FEB-2002; 2002EP-00075565.
XX
PA  (KWEK-) KWEK EN RESEARCHEBDRJUF AGRICO BV.
XX
PI  Van Der Vossen EAG, Allefs JHM;

```

```

XX      XX  MPI: 2003-714439/68.
DR      DR  P-PSDB; ADF17767.
XX      XX
PT  New resistance gene conferring resistance against an oomycete pathogen,
PT  useful for producing plants, especially potatoes and tomatoes, resistant
PT  against oomycete pathogens such as Phytophthora infestans.
XX      XX
PS  Example 5; SEQ ID NO 38; 86bp; English.
XX      XX
CC  This invention relates to novel isolated polynucleotides that confer
CC  resistance against late blight caused by the oomycete pathogen
CC  Phytophthora infestans, which threatens both tomato and potato crops.
CC  Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC  leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
CC  and which cause disease resistance to bacteria, fungi, nematodes etc.
CC  These R genes, namely Rpi-b1b, RGCI-b1b, RC3-b1b and RC4-b1b, can be
CC  described as plant growth regulators. They are useful in providing
CC  resistance to Phytophthora infestans, especially in Solanum tuberosum
CC  (potato) plants to protect against oomycete infection or to demonstrate
CC  disease susceptibility. Resistance can be conferred by transformation of
CC  existing potato and tomato cultivars with the gene, a procedure that is
CC  more straightforward and faster than conventional introgression breeding.
CC  This polynucleotide sequence is the Solanum bulbocastanum RGCI-b1b coding
CC  DNA containing an intronic sequence in an exemplification of the
CC  invention.
XX      XX
SQ  Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other:
XX      XX

Alignment Scores:
Pred. No.: 5,44e-304 Length: 3260
Score: 3648.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
Query Match: 71.15% Indels: 114
DB: 10 Gaps: 9

US-10-647-268-2 (1-988) x ADF17762 (1-3260)
QY      1  MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
DB      1  ATGGCTTAACCTTCTCTTCAAGTTCGTGCTAGATATCTCACTTTTTCATCCAAAGGGGAA 60
QY      21  LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
DB      61  CTTCGATTGGTTTGTGTTTCGAGAGGAGGTTTAAAACTTCAAGTATGTTTCAATG 120
QY      41  IleGlnAlaValLeuGluAlaPheAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn 60
DB      121  ATCCAACTGTGCTAGAGAGATGCTCAAGAGCACTGAAGTACAGGCAATTAAGAAC 180
QY      61  TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
DB      181  TGGTTACAGAACTGCATGTTGCTGCATATGATGATGATGATGATGATGATGATGATGAT 240
QY      81  ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
DB      241  ACTGAGGCA--GCMAATTCAGACAGGCTGTATGGGCGCTTATCTATCCAGGACATC 297
QY      101  ThrPheArgHisLysValIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
DB      298  ACTTTCGTTCACAAAGTGGGAAAAAGATGAAGAAATGATGAAAAAATAGATGCAATT 357
QY      121  AlaAlaGluArgLysPheHisLeuAspGluArgThrIleGluAlaGlnValAlaThr 140
DB      358  GCAGAGGAGACGAGGAATTTTCAATTATGATGAAGATTATGAGAGACAAAGCTGCTAGA 417
QY      141  ArgGlnThr----- 143
DB      418  CGGCAAC-AGTGCTCATCTTAATTTTATTTTAAAACAAATAAGTATACAAATTCGAG 476
QY      143  ----- 143

```

Db	477	AGAAACGAAGAAATTATATTCATTTTATTTTGGCAATTATCAAAAGTCATTTGGTTT	536
Qy	143	-----	143
Db	537	TTAACTGGGGAGAGTTTCAAAATATTTCTCTAGCTTAATGTTGTCTCACTCACTCA	596
Qy	143	-----	143
Db	597	GCATGATTTTCTCAATCCTTCACTTCAACTCCCCCTCTGTGCATTAATCTCTCAAT	656
Qy	144	-----	144
Db	657	TTCTGTGACTCCATATGAGCTTGAAATGAACAACATTTCTGTTTGGAGCAGGTTTGGT	716
Qy	147	LeuAenGluProGlnValTyrGlyArgAspGlyValSerGluValIleValIleLeu	166
Db	717	TTAACTGAGCCAAAGTTATGAGAGGAAAGAGATGAGATGAGATGAGAAATCTTGG	776
Qy	167	IleAsnValSerAsnIleGlnThrLeuProValLeuProIleLeuGlyMetGlyGly	186
Db	777	ATAAACATATGTTATGTTATCCGAAGAGTTCCATATCTCCCATATCTGGTATAGGGGGA	836
Qy	187	LeuGlyValThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPhe	206
Db	837	CTAGAAAGAGACCTTACGCCCAATATGTCCTTCAATATCAAAAGATTTATCTGACATTC	896
Qy	207	HisProIleIleTyrIleCysValSerGluAspPheAsnGluValArgLeuIleValSerGlu	226
Db	897	AATCAAAAGATATGGGTTTGTGTCTCAAGATATTTTATAGAAAGAGTTGATTAAGGCA	956
Qy	227	IleValGluSerIleGluGluValSerLeuGlyValMetAspLeuAlaProLeuGlnVal	246
Db	957	ATTGATGATCTATATGGAAGAAAGTCACCTGGTACATGAGCTTGGCTCCCTCCAGAA	1016
Qy	247	LysLeuArgAspLeuLeuAsnGlyValSerTyrLeuLeuValLeuAspAspValIleProAsn	266
Db	1017	AAGCTTCAGAGTTGTGATGAGAAAGAAATCTTTCTTGTGTGATGATGTTGTGAAAT	1076
Qy	267	GluAspGlnAspLysTyrAlaLysLeuArgGlnValLeuValGlyAlaSerGlyAla	286
Db	1077	GAAATCAAGAAAGTGGATTAATCTTAGAGCAGTATGAAAGTTGGAGTATGTGTCT	1136
Qy	287	SerValLeuThrThrThrArgLeuGluValGlySerIleMetGlyThrLeuGlnPro	306
Db	1137	TCAATTTCAATTTACTCTCTGCTTGAAGAAAAATTCATTTATGGAACCTTTCACACTA	1196
Qy	307	TyrGluLeuSerAsnLeuSerGlnGluAspCysTyrLeuLeuPheMetGlnArgAlaPhe	326
Db	1197	TATCAATTTCAATTTGTCTCAAGAGATTTGTGTGTGTCTTCAAGACACTGCTATTT	1256
Qy	327	GlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLysGluIleValLysLys	346
Db	1257	TGCACACAAACCGAACAAGTCTTAAACCTTAAGAAATCGAAGAGAGATTTGGAAGAA	1316
Qy	347	CysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlu	366
Db	1317	TGTGGGGGTGTGCTTACAGAGCCAAACCTTCGAGGCCCTTTTACGCTTCAAGAGGGA	1376
Qy	367	GluArgGlnTyrGluHisValArgAspSerGluIleTyrLysLeuProGlnGluSer	386
Db	1377	GAAAGTGAATGGGAACATGTGAGAGATGAGATTTGGAATTTTACCTCAAGATGAAAT	1436
Qy	387	SerIleLeuProAlaLeuArgLeuSerTyrHisIleLeuProLeuAspLeuArgGlnCys	406
Db	1437	TCTGTTTGTGCTCCCGAGAGCTGAGTTATCATCATCTTCCACTTGATTTGGAACAAAT	1496
Qy	407	PheThrTyrCysAlaValPheProLysAspThrGluMetGluLysGlyAsnLeuIleSer	426
Db	1497	TTTGCATATTTGGCAGATTTCCCAAGAGACCAAAATAGAAAGAAATATCTATCTCCT	1556
Qy	427	LeuTyrMetLysHisGlyPheIleLeuSerLysGlyAsnLeuGluLeuGluAsnValGly	446
Db	1557	CTCTGATGGCAACAGTTTCTTTTATCAAAAGAAACATGAGCTGAGAGATTTGGGC	1616

Qy	447	AsnGluValTyrAsnGluLeuTyrLeuArgSerPhePheGlnGluIleGluValLysSer	466
Db	1617	AATGAGATATGAGATGATTAATTAATCTTGAAGCTTTTTCCAAGAGATGAGTTAATCT	1677
Qy	467	GlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSer	486
Db	1677	GGTAAACTTATTTTCAAGATGACATGATCTATCCATGATGATTTGGCTACATCTATGTTTCA	1736
Qy	487	AlaSerThrSerSerSerAsnIleArgGluIle-----	497
Db	1737	GCAAGCGCATCAACAGATGATATCCCAATTAATGTAATAAGATGATGATGATGATG	1796
Qy	498	---IleValGluLeuTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSer	516
Db	1797	TTCAATTTAACAATTTAATAAGATATGATGATTCATTTGTTTCCCAAGTGTGTCTCT	1856
Qy	517	TyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIle	536
Db	1857	TACTCTCCTTCGCTCTTTAAGAGTTTGTCTGTTAAGGTCCTTATCTTAAGTACCTCA	1917
Qy	537	LysLeuLysGluLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu	556
Db	1917	GAATTTAACAAGTTACCGTCTCCGTTGAGATCTGTGATCATTTAAGATCACTTGACCTG	1976
Qy	557	SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln	576
Db	1977	TCTGTAT---AAATTTGTATCTTCCAAAGAGGTGTGACAGCTTCAAAATCTGAG	2037
Qy	577	ThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGluThrSerLysLeu	596
Db	2034	ACTCTTATCTATATTAATGTCAGTCACTTCTTGTTCGGAACAAACAGTAAAGCTT	2093
Qy	597	GlySerLeuArgAsnLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArg	616
Db	2094	TGTATGCTCCGAGATCTGTACTGATCACTG---CAATTACTTATATGACACCAAGA	2150
Qy	617	IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValGlyIleGlnLysLys	636
Db	2151	ATAGATATTTGACATGCGCTTAAGACACTAGGTTACTTTGTTGTAAGC---GAGAGGAA	2207
Qy	637	SerCysGlnLeuGlyGluLeuArgLeuAsnLeuTyrGlySerIleGluIleThrHis	656
Db	2208	GATTATCAACTTGTGTAACTACGAAATTTAAACCTCCGGGCGCAATTCATCAACAT	2267
Qy	657	LeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsn	676
Db	2268	CTTGAAGAGTGAAGAAATGATATGAGGCAAGAAAGCAATTTATCTGCAAAACCAAT	2327
Qy	677	LeuHisSerLeuSerMetLysTyrAspAspAspGluArgProArgIleTyrGluSerGlu	696
Db	2328	CTACACTCTTTAAGCATGATGGTGGAT-----AGACCAACAAGATATGATCCCA	2378
Qy	697	LysValGluValLeuGlnAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg	716
Db	2379	GAACTTAAAGCTTTAAGCCCTCAACACCATCCCAATCTGAATATTTTGAATTCATT	2438
Qy	717	GlyPheArgGlyIleArgLeuProAspTyrPheAsnHisSerValLeuLysAsnValVal	736

QY 796 AsnLeuYsglyLeuLeuYsglyGluGluGlnCysProValLeuGluGlu 815
 DB 2679 AATCTGAAGGATTCGACAGAAATGAAGAGCAGAGCAATCCCCGTCCTGGAAGATG 2738
 QY 816 GluIleYsgCysProMetPheValIleProThrLeuSerSerValValLeuVal 835
 DB 2739 AAGATTTCGAGATCCCTATGTTGTTTCCGACCCCTTCTTGTCMAAATTGAA 2798
 QY 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
 DB 2799 ATTGGGGGGG---GCAGATCGAGAGGTTTGAGCTCCATATCTAATCTGACACTTT 2855
 QY 856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLys 875
 DB 2856 ACATCCCTCAAGATTTTCAGTAAACACACAGTCACTTCACTGAAAGAGATGTTCAA 2915
 QY 876 SerLeuAlaAsnLeuYsglyTyrLeuAsnIleSerPheTyrPheAsnLeuYsglyLeuPro 895
 DB 2916 AACCTTGAAATTCATATCTGATGAGTCTCTTCTTGGAAGATCTCAAGAGCTGCT 2975
 QY 896 ThrSerLeuAlaSerLeuAsnAlaLeuYsglyHisLeuGlnIleHisSerCysTyrAlaLeu 915
 DB 2976 ACCAGCTCGCTAGCTCAACAATTGAAAGTCTGAGTATTCGTTATTGTTACGCACTA 3035
 QY 916 GluSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThr 935
 DB 3036 GAGAGTCTCCCGCAGAGAGGCTGGAAGTTTATCTTCACTCAAGACTTATTGTTGAA 3095
 QY 936 TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnHisLeuThrAlaLeuThrAsn 955
 DB 3096 CACTGTAAATGCTAAATGTTTACAGAGGAGATTCGAGCACTTAACAACCTCAAGT 3155
 QY 956 LeuSerValGluPheCysProThrLeuAlaLysArgCysGlyLysGlyIleGluAsp 975
 DB 3156 TTTAAATAATTCGGGATGTCACCACTGATCAAGCGGTGAGAAAGGAATGAGAAAGAC 3215
 QY 976 TrpTyrIleValLeuAlaHisIleProArgValPheIleTyr 988
 DB 3216 TGGCACAATAATTTCTCAGATTCCTTATGTGAATATATAT 3254
 RESULT 8
 ID ADH51534 standard; DNA; 3260 BP.
 AC ADH51534;
 XX 25-MAR-2004 (first entry)
 DT
 DE S bulbocastanum RGCl-b1b gene SeqID51.
 XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
 KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
 KM de; RGCl-b1b.
 XX Solanum bulbocastanum.
 OS
 XX US2003221215-A1.
 PN
 XX 27-NOV-2003.
 PD
 XX 07-FEB-2003; 2003US-00360522.
 PF
 XX 07-FEB-2003; 2003US-00360522.
 PR
 XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
 PA
 XX Aljefe JHM, Van Der Vossen EAG;
 PI
 XX WPI; 2004-010903/01.
 XX
 XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.

XX Claim 6; SEQ ID NO 51; 989p; English.
 PS
 CC This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of the S
 CC bulbocastanum RGCl-b1b gene which is related to the invention.
 XX
 SQ Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,44e-304 Length: 3260
 Score: 3648.00 Matches: 745
 Percent Similarity: 76.58% Conservative: 92
 Best Local Similarity: 68.16% Mismatches: 143
 Query Match: 71.15% Indels: 114
 DB: Gaps: 9
 US-10-647-268-2 (1-988) x ADH51534 (1-3260)
 QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlu 20
 DB 1 ATGGCTGAAGCTTTCCTTCAAGTCTCTGATATATCTCACTTTTTCATCAAGGGGAA 60
 QY 21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThr 40
 DB 61 CTGGATTTGGTTTGTGTTGTTGACAGAGAGGTTTAAACCTTCAAGTATTTTCATG 120
 QY 41 IleGlnAlaValLeuGlnAspAlaGlnLysGlnLeuLysAspLysAlaIleGlnAsn 60
 DB 121 ATCCAGCTGTGCTAGAAAGATGCTCAAGAGAGCACTGAGTCAAGGCAATTAAGAAC 180
 QY 61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
 DB 181 TGGTTACAGAAATCAATGTTGCTGCAATGAGTTGATGACATCTGGATGACGTAA 240
 QY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
 DB 241 ACTGAGCA---GCAAGATTCAAGCAGGCTGATTTGGGCGTTATCATCCAGACATC 297
 QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
 DB 298 ACTTTCTGTTCAGAGGTGGGAAAAAGATGAAGAAATGATGAAAACTAGATGCATTT 357
 QY 121 AlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
 DB 358 GCAGAGGAAACGAGAAATTTTCATTGTAGTAAAGATTATAGAGACCAAGCTGCTAGA 417
 QY 141 ArgGlnThr----- 143
 DB 418 CGGCAAC-AGTGCTCATCTTAATTTTAAACAAATTAAGTATTACAATTGCG 476
 QY 143 ----- 143
 DB 477 AGAAACGAGAAATTTATATCTTTTATTTTGGCAATTATCAAACTATTGTGTT 536
 QY 143 ----- 143
 DB 537 TTAAGCTGGGGGAAATTTCAATATTTTCTAGTCTTAATGTTTGTCTGACTCATCA 596
 QY 143 ----- 143
 DB 597 GCATGATTCTCAATCTTCACTTCAACTCCCTCACTGCTGCAAAATATCTTCTCTATT 656
 QY 144 -----GlyPheVal 146

Db 657 TTCTGTGACTCTTAATGAGCTTGAATGTAACAACATCTTGTGTGAGCAGAGTTTGT 716
Qy 147 LeuAenGluPProGlnValTyrGlyArgAspIleGlyAspGluIleValIleLeu 166
Db 717 TTAACGTGCGCAAAAGTTTATGAAAGGAAAGGAGATGATGATAAATCTTG 776
Qy 167 IleAsnValSerAsnIleGlnThrLeuProValLeuProIleLeuGlyMetGly 186
Db 777 ATAAACATGTTAGTATTCCGAAGAATCTCCAGTCTCCCAATCTTGATGGGGGA 836
Qy 187 LeuGlyIleThrThrLeuValGlnMetValPheAsnAspGlnArgValIleGlnIlePhe 206
Db 837 CTAGGAAGACGACTCTAGCCCAATGGCTTCAATGATCAAGAAATTAATGAGCATTC 896
Qy 207 HisProIleIleTyrIleCysValSerGluAspPheAsnGluValArgLeuIleIleGlu 226
Db 897 AATCTAAAGATATGGTTGTGTCTCAGATGATTTGATGAGAAAGGTTGATTAAGCA 956
Qy 227 IleValGluSerIleGluGluIleSerLeuGlyMetAspLeuValProLeuGlnIle 246
Db 957 ATTTGATGATCTATTGAAAGAAAGTCACTGGTGACATGACTGGCTCCCTCCAGAA 1016
Qy 247 LysLeuArgAspLeuLeuAsnGlyLysIleTyrLeuLeuValLeuAspAspValTyrAsn 266
Db 1017 AAGCTTCAGAGTTGTTGAATGAAAAAAGATACCTTCTGTTTGGATGATGTTGGAA 1076
Qy 267 GluAspGluAspIleTyrAlaIleIleAspArgGlnValIleIleValIleValIleSerGlyAla 286
Db 1077 GAAAGTCAAGAAAGGAGGATTAATCTTAGAGCAGATTAAGATTTGAGCTAGTGGTCT 1136
Qy 287 SerValLeuThrThrThrArgLeuGluIleValGlySerIleMetGlyThrLeuGlnPro 306
Db 1137 TCATTTCTAATTAATTAATCTGCTTGAATAAATTTGGATCAATTAATGGAATCTTGCACTA 1196
Qy 307 TyrGluLeuSerAsnLeuSerGlnGluAspCysTyrPleuLeuPheMetGlnArgAlaPhe 326
Db 1197 TATCAGTATCAAAATTTGTCTCAAGAAAGATTTGTTGTTCACAAACGTCATTT 1256
Qy 327 GlyIleAsnGluGluIleAsnLeuAsnLeuValAlaIleGlyLysGluIleValIleLys 346
Db 1257 TGCACCAACCAAGCAAGTCTTAATCTTAAGAAATCGAAAGAAAGATTTGTAAGAA 1316
Qy 347 CysGlyGlyValProLeuAlaAlaIleThrLeuGlyGlyIleLeuArgPheLysArgGlu 366
Db 1317 TGTGGGGGTGTGCTCTAGCAGCCAAACTCTTGGAGGCTTTTACGCTTCAAGAGGAA 1376
Qy 367 GluArgGlnTyrGluIleValIleArgAspSerGluIleTyrPleuProGlnGluIleSer 386
Db 1377 GAAAGTGAATGGAAACATGATGATGATGATTTGAATTTTCAACCAAGATGAAAT 1436
Qy 387 SerIleLeuProAlaLeuArgLeuSerTyrHisIleLeuProLeuAspLeuArgGlnCys 406
Db 1437 TCTGTTTTCCTGCTCGAGCTGAGCTTATCATCTTCCACTTGATTTAGACAATGT 1496
Qy 407 PheThrTyrCysAlaValPheProLysAspThrGluMetGluIleGlyAsnLeuIleSer 426
Db 1497 TTTGCATATTCGCGAGTATCCCAAGGACCAAAATTAAGAAAGATATCTATCGCT 1556
Qy 427 LeuTyrMetAlaHisGlyPheIleLeuSerLysGlyAsnLeuGluLeuGluAsnValGly 446
Db 1557 CTCGAGATGGCACACAGTTTCTTTATCAAAAGGAAACATGAGCTAGAGATCTGGGC 1616
Qy 447 AsnGluValTyrPheAsnGluLeuTyrLeuArgSerPhePheGlnGluIleGluValLysSer 466
Db 1617 AATGAAGATGAAATGAATTAATTAATCTGAGCTTTTTCAGAGAAATTTGAAGTTAAATCT 1676
Qy 467 GlyIleThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSer 486
Db 1677 GGTAAACTTATTTCAAGATGATGATCTCATTCATGATTTGGGTACATCATATGTTTCA 1736
Qy 487 AlaserThrSerSerSerAsnIleArgGluLe----- 497

Db 1737 GCAAGCGCATCAACAGAGTATACGCCAAATAATGTAAAAAGATGATGAAGATATGATG 1796
Qy 498 ---IleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSer 516
Db 1797 TTCAATTGTAACAAATTTATTAAGATATGATGCTCATTTGGTTTCTCCGAAGTGTCTTCT 1856
Qy 517 TyrSerLeuSerHisIleGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIle 536
Db 1857 TACTCTCCTTGCTCTTAAAGATTTGTCTCGTTAAGGGGTCTTAATCTTAATGTAATCTCA 1916
Qy 537 LysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisIleuArgTyrLeuAsnLeu 556
Db 1917 GAAATTTGAACGTTAACCGTCTTCGTTGAGATGTAGTACATTTTAAGATTAATCTTGACTG 1976
Qy 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
Db 1977 TCTGTATAT---AAATTTGATGCTTCCAAAGAGGTTTGCAAGCTTCBAATCTGCAG 2033
Qy 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGluThrSerLysLeu 596
Db 2034 ACTCTTGATCTATTAATTAATTTGACAGTCACTTCTGTTGCCGAACAACAAGATAGCTT 2093
Qy 597 GlySerLeuArgAsnLeuLeuAspGlyCysTyrGlyLeuThrCysMetProArg 616
Db 2094 TGTAGTCTCCGGAATCTTGATCTGATCACTGT---CCATTAAGCTTATGTCACAGAA 2150
Qy 617 IleGlySerLeuThrThrCysLeuLysThrLeuSerArgPheValIleGlyIleGlnLysLys 636
Db 2151 ATAGGATTTGATGATGATGCTTAAAGACATGATTAATCTTGTGTGATGAGC---GAAAGGAA 2207
Qy 637 SerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHis 656
Db 2208 GGTATATCAACTGTGTGAACATCAAGAAATTTAAACCTCCGTGTGCAATTTCAATCAACAT 2267
Qy 657 LeuGluArgValLysAsnAspMetAspAlaIleGluIleAsnLeuSerAlaLysGluAsn 676
Db 2268 CTTAGAGAGTGAAGAAATGATATGAGCAGAAAGCCAAATTTATCTGCAAAAGCAAT 2327
Qy 677 LeuHisSerLeuSerMetLysTyrAspAspAspGluArgProArgIleTyrGluSerGlu 696
Db 2328 CTACACTCTTTAAGCAATGAGTTGGAT-----AGACCAAACAGATATGATCCGAA 2378
Qy 697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
Db 2379 GAACTTAAAGTCTGTAAGCCCTCAAAACATCCCATCTGAATTTTGAATCAATT 2438
Qy 717 GlyPheArgGlyIleArgLeuProAspTyrMetAsnHisSerValIleLysAsnValIle 736
Db 2439 GACTTCTGTGATTTCTGTCTCTCCGACTGAGTGAATCACTCAGTTTGAAGAAATGTTGTC 2498
Qy 737 SerIleGluIleIleSerCysLysAsnCysSerCysLeuProPropheGlyGluLeuPro 756
Db 2499 TCTATTTCAATTAACGGTTGTGAAGAACTGCTCGTGTTCACACCTTGTGGAGCTGCT 2558
Qy 757 CysLeuLysSerLeuGluLeuTyrPheArgLysSerAlaGluValGluTyrVal---AspSer 775
Db 2559 TGTCTAGAAAGTCTGAGTTTACAGACGGGTCTGTGAGGGTGAATGTTGAAGATTTCT 2618
Qy 776 GlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArgGluPheGly 795
Db 2619 GGAATTCCTGACAAAGAAAGATTTCACTCCCTGAAAACTTCATATAGCTGGCTTTGT 2678
Qy 796 AsnLeuLysGlyLeuLeuLysLysGluGlyGluGlnCysProValLeuGluGluIle 815
Db 2679 AATCTGAAGAGATTTGACAGAGATGAAGAGCAAGCAATCCCGGTGCTTAAGAGATG 2738
Qy 816 GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLeuVal 835
Db 2739 AAGATTTCCGATTCCTTAATGTTGTTTCCGACCTTCTTCTGCAAGAAATTTGAA 2798
Qy 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
Db 2799 ATTTGGGGGAG---GCAGATGACGAGGTTTGAGCTTCATATTAATCTCAGCACTCTT 2855

```
QY 856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLys 875
DB 2856 ACATCCCTCAAGATTTCAGTAACACACAGACTTCACTACGTGGAAGATGTTCAA 2915
QY 876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
DB 2916 AACCTGTAAGAAATCTATATCTTGAAGTCTCTTCTTGGAGAAATCTCAAGAGCTGCTT 2975
QY 896 ThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeu 915
DB 2976 ACCAGCCCTGGAGTCTCAACAAATTGAAGTCTGTGAATTCGTTATGTTACGCACTA 3035
QY 916 GluSerLeuProGluGluGlyValLysGluLeuIleSerLeuThrGlnLeuSerIleThr 935
DB 3036 GAGAGTCTCCCGAGAGAGGCGTGAAGCTTATCTTCACTACAGATTAATTTCTTGA 3095
QY 936 TyrCysGluMetLeuGlnCysLeuProGluGluGlnHisLeuThrAlaLeuThrAsn 955
DB 3096 CACTGTACATGCTAAATGTTTACCAAGAGGATTGACAGACCTTAACAACCTCAAGT 3155
QY 956 LeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyTleGluLysP 975
DB 3156 TTAAATAATTCGGGAGTGTCCACAACTGATCAAGCGGTGTGAGAAAGGAAATGAGAGAAC 3215
QY 976 TrpTyrLysIleAlaHisIleProArgValPheIleTyr 988
DB 3216 TGGCAAAATTTCTCACATTCCTTAATGTGAATATATAT 3254

RESULT 9
ADP17760
ID ADP17760 standard; DNA; 3592 BP.
XX
XX ADP17760;
XX
XX 12-FEB-2004 (first entry)
XX
XX Solanum bulbocastanum Rpi-b1b genomic DNA.
XX
XX gene; ds, Rpi-b1b; Rpi-b1b gene cluster; growth regulator;
XX oomycete infection; introgression breeding; plant; late blight.
XX
XX Solanum bulbocastanum.
XX
XX Key Location/Qualifiers
XX CDS 1..3592
XX /*tag= a
XX /product= "Rpi-b1b protein"
XX /note= "This coding sequence contains one intron"
XX /transl_except= (pos: 1107..1108, aa: Gly)
XX intron 428..1106
XX /*tag= b
XX /number= 1
XX
XX EP134979-A1.
XX
XX 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Van Der Vossen EAG, Allefs JHM;
XX
XX MPI; 2003-714439/68.
XX
XX P-PEDB; ADP17765.
XX
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes and tomatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX
```

```
PS Example 5; SEQ ID NO 36; 86pp; English.
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b genomic
XX DNA of the invention.
XX
XX SQ Sequence 3592 BP; 1129 A; 659 C; 734 G; 1070 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 4.13e-303 Length: 3592
XX Score: 3638.50 Matches: 754
XX Percent Similarity: 68.03% Conservative: 78
XX Best Local Similarity: 61.65% Mismatch: 129
XX Query Match: 70.97% Indels: 262
XX DB: 10 Gaps: 9
XX
XX US-10-647-268-2 (1-988) x ADP17760 (1-3592)
QY 1 MetAlaGluAlaPheLeuGlnValLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
DB 1 ATGGCTGAAGCTTCATTCAGATTCGTGTAGACATCTCACTTCTTCTCAAGGGGAA 60
QY 21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
DB 61 CTGTATTTGCTTTTCGGTTTTCAGATGATGATCCAAAGGCTTTCAGCATGTTTTCACA 120
QY 41 IleGlnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsn 60
DB 121 ATTCAAGCGGTCTTGAAGATGCTCAGAGAAAGCACTCAACAAACAGCCCTTAGAAAT 180
QY 61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
DB 181 TGGTTGCAAAACCTCAATGCTGTACATATGATGATGATCATCTTGATGAATATATA 240
QY 81 ThrGluAlaProIleArgLysLysLysLysTyrGlyCysTyrHisProAsnValIle 100
DB 241 ACCAAGGCC--ACAAAGATTCCTCCAGCTGAATATGCGCCTTATCATCCAAAGGTTATC 297
QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
DB 298 CTTTCCGTCAAGAGTCGGGAAAGATGAGCAAGAGTGAAGAAACCTAAAGGCAAT 357
QY 121 AlaAlaGluArgLysLysPheHisLeuAspGluLysArgThrIleGluArgGlnValAlaThr 140
DB 358 GCTGAGAAAGAAAGAAATTTTCATTTTCACGAAAAAATGTAGAGAGCAAGCTGTAGA 417
QY 141 ArgGlnThrGly----- 144
DB 418 CGGAAACAGGTACTCATCTTAATTAATGATTACAAACAATAAGTTATATTCATTTT 477
QY 144 ----- 144
DB 478 TGGCAATATCAAAATTCAAGAAAGGTTAAATATATCATCATGTCTATCGTAATATGTGA 537
QY 144 ----- 144
DB 538 TATATACCTCTGTTGTTACTTTGATCTGAATATACTTTCGAATCTGGCAAGCTCAGAA 597
QY 144 ----- 144
DB 598 TCAATATATCAACCCCAACTTTTAATATATCATATCTTGAATATCACCCTGTCTACT 657
```



```
OY 144 ----- 144
Db 658 CATCACTACCAATCCCTTGGTCTTGAATCTTTCTTACCTATAAACTTGGAACACT 717
OY 144 ----- 144
Db 718 CGATCCGTTTGGCTTTCTTAAACAAGAGCTCAGAGAAAAGGTTTCTTATTCG 777
OY 144 ----- 144
Db 778 TTTCTCTGTGCTGCACTTGGGCTCTTAATCCATTAAAAACAGGCAATGTTAATCCCA 837
OY 144 ----- 144
Db 838 ACAGAGGTAGCCTTCTCTGACAGCTGACTTAATTTGTTCTAACAAAGAAAAAAGA 897
OY 144 ----- 144
Db 898 TTAGACATGTTTCTTCTGTATGATTAGCGTGAATTTCTTCAGAGTGGAACATAGG 957
OY 144 ----- 144
Db 958 GATATATTGACCAAAAGTAGAATGGGTATATTAAAGTATTTCTGATAGAACAGAG 1017
OY 144 ----- 144
Db 1018 TATATTGGCAAAATATCTCTATTTCTGTGTCTCTAATGAGTTGAAATGTAATA 1077
OY 145 -----Phe-ValLeuasnIuproGlnValTyrG1 154
Db 1078 TATTCATGTCGACATTTGCTTGACCAAGTTCTGTATTAACCGAACCGAGTTTATG 1137
OY 154 YARAspIyspGlnIysAspGlnIleValIysIleleuIleAspIleuValSerAsnIleG1 174
Db 1138 AAGAGACAAAGAAAGATGAGATGTAATAATCTTAATAACATGTTAGTGAATGCCCA 1197
OY 174 nThrIleuProValIleuProIleleuGlyMetGlyGlyLeuGlyIysThrThrIleuAlaG1 194
Db 1198 ACACCTTTCAGTCCCTCCCAATACCTGGTATGGGGGANTTAGAAAAACGACTCTTGCCA 1257
OY 194 nMetValPheAsnAspGlnIleValIleGlnHisPheHisProIysIleTrrIleCysVa 214
Db 1258 AATGTCCTTCATATACAGAGAGTTACTAGCAATTTCCATCCAAAATATGATTTGTGT 1317
OY 214 ISeGlnIAspPheAsnGlnIysArgLeuIleIysGlnIleValIleuSerIleGlnGlnIly 234
Db 1318 CTCGAAAGATTTTATGAGAAAGAGGTTTAAAGGCAATGTGATAGATCTATGAAAGAG 1377
OY 234 sSer--LeuGlyGlyMetAspIleuAlaProLeuGlnIysIysLeuArgAspLeuAs 253
Db 1378 GCCACTACTGTGAGATGAGACTTGGCTCCACTTCAAAAAGAGCTTCAGAGGTTGCGAA 1437
OY 253 nGlyIlyIysIleThrIleuIleuValIleuAspAspValTrrAsnGlnIAspGlnIlyTrrAl 273
Db 1438 TGGAAAAAGATACTGTGTCTTATGATGATGTTGAAATGAAATCAACAGAAAGTGGGC 1497
OY 273 alyIleuArgGlnIleuIysValIleGlyAlaSerGlyAlaSerValIleuThrThrTr 293
Db 1498 TAATTTAAGGCACTCTTGAAGGTTTGAAGCAAGGGGCTTCTGTCTTAACCACTACTCG 1557
OY 293 gLeuGlnIysValIleSerIleMetGlyThrLeuGlnProTrrIleuSerAsnLeuSe 313
Db 1558 TCTTGAAGAAGGTGGATCAATTATGAGACATTCACACATATGATGTCAATCTGTCTC 1617
OY 313 rGlnGlnAspCysThrIleuIleuPheMetGlnArgAlaPheGlyHisGlnGlnIleuIleAs 333
Db 1618 TCAAGAAAGATTGTGTGTGTTCATGCAACGTCGACATTTGGACCAACAAAGAAATAAA 1677
OY 333 nLeuAsnIleuValAlaIleGlyIysGlnIleValIysIleCysGlyGlyValProIleuAl 353
Db 1678 TCCAAACTCTTGCGCAATCGGAAGAGATTGTGAAAAAAAGTGGTGTGTGCTCTAGC 1737

OY 353 aAlaIysThrIleuGlyGlyIleleuArgPheIysArgGlnIleuArgGlnIrrGlnIleIysVa 373
Db 1738 AGCCAAAACCTTGAGAGATATTTTGCTTCAGAGAGAAAGAAAGACATGGGAACATGT 1797
OY 373 lArgAspSerGlnIleTrrPlyIleuProGlnIleGlnSerSerIleleuProAlaIleuAr 393
Db 1798 GAGAGACAGTCCGATTTGGAAATTTGGCTCAAGATGAAAGATTCATTTGCTGCTCGAG 1857
OY 393 gLeuSerTrrHisIleuProIleuAspLeuArgGlnCysPheThrTrrCysAlaValPh 413
Db 1858 GCTTAGTTACCATCAACTCCACTTGATTTGAAACAATGCTTTGGATGGATGGGGTGT 1917
OY 413 eProIysAspThrGlnMetGlnIysGlyAsnIleuIleSerIleuTrrMetAlaHisGlyPh 433
Db 1918 CCNAAAGATGCCAAAATGAAAAAGAAAAGCTTATCTCTCTGATGGCGCATGGGTTT 1977
OY 433 eIleLeuSerIysGlyAsnIleuGlnIleuGlnIleuValIAsnGlnIleValTrrAsnGlnIle 453
Db 1978 TCTTTATCAAAAGAAACATGAGAGCTTAGAGATGTGGCGGATGAACTATGAAAGATT 2037
OY 453 uTrrLeuArgSerPhePheGlnGlnIleGlnValIysSerGlyGlnThrTrrPheIysWe 473
Db 2038 ATACTGAGGCTTTTTCACAAGAGATTGAAGTTAAAGATGTAAACCTTATTTCAAGAT 2097
OY 473 tHisAspIleuIleHisAspIleuAlaThrSerIleuPheSerAlaSerThrSerSerSerAs 493
Db 2098 GCATGATCTCATCATGATGATTTGGCAACATCTGTGTTTCAGCAACACATCAAGACAGCA 2157
OY 493 nIleArgGlnIleIleValGlnAsnTrrIleHisIleMetSerIleGlyPheThrIysVa 513
Db 2158 TATCCGGAATTAATTAATAACACAGTTACACACATATGATGTCATTTGGTTCGCCAGAT 2217
OY 513 lValIserSerTrrSerIleuSerHisIleuGlnIysPheValSerIleuArgValIleuAsnIle 533
Db 2218 GGTGTGTTTTTACACTTTCCTCCCTTGGAAGATTTATCTCTGTAAAGTGTATATCT 2277
OY 533 uSerAspIleIysLeuIleIysGlnIleuProSerSerIleGlyAspLeuValHisIleuArgTrr 553
Db 2278 AGGTGATTCGACATTTTAATTAATGATTCATCTTCATTTGAGATCTAGTACATTTAAGATA 2337
OY 553 rIleuAsnIleuSerGlyAsnThrSerIleArgSerIleuProAsnGlnIleuCysIysLeuG1 573
Db 2338 CTGGAACCTGTATGGC---AGTGCATGCGTAGTCTTCCAAAGACATGTATGCAAGCTTCA 2394
OY 573 nAsnIleuGlnIleuIleuAspIleuHisGlyCysHisSerIleuCysIysLeuProIysGlnIuh 593
Db 2395 AAATCTGCAAACTCTTGATCTACATATTTGCACCAAGCTTTGTGTGTTGCCAAAAGAAAC 2454
OY 593 rSerIysLeuGlySerIleuArgAsnIleuIleuAspGlyCysTrrGlyLeuThrCysMe 613
Db 2455 AAGTAACCTTGGTATGATCTCGAAATCTTTACTTGATGATGACGATCATTTGACTGTAT 2514
OY 613 tProProAlaGlnIleGlySerIleuThrCysIleuIysThrIleuSerArgPheValIleGlyI1 633
Db 2515 GCCACCAAGATAGATGATCATTTGACATGCTTAAAGACTTCAAGGTCAATTTGTTGTGA-- 2572
OY 633 eGlnIysIysSerCysGlnIleuGlyGlnIleuArgAsnIleuAsnIleuTrrGlySerIleG1 653
Db 2573 -AGGAAGAAAGGTATCACTTGGTGAATCAAGAAACCTTAATTCCTATAGGCTCAATTTAA 2631
OY 653 uIleThrHisIleuGlnIleuArgValIlyAsnAspMetAspAlaIysGlnIleuAsnIleuSerAl 673
Db 2632 AATCTGCACTTTGAGAGAGTGAAGATGATTAAGGCGCAAAAAGAACCAATTTATTCGC 2691
OY 673 alyIysGlnIleuIleHisSerIleuSerMetIysTrrAspAspAspGlnIuhArgIleTrr 693
Db 2692 AAAAGGAATCTGCATTTCTTTAAGCATGAGTTGG--ATAATCTTTGAACCAATATATA 2748
OY 693 rGlnSerGlnIysValIleuValIleuGlnIleuAlaIleuIysProHisSerAsnIleuThrCysIle 713
Db 2749 TGAATCAAGAAAGATTAAAGTCTTGAAGCCTTCAAAACCAACATCTGACTTCTTT 2808
OY 713 uThrIleArgGlyPheArgGlyIleArgIleuProAspTrrPheAsnHisSerValIleuIy 733
```


Dh 358 GCTGAGAAAGAAAGATTTTCATTTCGACGAAAAAATTGTAGAGACAAGCTGTAGA 417
Qy 141 ArgGlnThrGly----- 144
Dh 418 CGGGAACAGAGTACTCATCTTAATAATAGTATTAACAACATGAAGTTATATTCATTTT 477
Qy 144 ----- 144
Dh 478 TGGCAATTATCAAAATTCAGAAAAAGGTTAAATATACTCATGTCCTATGCTAAATAGTGA 537
Qy 144 ----- 144
Dh 538 TAAATACCTCTGTTGACTTTCGATCGAATATACCTTGCAAAATCTGCAAGCTGAGAA 597
Qy 144 ----- 144
Dh 598 TCAATTAATCAACCCCACTTTTAAATACTGATATCTTTAGAAATCCACCTGTCTAACT 657
Qy 144 ----- 144
Dh 658 CATCCACTACCAATTCCTTTGCTTTGTAATCTTTCTTAACCTTAATAACTTGAACT 717
Qy 144 ----- 144
Dh 718 CGATCCGTTTGTCTTTCTTAACAAGCAGCTCAGAGAAAAAGGTTTCTTCTAATCTG 777
Qy 144 ----- 144
Dh 778 TTTCTCTGTGCTGCACTTGGGCTTAAATCCATTAAACAGGGAGTTAATCCCA 837
Qy 144 ----- 144
Dh 838 ACGAGGTAGCCTTCTGACAGCTGACTGAATTTGTCTAAACAAAGAAAAAAGA 897
Qy 144 ----- 144
Dh 898 TTAGACATGTTTTCTTGTGATTAAGCTGAGATTTCTTGAGGTGAGACATGAGG 957
Qy 144 ----- 144
Dh 958 GATATATTGACCAAAAGTAGAATGGTATATTTAAAGTATTTCTGATGAACAGAG 1017
Qy 144 ----- 144
Dh 1018 TATATTGCGAAATATCTCTATTTCTGTGTCCTAATGATTTGAATTAATAA 1077
Qy 145 ----- Phe-ValLeuAsnGluProGlnValTyrGly 154
Dh 1078 TATTCTCATGTGACATTTGCTTGACCAAGGTTCTGTATTAACCGAACCGGAGTTATGG 1137
Qy 154 YArgAspLysGlnLysAspGlnIleValLysIleLeuIleAsnAsnValSerAsnAlaGly 174
Dh 1138 AAGAGACAAAGAGAAAGATGATAGTAAATCTCTAATAAACAATGTAGTATGCCCA 1197
Qy 174 nThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLysThrThrLeuAlaGly 194
Dh 1198 AACACTTTCAGTCTCTCCCAATATCTGTATGTGGGGGATGAGAAAAACGACTCTTGCCCA 1257
Qy 194 nMetValPheAsnAspGlnArgValIleGlnLysPheHisProLysIleTrrIleCysVal 214
Dh 1258 AATGCTTTCAATATACACAGAGAGTACTGACATTTCCATTCCAAATAATAGATTTGTGT 1317
Qy 214 LserGluAspPheAsnGlnLysArgLeuIleLysGlnIleValGlnSerIleGlnGlnLys 234
Dh 1318 CTGCGAAGATTTTGATGAGAAGAGGTTAATTAAGCAATGTAGAAATCTATTGAAGAAG 1377
Qy 234 sSer---LeuGlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAs 253
Dh 1378 GCCACTAATTGGTGTAGATGACTTGGCTCCACTTCAAAAAGAGGCTTACAGAGTTGCTGAA 1437
Qy 253 nGlyLysLysTyrLeuLeuValIleuAspAspValTrrAsnGlnLysAspGlnAspLysTrrAl 273
Dh 1438 TGGAAAAAGATATCTTGCTTGTCTTAATGATGTTTGGAAATGAAGATCAACAGAAATGGGC 1497

Qy 273 aLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrThr 293
Dh 1498 TAATTTAAGACACTCTTGGAAGGTTGAGCAAGTGGCTTCTGTCTTAACCACTACTCTCG 1557
Qy 293 GLeuGlnLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLeuSerAsnLeuSe 313
Dh 1558 TCTTGAAGAGTTGGATTCATTAATGGAACATTTGCCAACATATGACATGTCAAATCTGTC 1617
Qy 313 rGlnGluAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlnGlnIleAs 333
Dh 1618 TCAGAAAGATTTGTGTGTGTGTTTCATGCAACGTCGATTTGGACACCAAGAGAAATAAA 1677
Qy 333 nLeuAsnLeuValAlaIleGlyLysGlnIleValLysCysGlyGlyValProLeuAla 353
Dh 1678 TCCAAACCTTGTCGCAATCGAAGAGATTTGGAAGAAAAAGTGTGTGTGCTTATGCG 1737
Qy 353 aAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlnLysArgGlnTrrGlnHisVal 373
Dh 1738 AGCCAAAACCTTGAGAGTATTTTGTGCTTCAAGAGAGAAAGAACATGGGAACATGT 1797
Qy 373 LArgAspSerGlnIleTrrLysLeuProGlnGlnGlnSerIleLeuProAlaLeuArg 393
Dh 1798 GAGAGACAGTCCGATTTGGAATTTGCTCAAGATGAAGTTCTAATCTGCTGCTCGAG 1857
Qy 393 GLeuSerTyrHisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPh 413
Dh 1858 GCTTAGTTACATCAACTTCACCTTGATTTGMAACAAATGCTTTGCGTATTTGGCGGTGT 1917
Qy 413 eProLysAspThrGlnMetGlnLysGlnAsnLeuIleSerLeuTrrPheAlaHisGlyPh 433
Dh 1918 CCCAAAGATGCCAAATATGAAAAAGAAAGCTAATCTCTCTGATGCGCATGTT 1977
Qy 433 eIleLeuSerLysGlyAsnLeuGlnLeuGlnAsnValGlyAsnGlnValTrrAsnGlnLe 453
Dh 1978 TCTTTATCAAAAGAAACATGAGAGTGAAGATGTGGGAGATGAAGATGAAGAAAT 2037
Qy 453 uTyrLeuArgSerPhePheGlnGlnIleGlnValLysSerGlyGlnThrTyrPheLysMe 473
Dh 2038 ATACTGAGGTCCTTTTTCACAGAGATGGAAGTTAAAGATGTTAAACATTATTTCAAGAT 2097
Qy 473 tHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAs 493
Dh 2098 GCATGATCTCATCAATGATTTGGCAACATCTCGTTTTGAGCAACACATCAAGCGAGCA 2157
Qy 493 nIleArgGlnIleIleValGlnAsnTyrIleHisMetMetSerIleGlyPheThrLysVal 513
Dh 2158 TATCCGTAATATAATTAACACAGTTACACACATATGATGTCATTTGGTTCGCCGAAGT 2217
Qy 513 ValSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLe 533
Dh 2218 GGTGTTTTTTTACACTTCCCTCCCTGGAAAGTTTATCTGTTAAGAGTCTTATATCT 2277
Qy 533 uSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgLys 553
Dh 2278 AGGTGATTCGACATTAATTAAGTATTCATCTTCATTTGAGATCTAGTCAATTAAAGATA 2337
Qy 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGly 573
Dh 2338 CTTGAACCTGTATGCG---AGTGGCATGCGTATGCTTTCCAAAGCAATTATGCAAGCTTGA 2394
Qy 573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGlnThr 593
Dh 2395 AATTCGCAAACTCTTGATCTACAAATATTGACACCAAGCTTTGTGTGTTTGCAAAAGAAC 2454
Qy 593 rSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMe 613
Dh 2455 AAGTAAACTTGTGTAGTCTCGAAATCTTTTACTGTAGTGTAGCCAGTCAATGACTTGTAT 2514
Qy 613 cProProArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyIle 633
Dh 2515 GCCACCAAGATAGATTCATTTGACATGCTTTAAGACTTATGATCAATTTGTTGTGGA--- 2572

```

Qy 633 eglnlyllyserCyseInleuglygluLeuArgAsnLeuAsnLeuTyrglyserilegi 653
Db 2573 -AGSAAAGAAAGTATATCACTTGTAAGTAAGAACTTAATCTTAATGCTCAATTA 2631
Qy 653 uileThiHleuGlulArgVallyAsnAspMetAspAlaIySGlulAlaenleuSeraI 673
Db 2632 AATCTCCATCTTGAGAGAGTAAGAAATGATTAAGACGCAAAAGCAATTAATCTGC 2691
Qy 673 elySGlulAsnleuHiseSerleuSerMetlySTPAspAspAspIuArgProArgileTy 693
Db 2692 AAAAGGAATCTGCAATCTTTAAGCAAGATTGG--AATTACTTTGGACCAATATA 2748
Qy 693 rGluSerGluIyValGluValleuGluAlaLeuIyProHiseSerAsnleuThrCySle 713
Db 2749 TGATCTGAGAAATTAAGTAAAGCTTGAAGCCCTCAACCACTCAATCTGACTTCTT 2808
Qy 713 uThrIleArgGlyPheArgGlyIleArgleuProAspTTPMetAsnHiseSerValleuTy 733
Db 2809 AAAAATCTATGGCTTCAGAGAAATCCATCTCCAGAGGAGTGAATCACTCAATTAAGAA 2868
Qy 733 eAsnValIySerIleGluIleIleSerCySlyAsnCySserCySleuProProphegi 753
Db 2869 AAAATATTCTCTATTTCTTAATTAAGCACTTCAGAAATGCTCAATGCTTACCACTTTGG 2928
Qy 753 yGluLeuProCySleuIySerleuGluLeuThrPArgIySeraIaGluValIyIyTyVa 773
Db 2929 TGATCTGCTTGTCTTAAGAAATCTTAAGATTACATGGGGGCTCTCGAGATGCGAGTATGT 2988
Qy 773 lAsp-----SergIyPheProThrThrArgArgPheProSeriIe 786
Db 2989 TGAAGAATGATATATGATTTGATTTGATCTGAGATCCCAAGAAATTAAGTTTCATCTT 3048
Qy 786 uArgIyLeuAsnIleArgGluPheGlyAsnLeuIyGlyleuLeuIySlySGlulIyGI 806
Db 3049 GAGGAAATCTGATATATGAGACTTTGTGATGCTAAAGATTTGTGAAAAAGAGAGAGA 3108
Qy 806 uGluGlyCySProValleuGluIleGluIleGlyleuCySProMetPheValIlePr 826
Db 3109 AGACCAATTCCTGTGCTTGAGAGATGATTAATTCAGAGATGCCCTTTTCG----- 3160
Qy 826 oThrLeuSerValIySlyLeuValIySergIyAspIySerAspAlaIleGlyPh 846
Db 3161 -ACCTTTCT----- 3169
Qy 846 eSerSerIleSerAsnleuMetAlaLeuThSerleuGluIleArgTyArgAsnIySGluAs 866
Db 3170 -----TCTATCTTAGGGCTTACTTCTTCCCTCAGAAATTTGCTAATTAAGTAGC 3219
Qy 866 pAlaSerleuProGluIyMetPheIySerleuAlaAsnleuTySTyIleAsnIleSe 886
Db 3220 TACTTCAATCCCAAGAGATGTCMAAAACCTTGCAATCTCAATATCTTGACAAATCTC 3279
Qy 886 rPheTyPheAsnleuIySGluLeuProThrSerleuAlaSerleuAsnAlaLeuIySHI 906
Db 3280 TCGGTGCAATATCTCAAGAGCTGCCCTACAGCTGCTGATGCTGATTTGAAAAG 3339
Qy 906 sLeuGluIleHiseSerCySTyAlaLeuGluSerleuProGluGluIyVallySGlyLe 926
Db 3340 TCTAAAAATCAATGTTGTTGCGCACTAGAGATCTCCCTAGAGAGAGGGCTGAGAGGTTT 3399
Qy 926 uIleSerleuThrGluIySerIleThrTyCySgluMetleuGluIyCysleuProGluI 946
Db 3400 ATCTTCACTCAAGAGATATTGTTGAACACTGTAACATGCTTAATTAATTTTACAGAGGG 3459
Qy 946 yLeuGluHiseleuThralaLeuThrAsnleuSerValGluPheCySProThrleuAlaIy 966
Db 3460 ATTGAGAGACTTAACAACCTCAACAAGTTAAAAATTCGGGAGTGTCCACAACATGATCA 3519
Qy 966 sArgCySglululysGlyIleGlyIyAspTTPTyIyIleAlaHiseIleProArgValPh 986
Db 3520 GCGGTGTGAGAGAGATAGAGAAAGCTGCGACAAAATTTCTCAATTTCTTAATTTGTA 3579
Qy 986 eIleTyT 988

```

```

Db 3580 TATATAT 3586
RESULT 11
ID ADH51533
ID ADH51533 standard; DNA; 5191 BP.
XX
AC ADH51533;
XX
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum Rpi-b1b partial gene SeqID50.
XX
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW ds.
XX
OS Solanum bulbocastanum.
XX
PN US2003221215-A1.
XX
PD 27-NOV-2003.
XX
PE 07-FEB-2003; 2003US-00360522.
XX
PR 07-FEB-2003; 2003US-00360522.
XX
PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
PI Allefs JHM, Van Der Vossen EAG;
XX
DR WPI; 2004-010903/01.
XX
PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
PS Claim 6; SEQ ID NO 50; 98bp; English.
XX
CC This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a fragment of the
CC S bulbocastanum Rpi-b1b protein which is related to the invention.
XX
SQ Sequence 5191 BP; 1673 A; 877 C; 941 G; 1700 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7,03e-303 Length: 5191
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: Gaps: 9
US-10-647-268-2 (1-988) x ADH51533 (1-5191)
Qy 1 MetAlaGluAlaPheLeuGluIyValleuLeuAspAsnleuThrCySPhelIeGluIyGlu 20
Db 1191 ATGCTGAGAGCTTTCATTAAGATCTCTGAGACATCTCACTTCTTCTCAAGAGGGGAA 1250
Qy 21 leuGlyleuIleleuGlyPheIyAspGluPheGluIySleuGluIySeraIlePheThr 40
Db 1251 CTGTATATGCTTCTTGGATTTTCAAGATGAGTTCCAAAGGCTTTCAGAGATGTTTCTACA 1310
Qy 41 IleGluAlaValleuGluAspAlaGluIySleuIySeraIySeraIleGluAsn 60

```



```

Qy 553 rLeuAsnLeuSerGlyAnthrSerIleArgSerLeuProAsnGluLeuCysGlyLeuG 573
Db 3528 CTTBAACCTGATGCG---ACTGGCAGCCGATGCTTCCAAAGCAAGTTATCCAAAGCTTCA 3584
Qy 573 nAsnLeuGlnThrLeuAspLeuH1sglyCysH1SerLeuCysCysLeuProGlyLeuH 593
Db 3585 AAATCTCAAACTCTTGATCTTACAAATATTTGCAACCAAGCTTGTTGTTGCAAAAGAAAC 3644
Qy 593 rSerLeuLeuGlySerLeuAsnLeuLeuLeuAspGlyCysGlyLeuThrCysGlyLeu 613
Db 3645 AAGTAACCTGGTGGTCTCCAAATCTTTACTGATGATGCAAGTCATTTAGCTGAT 3704
Qy 613 tProPArgIleGlySerLeuThrCysLeuLeuThrLeuSerAspPheValIleGlyI 633
Db 3705 GCCACCAAGGATAGGATCATTTGACATGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 3762
Qy 633 eGlnLeuLeuSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuGlySerIleG 653
Db 3763 -AGGAGAAAGGTTATCACTTGGTGAACCTGAAGAACTTAATCTCTATGCTCAATTA 3821
Qy 653 uIleThrH1leuGlnuArgValIlyAsnAspMetAspAlaIysGluIleAsnLeuSerH 673
Db 3822 AATCTCGATCTTGAAGAGAGAAAGATAGGACGCAAAAGAGCCAAATTAATCTGC 3881
Qy 673 alyeGluAsnLeuH1SerLeuSerMetLeuTrpAspAspArgIleuArgProArgIleTy 693
Db 3882 AAAAGGGAATCTGATCTTTTAAGCATAGCTTG---AATACTTTGAGCAACATATATA 3938
Qy 693 rGluSerGluLeuValGluValLeuGluValleuLeuAspProH1SerAsnLeuThrCysLe 713
Db 3939 TGATCTGAGAAAGATTAAGTGAAGCTTGAAGCCCTCAACCACTCAATCTGACTTCTTT 3998
Qy 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnH1SerValLeu 733
Db 3999 AAAAATCTATGCTTCAGAGAAATCCATCTCCAGAGGATGAATCACTCAGATTTGAA 4058
Qy 733 sAsnValIleSerIleGluIleIleSerCysAlaAsnCysSerCysLeuProPheG 753
Db 4059 AAAATATGCTCTCTTTCTTAATTAAGCACTTCAAGAAAGCTCTCAAGCTTCAAGCTTCAAG 4118
Qy 753 yGluLeuProCysLeuLeuSerLeuGluLeuTrpArgIlySerAlaGluValIleGlyI 773
Db 4119 TGATCTGCTTGTCTGAAGAACTTAAGATTAACATCGGGGGCTGGAGATGAGATATGT 4178
Qy 773 lAsp-----SerGlyPheProThrArgArgPheProSerIle 786
Db 4179 TGAAGAGTGAATATGATGTTCAATCTGATCCCAAGAAATTAAGCTTCAATCTCT 4238
Qy 786 uArgLeuLeuAsnIleArgGluPheGlyAsnLeuLeuGlyLeuLeuValGlyGluI 806
Db 4239 GAGGAAATCTGATATATGAGACTTGTGTAAGCTTGAAGAGATTTGCAAAAGAAAGAGGA 4298
Qy 806 uGluGlnCysProValLeuGlnGluIleGluIleLeuCysCysProMetPheValIlePr 826
Db 4299 AGAGCAATTCCTGCTTGAAGAGATGATATTAACAGAGGCTTTTTCG----- 4350
Qy 826 oThrLeuSerSerValIlyLeuValIleValSerGlyAspIlySerAspAlaIleGlyPh 846
Db 4351 -ACCTCTTCT----- 4359
Qy 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgIlyAsnLeuVal 866
Db 4360 -----CTATATCTTAGGGCTCTTACTTCCCTCAAGATTTGCTATTAATTAAGTAC 4409
Qy 866 pAlaSerLeuProGluGluMetPheLeuSerLeuAlaAsnLeuValIlyLeuAsnIleSe 886
Db 4410 TACTTCAATCCCAAGAGAGATTTCAAAAGCTTCAAAATCTCAAAATCTTGAACAATCTC 4469
Qy 886 rPheTyrrPheAsnLeuLeuValGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuValH 906
Db 4470 TCGGTGCAATATCTCAAAAGAGCTGCTTACAGCTTGGCTAGTGTGAATGCTTTGAAAG 4529

```

```

Qy 906 sLeuGlnIleHisSerCysTyralaLeuGluSerLeuProGluGluValIlyGlyLe 926
Db 4530 TCTAAATTCATATGTTGTCGACTAGAGAGCTCCCTCAGAGAGGGCTGAAAGCTTT 4589
Qy 926 uIleSerLeuThrGlnLeuSerIleThrTyrrCysGluMetLeuGlnCysLeuProGlu 946
Db 4590 ATCTTCACTCAACAGATTAATTTGTGAACACTGTAACTGTCTAAATGTTTACAGAGGG 4649
Qy 946 yLeuGlnH1leuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaI 966
Db 4650 ATTGAGACCTTAACAAACCTCACAAGTTTAAATTCGGGAGTGTCCACAACATGATCAA 4709
Qy 966 sArgCysGluLeuGlyIleGlyGluAspTrpTyrrIlyValIleAlaH1leProArgValPh 986
Db 4710 GCGGTGTGAGAAAGGAATAGAGAAAGACTGGCACAAATTTCTCAATCTCTAATGTGAA 4769
Qy 986 eIleTyrr 988
Db 4770 TATATAT 4776

RESULT 12
ADFI7761
ID ADFI7761 standard; DNA; 7349 BP.
XX
AC ADFI7761;
XX
DT 12-FEB-2004 (first entry)
XX
DE Solanum bulbocastanum BAC SPB4 genomic DNA fragment.
XX
KW ds; BAC SPB4; Rpi-b1b gene cluster; growth regulant; oomycete infection;
XX introgression breeding; plant; late blight.
XX
OS Solanum bulbocastanum.
XX
PN EP1334979-A1.
XX
PD 13-AUG-2003.
XX
PF 08-FEB-2002; 2002EP-00075565.
XX
PR 08-FEB-2002; 2002EP-00075565.
XX
PA (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PI Van Der Vossen ENG, Alléfe JHM;
PI WPI; 2003-714439/68.
DR
XX
PT New resistance gene conferring resistance against an oomycete pathogen,
PT useful for producing plants, especially potatoes and tomatoes, resistant
PT against oomycete pathogens such as Phytophthora infestans.
XX
PS Example 5; SEQ ID NO 37; 86pp; English.
XX
CC This invention relates to novel isolated polynucleotides that confer
CC resistance against late blight caused by the oomycete pathogen
CC Phytophthora infestans, which threatens both tomato and potato crops.
CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
CC and which cause disease resistance to bacteria, fungi, nematodes etc.
CC These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
CC described as plant growth regulants. They are useful in providing
CC resistance to Phytophthora infestans, especially in Solanum tuberosum
CC (potato) plants to protect against oomycete infection or to demonstrate
CC disease susceptibility. Resistance can be conferred by transformation of
CC existing potato and tomato cultivars with the gene, a procedure that is
CC more straightforward and faster than conventional introgression breeding.
CC This polynucleotide sequence is the Solanum bulbocastanum BAC SPB4
CC genomic DNA fragment, present in RGC2-b1b of the invention.
XX
SQ Sequence 7349 BP; 2508 A; 1139 C; 1218 G; 2484 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:	1,16e-302	Length:	7349
Score:	3638.50	Matches:	754
Percent Similarity:	68.03%	Conservative:	78
Best Local Similarity:	61.65%	Mismatches:	129
Query Match:	70.97%	Indels:	262
DB:	10	Gaps:	9

US-10-647-268-2 (1-988) x ADF17761 (1-7349)

```

Oy      1 MetValGluValPheLeuGlnValLeuLeuAspLeuThrCysPheIleGlnGlyGlu 20
Db      2648 ATGGCTGAAGCTTTTCATTCAGAGTCTGCTAGACATCTCATTCTTCTCTCAAGGGAAA 2707
Oy      21 LeuGlyLeuIleLeuGlyPheLeysAspGluPheGluIlyLeuGlnSerThrPheThrThr 40
Db      2708 CTGTGATTGCTTTTGGTTTTCAGAGTGAATCCAAAGGCTTTCAAAGCATGTTTCTTACA 2767
Oy      41 IleglnIaValLeuGluAspAlaGlnIlySylsGlnLeuIlySAspLysAlaIleGluAsn 60
Db      2768 ATTCAGAGCCGTCCTTGAAGATGCTCAGAGAGCAACTCAACACAAAGCTCTAGAAAT 2827
Oy      61 TrpLeuGlnIlySLeuAsnAlaAlaIatYrGluIaAspAspIleLeuAspGluCysLys 80
Db      2828 TGGTTGCAAAAACCTCAATGCTGCTACATATGAGTCAGATGACATCTTGATGAATATAAA 2887
Oy      81 ThrGluIaProIleArgGlnIlySAsnIlySylsYrGlyCysYrHisProAsnValIle 100
Db      2888 ACCAAGGCC---ACAAGATTCCTCCAGCTCGAATATGCGCGTTATCATCAAGAGTTATC 2944
Oy      101 ThrPheArgHisIleGlyIlySAspMetIlySylsIleMetGlnIlySLeuAspValIle 120
Db      2945 CCTTTCCTGCAAGAGTGGGAAAAGAGTGAACCAAGATGATGAAAACTAAAGCAATT 3004
Oy      121 AlaIaGluArgIleIlySAspHisLeuAspGluArgThrIleGluArgGlnValaIaThr 140
Db      3005 GGTGAGAAAAGAAAGAAATTTTCATTGGACGAAAAAATTGTAGAGAGCAAGCTGTAGA 3064
Oy      141 ArgGlnThrGly----- 144
Db      3065 CGGGAACAGGTACTCATCTTAAATAGTATTAACAACAATAAGTTATTCATTATTTT 3124
Oy      144 ----- 144
Db      3125 TGGCAATTATCAAAATTCAGAAAAGGTTAAATATCTCATGCTCTATGCTAAATAGTGA 3184
Oy      144 ----- 144
Db      3185 TATATACCTCTGTTGATCTTCGATCTGAATATACCTTGCAAAATCTGGCAGACTCAGAA 3244
Oy      144 ----- 144
Db      3245 TCAAAATTATCAACCCCACTTTTAAATACTCGATATCTTTAGAAAATCCACCTGTCTAACT 3304
Oy      144 ----- 144
Db      3305 CATTCACATACCATTCCTTTGCTTGAATCTTTTCTTACCTATTAACCTTGAAACACT 3364
Oy      144 ----- 144
Db      3365 CGATCCGTTTGGTTTCTTAAACAAGACACTCAGAGAAAAGAGTTTCTTCTAATTCG 3424
Oy      144 ----- 144
Db      3425 TTTCTCTGTGTGTGCTGCACTTGGTCTTAATCCCATTAACAAAGGCAATGTTAATCCCA 3484
Oy      144 ----- 144
Db      3485 AGCAGCGTAGCCTTTCTGACAGCTGACTGTAATTTTGTCTAACAAGAAAAAGAAAAAGA 3544
Oy      144 ----- 144
Db      3545 TTAGACATGTTTTTCTGTGATGATGATAGAGCTGATTTCTTTCAAGATGAAACATAGGG 3604

```

```

Oy      144 ----- 144
Db      3605 GATATATTGGACCAAAAAGTAAAGATGGGTATATATTAAAGTATTTCTGATAGAACAGAG 3664
Oy      144 ----- 144
Db      3665 TATATTGGCAAAAATATCTCTATTATTCTGTGTCTCTAATAGATGATGAATATATA 3724
Oy      145 ----- 144
Db      3725 TATTTTCATGTGACATTTGCTTGACACAGGTTCTGTATTAACCGAACCGAGTTATAG 3784
Oy      154 YrGAspIlySglIlySAspGluIleValIlySileLeuIleAsnAsnValSerAsnIaG 174
Db      3785 AAGAGCAAAAGAAAGATGATGATGAGAAATCTTATATAACAATGTTGATGATGCCCA 3844
Oy      174 nThrLeuProValLeuProIleLeuGlyMetGlyIlyLeuGlyIlySThrThrLeuIaG 194
Db      3845 AACCTTTCAAGTCTCCCAATACCTGGTATGGGGGATGAGAAAACGACTCTTGCCCA 3904
Oy      194 nMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrpIleCysVa 214
Db      3905 AATGCTCTCAATGACCAAGAGTACTGAGCAATTCATTCCAAATATAGATTTGTGT 3964
Oy      214 IserGluAspPheAsnGluIlySAspLeuIleIlySglIlyValIaGlnSerIleGlnGlu 234
Db      3965 CTGGAAATTTTTCATGATGAGAAAGGTTAATMAAGCAATTTGTAATCTATGAAGAGAG 4024
Oy      234 sSer---LeuGlyIlyMetAspLeuAlaProLeuGlnIlySLeuArgAspLeuAs 253
Db      4025 GCCACTACTTGTGATGATGACATTTGGCTGCCCACTCAAAAAGCTTCAGAGTTGCGAA 4084
Oy      253 nGlyIlySLeuThrLeuValLeuAspAspValITrPAsnGluAspGlnAspIlyStrAl 273
Db      4085 TGGAAAAGACTCTGCTGTCTTGAATGATGTTTGAATGAAGATCAACAGAAAGTGGC 4144
Oy      273 alyLeuArgGlnValLeuIlySValIaIaSerGlyValIaSerValLeuThrThrThr 293
Db      4145 TAAITTAAGACAGTCTTGAAGGTGAGCAAGGGCTTCTGTTCTTAACCACTACTCTG 4204
Oy      293 gLeuGlnIlySValIySerIleMetGlyThrLeuGlnProTyGlnLeuSerAsnLeu 313
Db      4205 TCTTGAAGAAGGTTGATCAATTAATGAGAACATTCGCAACATGATGCTCAAAATCTGTC 4264
Oy      313 rGlnGluAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlnIlyLeas 333
Db      4265 TCAAGAGATTTGTTGTTGTTGTTTCATCGAACGTGCATTTGAGACCAAGAGAAATATA 4324
Oy      333 nLeuAsnLeuValaIaIleGlyIlySglIlyValIlySylsCysGlyIlyValProLeuAl 353
Db      4325 TCCAAACCTTGTGCAATCGGAAGAGAGATTGTAAAAAAGTGGTGTGCTTAC 4384
Oy      353 aAlaIySThrLeuGlyIlyIleLeuArgPheIlySArgGlnGluArgGlnTrpGluHisVa 373
Db      4385 AGCCAAAACCTTGAGAGTATTTTGTCTTCAAGAGAAAGAAAGACAGATGGAAACATGT 4444
Oy      373 lArgAspSerGluIleTrpIlySLeuProGlnGlnIlySAspSerIleLeuProAlaLeu 393
Db      4445 GAGAGACGTCGATTTGGAATTTGCTCAAGATGAAAGATTCATTTCTGCTGCTCGAG 4504
Oy      393 gLeuSerTyHisIleuProLeuAspLeuArgGlnCysPheThrTyrcysAlaValPh 413
Db      4505 GCTTATGATACATCACTTCACCTTGATTGAATTAACAACATAGCTTTCGTAATGTGGGGTT 4564
Oy      413 eProIlySAspThrGlnMetGlnIlySglIlyAsnLeuIleSerLeuThrPheMetAlaHisGlyPh 433
Db      4565 CCCAAAGATCCCAAAATGAAAAGAAAGAAAGCTAATCTCTCTGATGGCGCATGGTTT 4624
Oy      433 eIleuSerIlySglIlyAsnLeuGluIlySValIaIySAsnGluValITrPAsnGluLe 453
Db      4625 TCTTTTATCAAAAAGAAACATGAGACTAGAGAGATGTGGCGCATGATGAGAAAGAAATT 4684

```



```

Qy 453 uTyrLeuArgSerPhehegIngluilegluVallysSerGlyGlnThrTyrPheLysMe 473
Db 4685 ATACTTGAGGCTCTTTTCCAAAGAGATTGAAGTTAAAGATGTTAAACTTATTTCAAGAT 4744
Qy 473 thiaapleuilehisapleuilaathrSerleuPheSerAlaSerThrSerSerSerSAs 493
Db 4745 GCAATGATCTCATGATGTTGGCAACATCTCTGTTTCACCAACACATCAACAGACAGAA 4804
Qy 493 nllaArgGluilelleValaGluAsnTyrlehisemecSerilegilePheThrLysVa 513
Db 4805 TATCCGTAATTAATAACACAGTTACACACATATGATGTCATTTGCTTTCGCCGAAGT 4864
Qy 513 lvalSerSerTyrSerleuSerHisleuGlnLysPheValaSerleuArgValaLysAsnle 533
Db 4865 GGTGTTTTTTTACACTTCTCCCTGGAAAGTTATCTCGTTTAAGAGGCTTAATCT 4924
Qy 533 useThrPleLysLysLysGlnleuProSerSerilegluAspLeuValHisleuArgTyr 553
Db 4925 AGGTGATTCGACATTATTAATAGTACCATCTTCATTTGAGATCTAGTACATTTAAGATA 4984
Qy 553 rleuAsnleuSerGlyAsnThrSerileArgSerleuProAsnGlnleuCysLysLysleuG 573
Db 4985 CTTAAACCTGATATGCG--AGTGGCATGCGTATGCTTCCAAAGCATTTATGCAAGCTTCA 5041
Qy 573 nasnleuGlnThrleuAspLeuHisgluCyAsHisSerleuCyGlySerProLysgluTh 593
Db 5042 AAATCTGCAAACTTTGATCTCAATATTTGCAACCAAGCTTTGTTGTTGCCAAAGAAAC 5101
Qy 593 rSerLysleuGlnleuSerleuAsnleuAsnleuAspGlyCysTyrGlyleuThrCysMe 613
Db 5102 AAGTAACTTGATGATGCTCCCAAACTTTTACTTGATGATGTCACAGTCATTTGATGAT 5161
Qy 613 tProPArgTleuGlySerleuThrCysleuLysThrleuSerArgPheValaGlyIle 633
Db 5162 GCCACCAAGATAGAGATCATTTGACATGCTTTAAGACTTACGTCATATTTGTTGGA-- 5219
Qy 633 eglnLysLysSerCysGlnleuGlnGluLeuArgAsnleuAsnleuTyrGlySerilegl 653
Db 5220 -AGGAAGAAAGGTATATCACTTGATGAACTGAACTTAATCTATATGCTCAATTA 5278
Qy 653 uileThrHisleuGlnLysValaLysAsnAspMetAspAlaLysGluAlaAsnleuSerAl 673
Db 5279 AATCTCGCATCTTGAAGAGATGAAAGATGATAGACGCAAAAGCAATTTATCTGCG 5338
Qy 673 alYsGluAsnleuHisSerleuSerMetLysTrpAspAspArgLysArgProArgileTy 693
Db 5339 AAAAGGGAATCTGATCTTTAAGCATGAGTTGG--AATTACTTTGACCACTATATA 5395
Qy 693 rGluSerGluLysValaGluValleuGluAlaLysLysProHisSerAsnleuThrCysLe 713
Db 5396 TGATCTGAGAGAAATTAAAGTCTTGAAGCCCTCAACCACTCAATCTGACTTCTTT 5455
Qy 713 uThrLleArgGlyPheArgGlyLleArgLeuProAspTrpMetAsnHisSerValaLysL 733
Db 5456 AAAAATCTATGCTTCAGAGGAATCCATCTCCAGAGAGATGATCACTCAGATTGAA 5515
Qy 733 aaenValaValaSerilegluilelleSerCysLysAsnCysSerCysleuProProPhegl 753
Db 5516 AAAATATTGTCCTATTTCTAATTAGCACTTCAGAAACGCTCACTTACCACTTCTTGG 5575
Qy 753 yGluLeuProCysleuLysSerleuGlnleuTyrArgGlySerAlaGluValaGluTyrVa 773
Db 5576 TGATCTGCTTGTCTTAAGAAAGTCTAGATTCACACTGGGGGCTCGGATGCGAGTATGT 5635
Qy 773 laap-----SergLysPheProThrArgArgPheProSerLe 786
Db 5636 TGAAGAAAGTGATATTGATTTTCATTTGATTCCTCCCAAGAAATTAAGTTTCCATCTT 5695
Qy 786 uArgLysLysAsnLleArgLysPheGlnPheAsnleuLysGlyLysleuLysLysGluGly 806
Db 5696 GAGGAAACTTATATTAAGGACTTTGATGATCTAAGAGATTTGCTGAAAAAGAGAGAGA 5755
Qy 806 uGluGlnCysProValleuGlnGluilegluileLysCysAspProMetPheVallePr 826

```

```

Db 5756 AGAGCAATTCCTCGTCTTGAAGAGATGATTAATTCACAGAGGCCCTTTCTG----- 5807
Qy 826 oThrLeuSerSerValLysLysLeuValaSerGlyAspLysSerAspAlailegluPh 846
Db 5808 -ACCTTTCT----- 5816
Qy 846 eSerSerileSerAsnleuMetAlaLeuThrSerleuGlnlleArgTyrAsnLysgluAs 866
Db 5817 -----TCTATCTTAGGGCTCTTACTTCCCTCAGAAATTGCTATATAAAGTAGC 5866
Qy 866 palAserleuProGluLysMetPheLysSerleuAlaAsnleuLysTyrleuAsnilleSe 886
Db 5867 TACTTCATTCGCCAGAGAGATGTTCAAAAACCTTGCAAACTCTCAAAATACCTTGACAATCTC 5926
Qy 886 rPheTyrPheAsnleuLysGluLeuProThrSerleuAlaSerleuAsnAlaLeuLysHis 906
Db 5927 TCGGTGCAATATATTCAAAGAGCTGCTTACCAGCTTGATGCTGATGCTTGAAG 5986
Qy 906 vleuGluileHisSerCysTyrAlaLeuGluSerleuProGluGluValaLysgluLe 926
Db 5987 TCTAAATTTCAATTTGTTGGCTTACCTAGAGAGTCTCCCTGAGGAGGCTCGAAGTTT 6046
Qy 926 uileSerleuThrGlnleuSerileThrTyrCysGluMetleuGlnCysleuProGluG 946
Db 6047 ATCTTCACTCAGAGATTAATTTGTTGAACACTGTAACATGCTTAATATGTTTACAGAGGG 6106
Qy 946 yLeuGlnHisleuThrLalaLeuThrAsnleuSerValaGluPheCysProThrLysAlaL 966
Db 6107 ATTGCACACCTTAACAAACCTTCACAAAGTTTAAAAATTCGGGAGATGTCACAACTGATCA 6166
Qy 966 sarGSGluLysgluilegluGluAspTrpTyrLysileAlaHisileProArgValaPh 986
Db 6167 GCGGTGAGAGAGGATAGAGAGAGACTGCGACAAAATTTCTCACTTCTAATGTGA 6226
Qy 986 eileTyr 988
Db 6227 TATATAT 6233

RESULT 13
ADFI7763
ID ADFI7763 standard; DNA; 3971 BP.
XX
AC ADFI7763;
XX
DT 12-FEB-2004 (first entry)
XX
DE S_bulbocastanum RGC3-b1b coding DNA containing an intronic sequence.
XX
KW gene; ds; RGC3-b1b; Rpl-b1b gene cluster; growth regulant;
KM oomycete infection; introgression breeding; plant; late blight.
XX
OS Solanum bulbocastanum.
XX
OS
XX
Key Location/Qualifiers
FT CDS 1..3971
FT /tag= a
FT /product= "RGC3-b1b protein"
FT /note= "this coding sequence contains one intron"
FT /transl_except= (pos: 1459..14560, aa: Gly)
FT intron 428..1458
FT /*tag= b
FT /number= 1
XX
XX EPI334979-A1.
XX
XX 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX (KWE- ) KWEK EN RESEARCHBEDRIJF AGRICO BV.

```

```

XX  Van Der Vossen EAG, Allele UHM;
XX  WPI; 2003-714439/68.
XX  P-PSDB; ADF17766.
XX  New resistance gene conferring resistance against an oomycete pathogen,
XX  useful for producing plants, especially potatoes and tomatoes, resistant
XX  against oomycete pathogens such as Phytophthora infestans.
XX  Example 5, SEQ ID NO 39; 86pp; English.
XX
CC  This invention relates to novel isolated polynucleotides that confer
CC  resistance against late blight caused by the oomycete pathogen
CC  Phytophthora infestans, which threatens both tomato and potato crops.
CC  Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC  leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
CC  and which cause disease resistance to bacteria, fungi, nematodes etc.
CC  These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
CC  described as plant growth regulators. They are useful in providing
CC  resistance to Phytophthora infestans, especially in Solanum tuberosum
CC  (potato) plants to protect against oomycete infection or to demonstrate
CC  disease susceptibility. Resistance can be conferred by transformation of
CC  existing potato and tomato cultivars with the gene, a procedure that is
CC  more straightforward and faster than conventional introgression breeding.
CC  This polynucleotide sequence is the Solanum bulbocastanum RGC3-b1b coding
CC  DNA containing an intronic sequence in an exemplification of the
CC  invention.
XX
SQ  Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.:      2.74e-300      Length:      3971
Score:          3606.50       Matches:     763
Percent Similarity: 63.02%    Conservative: 77
Best Local Similarity: 57.24%  Mismatches: 137
Query Match:    70.34%       Indels:      357
DB:             10           Gaps:        9
US-10-647-268-2 (1-988) x ADF17763 (1-3971)
OY  1 MetAlaGuaIaPheLeuGlnValIleuLeuSPaenLeuThrCysPheIleGlnGlyGu 20
DB  1 ATGGCTGAGGCTTTCATTCAAGTGTGCTAGACAAATCTCATTCTTCTCAAGGGGAA 60
OY  21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGlyIleuGlnSerThrPheThrThr 40
DB  61 CTTCATTGCTTTTCGTTTCAGATGAGTCCAAAGCTTTCAGAGATGTTTCTACA 120
OY  41 IleglnAlaValIleuGlnAspAlaGlnIleuGlnLeuIleuAspIleuAlaIlegln 60
DB  121 ATCCAAAGCGCTCTTGAAGATGCTCAAGAGAGCAATCAAGCAAGACCTTAAAGAAAT 180
OY  61 TrpLeuGlnIleuLeuAsnAlaAlaIleuTyrgIuaIaAspAspIleuAspGluCys 80
DB  181 TGGTTGCAAAAACCTCAATGCTCTCAATATGAAGTCAATGATCATCTGGATGAATATAA 240
OY  81 ThrGluAlaProIleArgGlnIleuAsnIleuTyrgIuGlyCysTygHisProAsnValIle 100
DB  241 ACTAAGGCC---ACAAGATTTCTTGAGCTGTAATGCGCTTATCATCCAAAGGTATAC 297
OY  101 ThrPheArgHisIleuIleGlyLysArgMetIleuIleMetGlnIleuAspValIle 120
DB  298 CCTTTCCTGACAAAGGTTGGAAAAGATGACCAAGTCAATGAAAACCTGAATGCAAT 357
OY  121 AlaAlaGluArgIleuAspHisIleuAspGluArgThrIleGluArgGlnValAlaThr 140
DB  358 GGTGAGGAACGAAGAATTTTCATTTCGAAAGAAAGATTATAGAGACAAAGCTCTACA 417
OY  141 ArgGlnThrGlyPhe----- 145
DB  418 CGGGAACAGGTAC-TCATCTTAATTAGTATTACAATTAGTTATATTCATTGTTT 476

```

```

OY  145 ----- 145
DB  477 GGGCAATGATCAATATTATGTAAAGTCAATATATCTAGTACTAGTAAATATGTTTAA 536
OY  145 ----- 145
DB  537 ATATACCTTAGTATATATCTATAGTACGAACATATCTCTCCATATATCTTGGACAAAT 596
OY  145 ----- 145
DB  597 ATTCCCTTAACGAATATAGACACGTGAAGTTCAGATTCAATTTATCCACCCATTT 656
OY  145 ----- 145
DB  657 TAAAGTCTGATTTCTTTAGGAAACCACTCATCTCTCCGTTTGAATTCTTAAAGAA 716
OY  145 ----- 145
DB  717 GCTCAGAAAAAGAGTTTCTCTGTTCTGTTTCTGTCGATTTTGTCTTAATCCAAT 776
OY  145 ----- 145
DB  777 AACAAACATACAAATTAATATATATGTTCAAGATGAGGTAGTCTTTCTAGCTACATG 836
OY  145 ----- 145
DB  837 AACTAGTGTAAATTTTGTTTTAAAGAAAGAAAGAAATGATTAGCTGATTTCTTTCA 896
OY  145 ----- 145
DB  897 GAGTGAATATAGGGGATTAAGTTGAGACATAGATGATTCATGTTATTTCTTCTTA 956
OY  145 ----- 145
DB  957 AAGTAAAGTTTCAAAATATGATATCAAGGTACGTAATGAAATATTATAGACAGTTC 1016
OY  145 ----- 145
DB  1017 TAACTACAAAATATGATATGAAATCTTAATATATCACTGACAAATATCTTAAATPAA 1076
OY  145 ----- 145
DB  1077 GCTACAAATTAATATCATGATACAGAGAAAGAAACCAAAAAATTAGGGTGAATTTT 1136
OY  145 ----- 145
DB  1137 GATTCATGCTTATCATCATGCTTCCATCAACATCAAGAAATTTGSCAAAGTAT 1196
OY  145 ----- 145
DB  1197 AAACGGTCGGTATATTTGATTGAAAGTAAACAGAGATACATTTGACTAAAGTA 1256
OY  145 ----- 145
DB  1257 TAACAATATATATTTGATGATCTTTATGATCAAAATTCATGTCGTTTGGGAGAAG 1316
OY  145 ----- 145
DB  1317 GAAATTCATATGTTTCAATGCTGCTCATGTCATCCATATCTTTATTTGCAAAAC 1376
OY  145 ----- 145
DB  1377 CCTTCTATTTAACTATTTTTCGCCGACTCTATAGACTTGAATGATTAACATATTTCTC 1436
OY  146 ----- 146
DB  1437 ATCTGACATTTGCTTGACACAGGTTCTGTGTTAACTGAACCAAGTTTATGGAAGGAC 1496
OY  157 LysGlnIleuAspGluIleValIleIleuIleAsnValIleSerAsnAlaGlnThrIleu 176
DB  1497 AAAGAAAAGATGATGATGATAAATCTTATTAACAATGTATGATGCCCAAAATCTC 1556
OY  177 ProValIleuProIleuGlyMetGlyGlyLeuGlyLysThrThrIleuAlaGlnMetVal 196

```

1557 TCAGTCCCTCCCAATCTGTATGGGGGAGCTAGAGAAAGACAACCTCTTCCCAAAATGGTC 1616
197 PheAanApGlnAnArgValIleGluHisPheHisProLysIleThrPileCysValSerGlu 216
1617 TTCAATGATGACAGAGATGAACTGAGCGTTTCTATCCCAAAATGGAATTTGGCTCTCGAAT 1676
217 AspPheAnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeu 236
1677 GATTTTGATGAGAAAGCTGTGATTAAGGCATATGATGATCTATTTGAAAGGAAAGTCCCTC 1736
237 GlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAnGlyLysLys 256
1737 AGTGCATGAGACTGGCTCCCACTTCAAAAGAGCTTCAAGAGTGGCTGATGAGAAAAGA 1796
257 TyrLeuLeuValLeuAspAspValITrpAsnGluAspGlnAspLysITrpAlaLysLeuArg 276
1797 TACTTCTTGTCTTGTGATGATGTTGGAAATGAAATCAACATAACTGGGCTTAATTTAAGA 1856
277 GlnValLeuLysValGlyValAsnSerGlyAlaSerValLeuThrThrArgLeuGluLys 296
1857 GCAGTCTTGAAAGCTTGACAGATGCTGCTATTTGTTCTACTACTACTGCTCTTGAAAAG 1916
297 ValGlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnLysAsp 316
1917 GTTGATCAATTAATGGAACATGCAACCATATGATGATTTGCTCAATCTGCTCAGAGGAT 1976
317 CysITrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAnLeu 336
1977 TGTGTGTTTTGTTGATGACGCTCATTTGGACACCAAGAAATTAATCAACCTT 2036
337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThr 356
2037 GTGGCAATCGGAAAGAGATGTGAAAATGTGGTGGTGGCTCTTACACCCAAAGACT 2096
357 LeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnITrpGluHisValArgAspSer 376
2097 CTGGAGGATATTTTCCGCTTCAAGAGAGAAAGAAATGGAACATGCTGAGAGACAGT 2156
377 GlnIleITrpLysLeuProGlnGluGluSerIleLeuProAlaLeuArgLysSerTyr 396
2157 CCGATTTGGAAATTTCCCTCAAGATGAAAGTTCTATTTCTGCCCTGAGGCTTGAATAC 2216
397 HisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAsp 416
2217 CATCATCTTCCACTTGATTTGACACATGCTTGTGATATGCGGATATCCCAAGGAC 2276
417 ThrGluMetGluLysGlyAsnLeuIleSerLeuITrpMetAlaHisGlyPheIleLeuSer 436
2277 ACCAAAATCGCAAAAGAAAATCTTATCGCTTTTGGATGGCACATGCTTTCTTTATCG 2336
437 LysGlyAsnLeuGluLeuGluLysAnValGlyAsnGluValITrpAsnGluLeuTyrLeuArg 456
2337 AAAAGAAATTTGGACCTAGAGATGATGAGTATGAAGTATGAAATGAATTAATTAAGG 2396
457 SerPhePheGlnGluIleGluValLysSerGlyGlnITrpPheLysPheHisAspLeu 476
2397 TCTTCTTCCAAAGAAATGAAATGATGATGTAATAAATTAATTAAGTGAATACCTC 2456
477 IleHisAspLeuAlaIThrSerLeuPheSerAlaSerIThrSerSerSerAnIleArgGlu 496
2457 ATCCATGATTTGGCTACATCTCTGTTTTCAGCAACACATCAAGACGCAATTTGCTGAA 2516
497 IleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSer 516
2517 ATAAATGCTAATTAATGATGATATATGATGATGATGATTTGCTGAAGTGGTATCTTCT 2576
517 TyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAnLeuSerAspIle 536
2577 TACTCTCTTCACTCTTGGAAAAGTTGTCTCATTAAGGCTCTTAATTAAGAAACTCG 2636
537 LysLeuLysGluLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAnLeu 556

2637 AACCTAAATCAATTAACATCTTCCATTTGGAGATCTAGTACATTTAAGATPACTGGACTTG 2696
557 SerGlyAnThrIThrSerIleArgSerLeuProAnGlnLeuCysLysLeuGlnAsnLeuGln 576
2637 TCTGGCAATTTAGAAATTCGTATATCTTCCAAAAGATTAATGACGCTTCAAAATTTGACG 2756
577 ThrLeuAspLeuHisGlyCysHisSerLeuCysLeuProLysGluIThrSerLysLeu 596
2757 ACTCTTAATCAATTAATTAATGAGACTCTCTTCTTGTGGCCAAAACAAGATTAACCTT 2816
597 GlySerLeuArgAnLeuLeuLeuAspGlyCysTyrGlyLeuIThrCysMetProProArg 616
2817 GGTACTCTCCGAAATCTTTACTTGATGCTGT---TCATTAACCTCAACGCAACAGG 2873
617 IleGlySerLeuIThrCysLeuLysIThrLeuSerArgPheValIleGlyIleGlnLysLys 636
2874 ATAGATTTGATGACATGCTTAAAGCTTAAAGTCTTTGTTATTTGGC---AAGGAAA 2930
637 SerCysGlnLeuGlyGluLeuArgAnLeuAnLeuTyrGlySerIleGluIleThrHis 656
2931 GGTATCAACTTGGTGAACCTAAACCTAAATCTCTATGGCTCAATTCATCACAAAA 2990
657 LeuGluArgValLysAsnAspMetCaspAlaLysGluAlaAsnLeuSerAlaLysGluAn 676
2991 CTGACAGAGTGAAGAAAGATAGCGATGCAAAAGAGCTAATTTATCTGCTAAACCAAT 3050
677 LeuHisSerLeuSerMetLysITrpAspAspArgGluArgProArgIleTyrGluSerGlu 696
3051 CTGACCTTTTATGCTTATGCTTATGAGTGGACCTTGATGAAAACATAGA---TATCATTTCA 3104
697 LysValGluValLeuGluAlaLeuLysProHisSerAnLeuIThrCysLeuThrIleArg 716
3105 -----GAAGTTCTTGAAGCCCTCAACACACCTCAATCTGAATATTAGAAATCAT 3158
717 GlyPheArgGlyIleArgLeuProAspITrpMetAsnHisSerValLeuLysAnValVal 736
3159 GGCTTCGAGAGAAATCCGCTCCAGATTTGATGATCAATCATCGTTTGAAAATTTTGC 3218
737 SerIleGluIleIleSerCysLysAnCysSerCysLeuProProPheGlyGluLeuPro 756
3219 TCTATTAAGAAATTAAGGTTTGGAAGAACTGCTCATCTTCAACCCCTTGTGTAGCTGCT 3278
757 CysLeuLysSerLeuGlnLeuITrpArgIleSerAlaGluValGluTyrVal---AspSer 775
3279 TGTCTGAAGAACTTGAAGTTTACACACCGGCTAGCAGATGAGATATGTTGAAGTAT 3338
776 GlyPheProIThrArgArgPheProSerLeuArgLysLeuAnIleArgGluPheGly 795
3339 GTTCATCTCT-----GGAAGGTTTCCATCTTGAAGAAACTGTTATATGGAACCTTTAGT 3392
796 AnLeuLysGlyLeuLeuLysGluGluGluGluGlnCysProValLeuGluGluIle 815
3393 AATCTAAAGAAATGCTGTAAGAAAGAGAAAGAAAGCAATTCCTGTGCTTGAAGAGATG 3452
816 GlnIleLysCysCysProMetPheValIleProIThrLeuSerSerValLysLeuVal 835
3453 ACATTTTACTGGTCCCTATGTTTGTATTCGACCTTTCTTCTGTAAGCATTTGAAA 3512
836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
3513 GTTATTGGG-----ACAGATGCAACAGTTTGAAGTCCATATCTTAATCTTGGGCTCTT 3566
856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGlnGluMetPheLys 875
3567 ACTTCCCTTGAACATTAAGCAATTAAGCAAGCTACTTCACTCCCAAGAAAGATGTTCAAA 3626
876 SerLeuAlaAsnLeuLysTyrLeuAnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
3627 AGCTTGAATTCATCAATTAATCTGAAATATCTTTCTTTAGGAATCTCAAGAGATGGCT 3686
896 ThrSerLeuAlaSerLeuAnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeu 915
3687 ACCAGCTGGCTAGTCAATGCTTGTGAAGAGTCTCAATATTGAATTTGTTGAACGACATA 3746

Oy	916	GIUSerLeuProGluGluGlyVallyesGlyLeuIleSerLeuThrcIleuSerIleThr	935
Db	3747	GAGAGTCTCCACGAGGAAAGGAGTTTAACTTCACTACCGAGTGTCTGCAGT	380
Oy	936	TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnHisLeuThrAlaLeuThrAsn	955
Db	3807	AACTGTATGATGACTTAAATAGTTTACCGAGGAGATTGCACACCTAACAGCCCTCACACT	386
Oy	956	LeuSerValGluPheCysProThrLeuAlaIysArgCysGluIuIleGlyGluAsp	975
Db	3867	TTAAACAATTACTCAATGTCTCAATTGATTTCAAGCGGTGTGAGAGAGAAATAGAGAAAGAC	392
Oy	976	TrpTyrIlysIleAlaHisIleLeuProArgValPheIleTyr	988
Db	3927	TGGCACAATAATGCTCACATTTCCATTGTGACTCTATAT	3965
RESULT 14			
ID	ADH51535	ADH51535 standard; DNA; 3971 BP.	
XX	ADH51535;		
XX	ADH51535;		
XX	25-MAR-2004	(first entry)	
XX	S	bulbocastanum RGC3-dlb gene SeqID52.	
XX	DE		
XX	KW	plant disease; oomycete infection; Phytophthora infestans; fungicide;	
XX	KW	Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;	
XX	ds;	RGC3-dlb.	
XX	Solanum	bulbocastanum.	
XX	US2003221215-A1.		
XX	27-NOV-2003.		
XX	07-FEB-2003;	2003US-00360522.	
XX	07-FEB-2003;	2003US-00360522.	
XX	(KWEK-)	KWEK EN RESEARCHBEDRIJF AGRICO BV.	
XX	Allefs JHMH,	Van Der Vossen EAG;	
XX	WPI;	2004-010903/01.	
XX	PS	Claim 6; SEQ ID NO 52; 98pp; English.	
XX	PT	New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful	
XX	PT	for providing members of the Solanaceae family e.g. Solanaceae tuberosum	
XX	PT	with resistance against oomycete infection.	
XX	CC	This invention relates to a novel DNA sequence in the field of plant	
XX	CC	disease, in particular oomycete infections. The DNA sequence encodes a	
XX	CC	protein which may provide a plant or its progeny with at least partial	
XX	CC	resistance against an oomycete infection caused by Phytophthora	
XX	CC	infestans. The invention may be useful for the development of compounds	
XX	CC	with a fungicide activity. The DNA sequence of the invention encodes an	
XX	CC	Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,	
XX	CC	cell, protein or binding molecule is useful for providing a plant or its	
XX	CC	progeny with resistance against an oomycete infection such as late blight	
XX	CC	(a disease of major importance to production of Solanaceae such as potato	
XX	CC	and tomato cultivars). The present sequence is that of the S	
XX	CC	bulbocastanum RGC3-dlb gene which is related to the invention.	
XX	Sequence	3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;	
Alignment Scores:			
Score:	2,74e-300	Length:	3971
Score:	3606.50	Matches:	763
Percent Similarity:	63.02%	Conservative:	77
Best Local Similarity:	57.24%	Mismatches:	137

Query Match:	70.34%	Indels:	357
DB:	12	Gaps:	9
US-10-647-268-2 (1-988) x ADH51535 (1-3971)			
QY	1 MetLlaGlnuAlaPheLeuGlnValIleLeuAspAsnLeuThrCysPheIleGlnGlu	20	
DB	1 ATGGCTGAAGCTTTCATTCAAGTTGTGTGACACATCTCACTTCTTCTTCAAGGGGAA	60	
QY	21 LeuGluLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr	40	
DB	61 CTGTATGTGCTTTTCGGTTTTCAGAGTAGAGTCCAAAGGCTTTCAAGCATGTTTCTTACA	120	
QY	41 IleGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn	60	
DB	121 ATCCAGCCGCTCTTGAAGATGCTCAAGAGAGCACTCAACGAAAGCTTGAAGAAAT	180	
QY	61 TripleGlnLysLeuAsnAlaAlaAlaTyrGluLaaAspAlaIleLeuAspGluCysLys	80	
DB	181 TGGTTGCAAAACCTCAATGCTGCTACATATGAATCGATGACATCTTGATGAATATATA	240	
QY	81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle	100	
DB	241 ACTAAGGCC--ACAAAGATCTTGACATCGAATATATGCGTTATATCAACAAAGTATATC	297	
QY	101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle	120	
DB	298 CTTTCCGTCCAAAGTTGGGAAAAGATGAGCAACAGATGAGAAAACCTGAATGCATTT	357	
QY	121 AlaAlaGlnuArgLysPheHisLeuAspGluLysThrIleGluArgGlnValAlaThr	140	
DB	358 GCTAGAGAGCAAGAAATTTTCATTTCAGAAAGATTTATAGAGAGCAACAGCTGTACA	417	
QY	141 ArgGlnThrGlyPhe-----	145	
DB	418 CGGAAACAGGTAC-TCATCTTAATTAAGTATTAACAATTAGTTATATTCATTGTTTT	476	
QY	145 -----	145	
DB	477 GGGCAATGATCAAAATTATGTAAAGTCAAAATATATCTATGATCTACGAAATATGTTAA	536	
QY	145 -----	145	
DB	537 ATTATACCTTAGTTATACATAATTAGTACGAACATCTCTCCATATCTTTGGAACAAAT	596	
QY	145 -----	145	
DB	597 ATTCCCTTAAAGAAATAGACACGTGAAGAAAGTTCAATTCAAATTATTCACCTCAATTT	656	
QY	145 -----	145	
DB	657 TAAATCTGATTTCTTAGAAGAAACCACTCATCTCTCCGTTTGAGTCTTAAAGAAACA	716	
QY	145 -----	145	
DB	717 GCTCAGAAAAAGAGTTTCTTCTGTCTGTCTGTCTGTGCATTTGTCCTTAATCCAAAT	776	
QY	145 -----	145	
DB	777 AACAAACAATACAAATTAATTAATTAATGTTCACGATGAGGATGCTTTCTTAGCTAGACATG	836	
QY	145 -----	145	
DB	837 AACGAGGTAAATTTTGTTTTAAGAAAGAAAGAAATGATTAAGCTGATTTCTTTCA	896	
QY	145 -----	145	
DB	897 GAGTGAATATAGGGGATAAAGTTGAGAGATAGAGTTCAATCGTTATTTCTTCTTA	956	
QY	145 -----	145	
DB	957 AAGTAAACAAGTTCAACAAAATGATATATCAAGGTACGGTAATGGAATAATTAATTAGACACGTC	1016	

QY 145 ----- 145
Db 1017 TAAACTAATAATGATAGAACTTAATATATGAGACAATATCATCTTTAATAA 1076
QY 145 ----- 145
Db 1077 GCTACCAATTTAATCATGATACAGAGAGAAACCAAAAAATTAGGGGTGAATTATT 1136
QY 145 ----- 145
Db 1137 GATTCTATGCTTATCATGTCTTCCATCAACATCAAGAAAAATTGTGCCAAAGTAT 1196
QY 145 ----- 145
Db 1197 AAAGGTGCGGTATTTGGATTTGAAGTAAACAGAGAGATPACATTTGACTAAAGTA 1256
QY 145 ----- 145
Db 1257 TAAACAATAGTATATTGATCATTTTATGATCAAAATTCATGTGGTTTGGGAGAAAG 1316
QY 145 ----- 145
Db 1317 GAAGTTCAATGTTTCAATCTGCTCTCATCTCATCAATCTCTTTATTGTGCAAAAC 1376
QY 145 ----- 145
Db 1377 CCTTCTATTTAATAATTTTCTGCGGACTCTTAATGAGCTTGAATGAACAATTTCTC 1436
QY 146 ----- 145
Db 1437 ATCTGACATTTGCTTGACACAGGTTCTGTGTTAACTGAACCAAGTTTATGGAAGGAGC 1496
QY 157 LysGluYAspArgLuiLeuValLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 176
Db 1497 AAAAGAAAAAGATGAGATGATAAAATCTTAATAACATGTAGAGCCCAAAACTTC 1556
QY 177 ProValLeuProLeuGluYMetGlyLeuGluYLeuThrThrLeuAlaGluMetVal 196
Db 1557 TCACTCCCTCCCAATCTTGATGTGGGGGACTAGGAAGAACACTCTTCCCAATGCTC 1616
QY 197 PheAsnArgLniArgValLLeuLniAspPheLsProLysLLeuTrpLLeuValSerL 216
Db 1617 TTCAATGATCAGAGAGTAAGTGAAGGCTTCAATCCCAAAATATGGAATTTGCGTCCGAT 1676
QY 217 AspPheAsnGluYAspArgLuiLeuGluYLeuValGluSerLLeuGluYLeuSerL 236
Db 1677 GATTTTGTGAAGAAGGTGTATTAAGCAATAGTAAGATCTATTGAAGGGAAGCCCTC 1736
QY 237 GlyGluMetAspLeuAlaProLeuGluYLeuYAspLeuLeuLeuLeuLeuLeuLeu 256
Db 1737 AGTGCATGAGCTTGCGCTCCATTCANAAAGAGCTTCAAGAGTTGCTGAATGGAAGAA 1796
QY 257 TyrLeuLeuValLLeuAspAspValTrpAsnGluYAspArgLniAspLLeuYLeuArg 276
Db 1797 TACTTCCCTGCTTATGATGATGTTTGAATGAAGTCAACATAGTGGCTAATTAGA 1856
QY 277 GluValLeuYValGlyAlaSerGlyAlaSerValLeuThrThrArgLeuGluY 296
Db 1857 GCAGTCTTGAAGGTGGAGCAAGTGTGCATTTGTTCTTAACATACTACGCTTGAAG 1916
QY 297 ValGlySerLLeuMetGlyThrLeuGluYProYArgLLeuSerAspLeuSerGluYAsp 316
Db 1917 GTTGATCAATTTATGGGAACATGCAACCATATGATGATGCAATCTGTCTCCAGAGAT 1976
QY 317 CysTrpLeuLeuPheMetGlnArgLAspGluYAsnGluYLeuValLeuValLeuVal 336
Db 1977 TGTGGTGTTTTGTTCATGCAAGGTGCATTTGGACACCAAGAAATTAATCAAACTT 2036
QY 337 ValAlaLLeuGlyYLeuGluYLeuValLysLysCysGlyGlyValProLeuAlaLysThr 356
Db 2037 GTGGCAATCGGAAGAGATGTTGAAAAATGTGTGTGTGTGCTGTGAGCCCAAGCT 2096
QY 357 LeuGluYLeuLeuArgPheYAspArgLuiGluYAspGluYLeuValAlaArgSer 376

Db 2097 CTTGAGGATATTTTCCGCTTCAGAGAGAGAAAGAGATGGAACATGTAGAGACAGT 2156
QY 377 GluLLeuTrpLysLeuProGluYLeuGluSerLLeuProAlaLeuArgLeuSerY 396
Db 2157 CCGATTTGGAATTTGCTCCAGAGATGAAGTCTATCTGCTGCGCTGAGGCTTAGTTAC 2216
QY 397 HisLsLeuProLeuAspLeuArgLniCysPheThrYrCysAlaValPheProLysAsp 416
Db 2217 CATCATCTCCATCTTGAATTTGAGCAATGCTTTGTGATGTGGGATTTCCAAAGGAC 2276
QY 417 ThrGluMetGluYLeuValLeuLLeuSerLeuTrpMetAlaHisGlyPheLLeuSer 436
Db 2277 ACCAAAAATGGCAAGAAAAATCTATGCGCTTTTGGATGCGACATGTGTTCTTTATCG 2336
QY 437 LysGluYAsnGluYLeuGluYAsnValGlyAsnGluValTrpAsnGluYLeuYLeuArg 456
Db 2337 AAAGAAAAATTTGGAGCTAGAGAGATGATGATAGATGAATGAATTAATCTAGAG 2396
QY 457 SerPhePheGluYLeuValLysSerGlyGluThrYrPheYMetHisAspLeu 476
Db 2397 TCTTTCTTCCAAAGATTTGAAGTTGAATCTGTGTAACCTTATTCAGATGCATGACCTC 2456
QY 477 LLeuLsAspLeuAlaTrhSerLeuPheSerAlaSerThrSerSerSerAsnLLeuArgL 496
Db 2457 ATCCATGATTTGGCTACATCTCTGTTTCAAGCAACATCAGACAGCAATATTCGTAA 2516
QY 497 LLeuValGluYAsnYrLLeuHisMetMetSerLLeuYrPheThrYValValSerSer 516
Db 2517 ATTAATGCTAATTTATGATGATATATGATGATGATGATGATGATGATGATGATGAT 2576
QY 517 TyrSerLeuSerHisLLeuGluYLeuPheValSerLeuArgValLeuLeuSerAspLLe 536
Db 2577 TACTTCTTCACTTCCAAAAGTTTGTCTCATTTAAGGCGCTTATCTTAAGAACTCG 2636
QY 537 LysLeuYAsnGluYLeuProSerSerLLeuYAspLeuValHisLLeuArgYrLeuAsnLeu 556
Db 2637 AACCTAATCAATTAACATCTTCCATGAGAGATCAAGTAACTTAAGATCACTGAGACT 2696
QY 557 SerGlyAsnTrhSerLLeuYAspLeuProAsnGluYLeuYAspLeuGluYLeuGluY 576
Db 2697 TCTGCAATTTTGAATTCGTAATCTTCCAAAGAGATTAATCAGGCTTCAAAATCTGAG 2756
QY 577 ThrLeuAspLeuHisGlyCysHisSerLeuYAspLeuProYAspLeuThrSerYLeu 596
Db 2757 ACTCTGATCTACATTTATGAGACTCTTCTTGTGTCCAAAACAAACAGTAACCTT 2816
QY 597 GlySerLeuArgAsnLeuLeuLeuAspGlyCysYrGlyLeuThrCysMetProProArg 616
Db 2817 GGTAGTCTCCGAATCTTTTATCTTGATGGCTGT---TCATTGAGGTCAACGCCAACAGG 2873
QY 617 LLeuYSerLeuThrCysLeuYLeuThrLeuSerArgPheValValGlyLLeuLysLys 636
Db 2874 ATAGAGATTTGTAATGCTTAACTGCTTAAGTGTCTTGTGTTATGGC---AAGGAAAA 2930
QY 637 SerCysGluYLeuGluYLeuYAsnLeuYAsnLeuYrGlySerLLeuLLeuHis 656
Db 2931 GGTATCAACTTGTGTGAACCTTAATAACCTTAATCTTATGCTCAATTCACAA 2990
QY 657 LeuGluYrValLysAsnAspMetAspAlaYAsnGluYAsnLeuSerAlaYAsnGluYAsn 676
Db 2991 CTTGACAGAGTGAAGAAAGATAGCGATGCAAAAGAGTATTTATCGCTAAGCAAT 3050
QY 677 LeuHisSerLeuSerMetLysTrpAspAspArgLuiArgProArgLLeuYrGluSerGlu 696
Db 3051 CTGCACCTTTATCTCGAGTGTGGACCTTGATGAAGAACTAAG---TATGATTTCA--- 3104
QY 697 LysValGluYValLeuGluYAlaLeuYrProHisSerAsnLeuThrCysLeuThrLLeuArg 716
Db 3105 -----GAAGTCTTGAAGCCCTTAACCAACATCTCAATCTGAATATTGAATCAAT 3158
QY 717 GlyPheArgGlyLLeuYrLeuProAspTrpMetAsnHisSerValLeuYAsnValVal 736

```

Db      3159 GGCCTCGAGAGATCCGCTCCAGATTGATGATCAATCATGTTTGGAAAAATGTTGTC 3218
Qy      737 SerIleGluIleIleSerCysValAsnCysSerCysLeuProPheGluLeuPro 756
Db      3219 TCATATTAGAAATTAGAGGTTGTGAAAACTGCTCATGCTTACACACCTTTGGTGGCTGCT 3278
Qy      757 CysLeuYsSerLeuGluLeuTyrArgSylSerIleGluValGluTyrVal---AspSer 775
Db      3279 TGTCTAGAAATCTTAGAGTTACACCGCGGTGAGAGATGTGGATGTTGAAGATATAT 3338
Qy      776 GlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIleArgGluPheGly 795
Db      3339 GTTCATCCT-----GGAAAGTTTCCATCCCTTGAAGAACTGTATATGGACTTTAGT 3392
Qy      796 AsnLeuYsGlyLeuLeuLysGluGluGluGluGluGluGluGluGluGlu 815
Db      3393 AATCTTAAAGGATTTGCTGAAAAAGAGAGAAAAAGCAATTCCTGTGTGAAAGAGATG 3452
Qy      816 GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLeuVal 835
Db      3453 ACATTTTACTGTGCTCCATGCTTTCTTATTCGACCCCTTTCTGTCAAGACATTGAAA 3512
Qy      836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
Db      3513 GTTATTGGC-----ACAGATGCAACAGTTTGAAGTCCATATCTTAATCTTGAAGGCTCTT 3566
Qy      856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluMetPheLys 875
Db      3567 ACTTCCTTGACATTAGCAATTAAGCTAAGCTTACTTACCCAGAAAGAGATGTTCAA 3626
Qy      876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
Db      3627 AGCCTTGCAATTCCTCAATTAATCTTCTTTCTTAGAAATCTCAAAAGAGTGGCT 3686
Qy      896 ThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeu 915
Db      3687 ACCAGCCCTGGCTAGCTCAATGCTTTGAAGAGTCCAAATTTGAATTTTGAACGCACTA 3746
Qy      916 GluSerLeuProGluGluGluValLysGlyLeuLeuSerLeuThrGlnLeuSerIleThr 935
Db      3747 GAGAGTCTCCAGAGAGAAAGGAGTGAAGGTTTAACTTCACTCAACGACTTGTCTGCT 3806
Qy      936 TyrCysGluMetLeuGlnCysLeuProGluGluGlnHisLeuThrAlaLeuThrAsn 955
Db      3807 AACTGTATGATGCTAAATGTTTACCGAGGAGATTGACGACACTTAACGCTCAACACT 3866
Qy      956 LeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIleGlyGluAsp 975
Db      3867 TTAAACAATTACTCAATGCTCAATAGTATTCAAGCGGTGTGAGAGGAATAGAGAAAGAC 3926
Qy      976 TrpTyrLysIleAlaHisIleProArgValPheIleTyr 988
Db      3927 TGGCACAAAATTGCTCAATTCATATTGACTTAAT 3965

```

```

RESULT 15
ADFI17764 ID ADFI17764 standard; DNA; 3899 BP.
AC ADFI17764;
DE 12-FEB-2004 (first entry)
DE s_bulbocastanum RGCA-b1b coding DNA.
XX
XX gene; ds; RGCA-b1b; Rpi-b1b gene cluster; growth regulant;
XX oomycete infection; introgression breeding; plant; late blight.
XX Solanum bulbocastanum.
XX
XX Key Location/Qualifiers
XX CDS 1..3899
XX FT /*tag= b
XX FT /product= "RGCA-b1b protein"

```

```

FT      /note= "This sequence contains 3 introns and some
FT      translation exceptions"
FT      1..433
FT      exon /*tag= a
FT      /number= 1
FT      434..510
FT      intron /*tag= c
FT      /number= 1
FT      511..542
FT      exon /*tag= d
FT      /number= 2
FT      543..618
FT      intron /*tag= e
FT      /number= 2
FT      619..742
FT      exon /*tag= f
FT      /number= 3
FT      743..1365
FT      intron /*tag= g
FT      /number= 3
FT      1366..3899
FT      exon /*tag= h
FT      /number= 4

```

```

EP1334979-A1.
13-AUG-2003.
08-FEB-2002; 2002EP-00075565.
08-FEB-2002; 2002EP-00075565.
(KWEE-) KWEEK EN RESEARCHBEDRIJF AGRICO BV.
Van Der Vossen ENG, Alléfs JHM;
WPI; 2003-714439/68.
P-PSDB; ADFI17768.
New resistance gene conferring resistance against an oomycete pathogen,
useful for producing plants, especially potatoes and tomatoes, resistant
against oomycete pathogens such as Phytophthora infestans.
Example 5; SEQ ID NO 40; 86bp; English.
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGCA-b1b, RGCA-b1b and RGCA-b1b, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum RGCA-b1b coding
XX DNA containing an intronic sequence in an exemplification of the
XX invention.
XX
XX Sequence 3899 BP; 1186 A; 678 C; 846 G; 1189 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.72e-282 Length: 3899
XX Score: 3400.00 Matches: 717
XX Percent Similarity: 62.94% Conservative: 105
XX Best Local Similarity: 54.90% Mismatches: 159
XX Query Match: 66.32% Indels: 326
XX DB: 10 Gaps: 10

```

US-10-647-268-2 (1-988) x ADFI17764 (1-3899)

QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspLeuThrCysPheIleGlnGlyLeu 20
 Db 1 ATGGGGAGAGCTTTCTTCAGATTCTGCTAGAAAATCTCATTCTTCATCGAGATATAA 60
 QY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGlyLeuLeuGlnSerThrPheThrThr 40
 Db 61 CTGTATTGATTCTTCGTTTCGAAAAGATGTGAAAAGCTGTGAGTGTGTTCACA 120
 QY 41 ILeuGlnAlaValLeuGluAlaAspAlaGlnLeuLeuAspLeuAlaIleGlnAsn 60
 Db 121 ATTCAAGCTGTGCTTCAGATGCTCAGAGAAAGCAATTGAAAGCAAGCAATTGAGAT 180
 QY 61 TTrpLeuGlnLeuLeuAsnAlaAlaIleTyrgluAlaAspAspIleLeuAspGluCysLeu 80
 Db 181 TGGTTCAGAAAACCTAATTCGTCTCTATGAAAGTTGATGATATATTTGGCGAATGTAAA 240
 QY 81 ThrGluAlaProIleArgGlnLeuLeuAsnLeuTyrglyCysTyrlsProAsnValIle 100
 Db 241 AATGAGCA---ATTAAGATTGAGCAGCTCGATTAGGGTTTATCACCCAGGATATATC 297
 QY 101 ThrPheArgHileuIleGlySarGmetLeuLeuIleMetGlnLeuLeuAspValIle 120
 Db 298 AATTTCCCTCACAATAATGGAGAGATGAAAGATTAAGAGAACTTGAATGCATA 357
 QY 121 AlaIleGluArgIleLeuPheHileuAspGluArgThrIleGluArgGln----- 137
 Db 358 TCTGAGAAAGAGAGAGATTTCATTCTCTGAAAAAATTACAGAGACAAAGCTGCCGCT 417
 QY 137 ----- 137
 Db 418 GCTACGCTGAAACAGGTGTGAGTACTGATAATTGACTTAAATTCAATTGT 477
 QY 137 ----- 137
 Db 478 TACCAATCATGTGTTCACCGTGATCTCTACAGTAGAGATGGCGCTGGCGAGGT 537
 QY 137 ----- 137
 Db 538 TGSAGGTGTGAGGTGTGGGCAACCCCACTTGAGTCTACATAAGTAGTACTTAA 597
 QY 137 ----- 137
 Db 598 ATTGTATAGATTGAACAAGTACAAACGCTCCTACTTGTCCTTATCGTATTATG 657
 QY 137 ----- 137
 Db 658 TCACCTAGAGATGATGTGTCTACTTGTCAACTTATATGAGTTAAAGTTCTACTGTGC 717
 QY 137 ----- 137
 Db 718 ACACCCAAAGTTGAGCGCGTAGATGTCAATTGATCCAAAGTTAAAGGCAATTATG 777
 QY 137 ----- 137
 Db 778 AATTATGCTTAAATATATGATCAATTTGTATCAAGTCTGCCAAATATATGTTCTAGTG 837
 QY 138 -----ValAlaThrArgGln 142
 Db 838 AAAAGTGTAAACCTTAGTCTGATCTGTATTGAAAGTGAATTTTGTGGC-ACATAAACAA 896
 QY 142 ----- 142
 Db 897 TGCATAGGCTGTGATTCATTTTTCATTAACCTTTTGTAGACGATTTTCTTATTCGAA 956
 QY 142 ----- 142
 Db 957 TTTTACTGTCTAAATGAGAAAGCAAGAAATAAGAGTATACAGAGGCTGACTCTTC 1016
 QY 142 ----- 142
 Db 1017 ATAGATCTATCATATAAAAAAAGCATGTGATTACTAGATATAGGTTCTTTTAAATTAC 1076

QY 142 ----- 142
 Db 1077 AAATTGTAGATTAAAAACAGTTCTGTGGGAGAGATTAGATACAGTGTATGATCTA 1136
 QY 142 ----- 142
 Db 1137 GAAGTTTTTTAAATAAAAAATTAGCAAAATTATGCGGGCTGGGGCGGTGAAAAACAGCA 1196
 QY 142 ----- 142
 Db 1197 ACTTTCAGAGCTTGGGGGTCGAATCTTTGCAAGTTTGTGTGGGTTTGGCTTCACCA 1256
 QY 142 ----- 142
 Db 1257 CCCAATCTGCATTCTGTCTAAATGTTTGTGTCTAATTCCTTCGACTCAATCT 1316
 QY 143 -----ThrGlyPheValLeu 147
 Db 1317 AATGAGCTCAATTGTAAACAATTTCTTGTGTCCACATTAATTGGAACAAGTTTGTGTTA 1376
 QY 148 AsnGluProGlnValTyrglyArgAspLeuLeuAspGluIleValIleLeuIle 167
 Db 1377 ACTGACCCAAAGCTACAGAGAGCAACAGAGAGATGATAGTGAATAATTCGTATA 1436
 QY 168 AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyLeu 187
 Db 1437 AACATGTATATGTTGCCAAGAACTTCAGTCTCCCTTAATTTGATATGGGGGACTA 1496
 QY 188 GlyThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHilePheHile 207
 Db 1497 GGAAGACGACACTGGCCCAAAATGATCTTCACATGAGAGAGTAACTAGCAATTCAT 1556
 QY 208 ProIleIleTrpIleCysValSerGluAspPheAsnGluSarGlyLeuIleLeuGly 227
 Db 1557 CCCAAATATAGGTTGTGTCTCAGATGATTTGATAGAAAGCTTATTAAGACAT 1616
 QY 228 ValGluSerIleGlnGluLeuSerLeuGlyGlyMetAspLeuAlaProLeuGlnLeu 247
 Db 1517 ATAGAAATATGAAAGAGATTCTCTCATGTTGAGAGCTTGCTTCATTTACAGAAAG 1676
 QY 248 LeuArgAspLeuLeuAsnGlyLeuLeuTyrlleuLeuValLeuAspAspValTrpAsnGlu 267
 Db 1677 CTCAGAGATTATGAAATGAGAAACGATACTGTTCTTGAATGATGTTTGAATGAT 1736
 QY 268 AspGlnAspLeuTrpAlaLeuArgGlnValLeuLeuValGlyAlaSerGlyAlaSer 287
 Db 1737 GATCTAGAAAAGTGGCTTAAGTTAGACAGCTTAACTGTTGAGCAAGAGGCTTCT 1796
 QY 288 ValLeuThrThrThrArgLeuGluLeuValGlySerIleMetGlyThrLeuGlnProTy 307
 Db 1797 ATTCTACTACTACTCTGCTTGAAGAGTTGATCATTTATGGAAAGCTTGCAACCAT 1856
 QY 308 GluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArgAlaPheGly 327
 Db 1857 CATTTGCAAAATTTGTCTCCACATGATGATTTACTTTGTTTATGCAACCGCATTTGGG 1916
 QY 328 HisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLeuGluIleValLeuLeuCys 347
 Db 1917 CAACAAAAGAGCAAAATCTTAATCTAGTGCCCATGGAAGAGATTTGGAAGAAATGT 1976
 QY 348 GlyGlyValProLeuAlaAlaLeuThrLeuGlyGlyIleLeuArgPheLeuSarGluGlu 367
 Db 1977 GGTGTGTGCTTATAGAGCCCAAGACTCTTGGTGTCTTTACGCTTCAAGAGAGAGAG 2036
 QY 368 ArgGlnTrpGluHisValArgAspSerGluIleTrpLeuLeuProGlnGluSerSer 387
 Db 2037 AGTGAATGGAACATGAGAGATAATGAGATTTGAGTCTGCTCAAGATGAAGTTCT 2096
 QY 388 IleLeuProAlaLeuArgLeuSerTyrlleHisLeuProLeuAspLeuArgGlnCysPhe 407
 Db 2097 ATTTTGTCTCTCTTAAGACTGAGATTATCATCACTTCATTATTTGAGACAAATGCTTT 2156
 QY 408 ThrTyrcysAlaValPheProLeuAspThrGluMetGlnLeuGlyAsnLeuIleSerLeu 427


```

Db 2157 GCGATGTCGAGATTCCTCCAAAGACACCAAAATGATMAAGAAATCTATCTCTC 2216
Qy 428 TTPMCAIAHISGLYPHEILEUSERISGLYASNLEUGLUEGLUASNVALISGLYASN 447
Db 2217 TGGATGGCGGATGGTTTCTTTTATCAAAAGGAAACTTGAGCTAGAGAGATGGGTAT 2276
Qy 448 GLUVALTPPANGLULEUTYRLEUARGSERPHEPHEINGIUILEGLUVALISERGLY 467
Db 2277 GAAATATGGAATGAAATTAATCTTAGAGCTTTCTTCCAAAGAAATGAAAGCTAAATGGGGT 2336
Qy 468 GLINHTYRPHLYMETHIASPLEULEHISAPLEUALATHRSERLEUPHESEALA 487
Db 2337 AATCTTATTTCCAGATACATGATCTATCCATGATTTGGCTACATCTCTCTTTCCGCA 2396
Qy 488 SerThrsSerSerAsnIleArgIUIleIleValIGluAsnTYRLeuMetMetSer 507
Db 2397 AGCGCATCATCGCGCATATATCCGCAATTAATGCAAAAGATTATTAACCATACAGTGTCC 2456
Qy 508 ILeGLYPHEHTYRISGLYVALISERSETYRISERLEUSERTHISLEUGLULYSPHEVALSER 527
Db 2457 ATTGGTTTCGTCGAGTGCTGTCTTACTCTCTCTGCTCTTGAAAGATTTGTCTCG 2516
Qy 528 LeuArgValLeuAsnLeuSerAspIleTySLeuLYSGlueuProSerSerIleGLYASP 547
Db 2517 TTAAAGGTCCTTAATCTAAGTTACTCAAAACTTGAGCAATTAACGCTCTTCCATTCGAGAT 2576
Qy 548 LeuValHisLeuArgTYRLeuAsnLeuSerGLYAsnThrsIleArgSerLeuProAsn 567
Db 2577 CTATTAACATTAAAGTATCTGGAACCTGTCTTGCAAT--AACTTCGTAAGCTTCCAAAG 2633
Qy 568 GlueuCYSLYISLEUGLULASnLeuGlnThrsLeuAspLeuHisGLYCYHISERLEUCYS 587
Db 2634 AGGTTGTCAGACTTCAAAATCTTCAACTCTTGATGACATTAATGCTTACTCACTTAAT 2693
Qy 588 CysLeuProLYSGlueuThrsIleSerLeuArgAsnLeuLeuAspLYCYS 607
Db 2694 TGTTCGCCAAACAAACAAAGTAACTTAGTAGTCTCCGACATCTTGTGTGATGGCTGT 2753
Qy 608 TYRGLYLeuThrsCysMetProProArgIleGLYSERLeuThrsCysLeuLYSThrLeuSer 627
Db 2754 ---CCATTGACTTCTACTCCACCAAGAGATGATGTTGACATGCTTAAGACTCTTAGGT 2810
Qy 628 ArgPheValIleGLYIleGlnLYSISerCysGlnLeuGLYGLUAsnLeuAsn 647
Db 2811 TTTCTTATTTGGGGA---AGCAAGAAAGTTATCACTTGTGAACCTGAACCTTAAT 2867
Qy 648 LeuTYRGLYSERILEGLUIleThrsISLEUGLULATGVALISASNAspMetAspALALYS 667
Db 2868 CTTCGCGGCTCAATTTCAATCAACACCTTGAGAGAGTGAAGAAAGATACGATGCA--- 2924
Qy 668 GluAlaAsnLeuSerAlaLYSGlueuAsnLeuHisSERLeuSerMetLYSThrAspAsp 687
Db 2925 GAAGCCAAATTAATCTGCAAAAGCAATCTGCAATCTTTAAGCATGATGGATTAACAT 2984
Qy 688 GluArgProArgIleTYRGLISERGLYISValIGluValIleuGluAlaLeuLYSPromet 707
Db 2985 ---GGACCAACACAGATATGAAATCCAAAGAGTTAAAGTCTTGAAGCACTCAACCAAC 3041
Qy 708 SerAsnLeuThrsCysLeuThrsIleArgGLYPHEARGGLYIleArgLeuProAspTPMet 727
Db 3042 CCCAATCTGAATATTTAGAGATCATTCGCTTCGAGAGATTCGTTTCCAAAGCTGAGATA 3101
Qy 728 AsnHisSERValLeuLYSAsnValISerILEGLUIleISerCysLYSAsnCYSSer 747
Db 3102 AATCACTCAGTTTGGAGAGCTCATCTCTTGAATTTAAAGCTGCAAAAATGCTGTG 3161
Qy 748 CysLeuProProPheGLYGLUeUProCysLeuLYSLeuGLUeUThrsArgGLYSer 767
Db 3162 TGTCTTACCACTCTTGGAGGCTCTCTGTCTAGAAATCTAGAGATTACAAAACGAGATCT 3221
Qy 768 AlaGluValGluTYRValAsp-----SerGLYPheProThrsArgArg 782

```

```

Db 3222 GCGAGGTGAGATATGTTGAAGAGATGATGCCATTTAGATTTCTCCACAGAAAGC 3281
Qy 783 PheProSerLeuArgLYSLeuAsnIleArgGLUPHEGLYASNLeuLYSGLYLeuLYS 802
Db 3282 TTTTCATCTCTGAAAAAATCTGTAATGCTTCTTCGCAAGTTGAAAGGCGTATGAAA 3341
Qy 803 LYSGLUIGLYGLUGLINCYSProValIleuGLUGLUIleGLUIleLYSCYSProMet 822
Db 3342 GAGAGAGAGAAAGAAATTCCTCATGCTTGAAGAGATGCGAATTTATATGTCCTCTG 3401
Qy 823 PheValIleProThrsLeuSerSerValLYSLeuValISerGLYAspLYSAsp 842
Db 3402 TTTGTTTTCCAACCTCTTCTCTGTCACAAAGATTGAACATTCAGGCAAC--ACAAC 3458
Qy 843 AlaIleGLYPheSerSerIleSerAsnLeuMetAlaLeuThrsSerLeuGlnIleArgTYR 862
Db 3459 ACTAGAGTTTGAAGCTCAATATCTTAATCTTAGACACTTTACTCTTCCGCAATTTGGTCT 3518
Qy 863 AsnLYSGlueuAspAlaSerLeuProGLUGLUMetPheLYSLeuAlaAsnLeuLYSTYR 882
Db 3519 AACTACAGAGGCACTTCACTCCGAGAGAGATGTTCAAGTCTTACAAATCTCGAATTC 3578
Qy 883 LeuAsnIleSerPheTYRPhAsnLeuLYSGlueuProThrsSerLeuAlaSerLeuAsn 902
Db 3579 TTTGATTTCTTTGACTTCAAGAAATCTCAAGATCTGCTTCCAGCCTGACTAGTCTAAT 3638
Qy 903 AlaLeuLYSHISLEUGLUIleHISerCysTYRAlaLeuGLUSerLeuProGLUGLUIY 922
Db 3639 GCTTGAAGGCTCTCCAAATTTGAAGTTGTGACTCAGCTAGAGATTTCCCTGAAACAGGG 3698
Qy 923 ValLYSGLYLeuIleSerLeuThrsGlnLeuSerILEThrsTYRCSGLUMetLeuGlnCYS 942
Db 3699 CTAGAGGTTTAACTTCACTCACACAGATGTTGTGTAATATCTGTAAGAGCTTAATAATGT 3758
Qy 943 LeuProGLUGLYLeuGlnHISLeuThrsAlaLeuThrsAsnLeuSerValIGluPheCysPro 962
Db 3759 TTACCCAGAGGATTTGACAGCACTTAACAGCCCTCAAAATTTAGAGATTTCTGTTGTCCA 3818
Qy 963 ThrLeuAlaLYSARGCYSGLUIGLYIleGLYGLUAspTPTYRISLeuAlaHisILE 982
Db 3819 GAAATGAAAAAGCCTGTGATTAAGAAATAGAGAAAGATGCGCAAAAATTTGTCACATT 3878
Qy 983 ProArgValPheIleTYR 988
Db 3879 CCAATCTGATATTCTAT 3896

```

Search completed: April 17, 2005, 00:24:46
 Job time : 1241 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

CM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 23:37:44 ; Search time 385 Seconds
(without alignments)
4199.069 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1.MAEPFLQVLDNLTCTFIOGE.....EKIGEDWYKXIAHPRVFYI 988

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+.p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10647268/runat_15042005_154720_26521/app_query.fasta_1.1159
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647268 @CGN 1.1 105 @runat_15042005_154720_26521 -NCPU=6 -ICPU=3
-NO_MMAP -LARGECQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	24.2	4465	3	US-08-930-996A-3
2	1198	23.4	4946	3	US-08-930-996A-1
3	1028.5	20.1	4208	3	US-09-004-838-1
4	1008.5	19.7	4163	3	US-09-004-838-70
5	966.5	18.9	2353	3	US-09-004-838-2
6	715	13.9	1662	3	US-09-004-838-6
7	609.5	11.9	3997	3	US-08-947-823-2
8	609.5	11.9	51952	3	US-08-947-823-1
9	575.5	11.2	9870	4	US-09-245-928A-15
10	571.5	11.1	3982	4	US-08-947-823-4
11	553.5	10.8	3099	3	US-09-360-186-2
12	553.5	10.8	3099	4	US-09-864-680A-2

13	550.5	10.7	2718	3	US-09-360-186-4	Sequence 4, Appli
14	550.5	10.7	2718	4	US-09-864-680A-4	Sequence 4, Appli
15	550.5	10.7	31491	3	US-09-360-186-1	Sequence 1, Appli
16	550.5	10.7	31491	4	US-09-864-680A-1	Sequence 1, Appli
17	530	10.3	3925	3	US-09-330-330-2	Sequence 2, Appli
18	528.5	10.3	3741	4	US-09-803-286A-1	Sequence 1, Appli
19	512.5	10.0	2903	2	US-08-310-912A-1	Sequence 1, Appli
20	512.5	10.0	2903	3	US-08-841-089-1	Sequence 1, Appli
21	512.5	10.0	2903	3	US-09-301-085-1	Sequence 1, Appli
22	512.5	10.0	2903	5	PCT-US95-04570-1	Sequence 1, Appli
23	512.5	10.0	2903	5	PCT-US95-04589-1	Sequence 1, Appli
24	489	9.5	3432	2	US-08-310-912A-141	Sequence 14, App
25	489	9.5	3432	3	US-09-301-085-141	Sequence 14, App
26	489	9.5	3432	5	PCT-US95-04589-141	Sequence 14, App
27	474.5	9.3	10322	3	US-09-330-330-3	Sequence 3, Appli
28	473.5	9.2	5475	2	US-08-680-377-1	Sequence 1, Appli
29	473.5	9.2	5475	2	US-09-228-246-3	Sequence 1, Appli
30	454	8.9	1238	2	US-08-414-938A-3	Sequence 3, Appli
31	449	8.8	10968	2	US-08-680-377-2	Sequence 2, Appli
32	449	8.8	10968	3	US-09-228-246-1	Sequence 1, Appli
33	436.5	8.5	1036	3	US-09-004-838-3	Sequence 3, Appli
34	436.5	8.5	5222	4	US-09-336-946B-68	Sequence 68, Appli
35	436.5	8.5	5222	4	US-09-993-170-57	Sequence 57, Appli
36	436.5	8.5	5696	4	US-09-993-170-60	Sequence 60, Appli
37	419	8.2	5134	2	US-08-310-912A-157	Sequence 157, App
38	419	8.2	5134	3	US-09-301-085-157	Sequence 157, App
39	419	8.2	5134	5	PCT-US95-04589-157	Sequence 157, App
40	376.5	7.3	13149	3	US-09-004-838-87	Sequence 87, Appli
41	367.5	7.2	5829	3	US-09-004-838-109	Sequence 109, App
42	367.5	7.2	10815	3	US-09-004-838-21	Sequence 21, Appli
43	367	7.2	3756	4	US-09-813-742A-2	Sequence 2, Appli
44	367	7.2	3760	1	US-08-261-663A-3	Sequence 3, Appli
45	367	7.2	3760	3	US-09-357-206A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-3
Sequence 3, Application US/08930996A
Parent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930.996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 3:


```

Db      2052 CCAGATTCATTGTTGTTGTTATTAACCTGGAGACACTTCCTTCATCTGT---AAA 2108
Qy      586 LeuCySLeuProLysGluThrSerLysLeuGlySerLeuArgAsnLeuLeuLeuAsp 605
Db      2109 CTTGAGAGCTACCCCTGAGATGAGAGAGATTGATTAACTTCGCTCATCTTACACATAAGC 2168
Qy      606 GlyCyTyGlyLeuThrCysMetProProArgIleGlySerLeuThrCysLeuTyThr 625
Db      2169 AACACTGGCACTTAAAG---ATGCCACTACATCATGAGAGAGTTGAAAAGCTCCCAAGTG 2225
Qy      626 Leu---SerArgPheValValGlyIleGlnLysLysSerCysGlnLeuGlyLeuLeu 643
Db      2226 TTGGTGGAGGCCAGATTTCTTGTAGGTGTTGGCAAAATGAA---GATTTGGGTAAACA 2282
Qy      644 ArgAsnLeuAsnLeuTyGlySerIleGlnIleThrHisLeuGlnArgValLysAsnAsp 663
Db      2283 CAA-----ACTTATATGATCTCTATCATAGTTGAAAGTTGAAAAGTGGTATATAGA 2336
Qy      664 MetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLys 683
Db      2337 AGGGAAGCTGTGAGCCAAAGATGAGGAGGAGGAAGATCATGTTGAGCAATATATCATGGAG 2396
Qy      684 TrpAspAspAspGluArgProArgIleTyrgLysSerGluLysValGluValLeuGluAla 703
Db      2397 TGGAGTGAAGAGCATTAAGTCTGACAAATTCACAAAGAAAGA---GACATATCTTATATAG 2453
Qy      704 LeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIleArgLeu 723
Db      2454 CTACCCCAATMAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2513
Qy      724 ProAspTrpMetAsnHisSerValLeuLysAsnValLysIleGlnIleIleSerCys 743
Db      2514 CCCAATTTGGGTAGCTGATCCTTTGTTTCTTAAGCTGGTGAATTTGTTCTTGAAGAACTGC 2573
Qy      744 LysAsnCySerCysLeuProProPheGlyGluLeuProCysLeuLysSerLeuGluLeu 763
Db      2574 AAGGACTGTACTCTCTGCGACACTAGAGCAAACTCCCTGTTGAAATTCCTTCCCTT 2633
Qy      764 TrpArgLysSerAlaGluValGluTyrgValAspSerGlyPhe-----ProThr 779
Db      2634 ---AAAGGAGTGCATGAAATTAAGAGTGTGACGGAAGAAATTTACGCGAATGTCCTCC 2690
Qy      780 ArgArgArgPheProSerLeuArgLys----- 788
Db      2691 AAAAAGCCTTTTAATGTCCTTGAGAGCTGGAATTTGAAGATGACAGAGTGAAGCAA 2750
Qy      789 -----LeuAsnIleArgGluPheGlyAsnLeuLysGlyLeu----- 800
Db      2751 TGGCAGCAGCTAGGAATTTGAGAGTTCCTTACACTTGAAGAGCTTTCAATTATAAATTC 2810
Qy      801 -----LeuLysLysGluGluGluGlu 807
Db      2811 CCTGAGCTCAGTTGGAGATACCGATCCAAATTTCAAGTTTAAAAAGTTTAAAGGTTTTT 2870
Qy      808 GlnCysProVal----- 811
Db      2871 GGTTCCTCAAGTTGTTTTTATGATGCTCAAGTTTAAGATCCCAACTGGAGGAATGAAG 2930
Qy      812 ---LeuGlnGluIleGlnIleLysCysCys-----ProMetPheVal 824
Db      2931 CAGATTGAGGAATATATATATCGTATTTAACTCTGTACCTCTCTCTTTTATGACATA 2990
Qy      825 IleProThrLeuSerSerValLysLysLeuValLysGly----- 838
Db      2991 CTGCCAACT---ACCTTGAAGCAATTAAGACATATCTGTTGCCCAAAATTTGAATTTG 3044
Qy      838 ----- 838
Db      3045 GAGGCGCAAGTTTGTAGATGATGATGTTTCTGAGGAATTTAGTGTGAAGAAATGTGCT 3104
Qy      838 ----- 838

```

```

Db      3105 TGTGATACCTGAGTTTCTCCCAAGACAGCTGAATTGAGAATTGGGAATTTGCCAAC 3164
Qy      839 -----AspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeu 852
Db      3165 GTAAGTTTTTATGATCTTACTAGCCACTGAATCTCAATTCGGAATTTGAGAAATGTT 3224
Qy      853 -----MetAla-----LeuThrSerLeuGlnIleArgTy 862
Db      3225 GAAAACTATGATGAGTGTGAGAGAGCTCCAGCTGACATCATCTGATATATTTCCGGA 3284
Qy      863 AsnLysGluAspAlaSerLeuProGlu----- 871
Db      3285 TGTAAAGAGCTCAAGTGTCTTCCAGAACTCTTCATCTCTCAAGAACTGCACACTACT 3344
Qy      871 ----- 871
Db      3345 AATTGTCCGAATATAGAAGAGAAATTACCTTCAATTACAAAACCTATATACAGAT 3404
Qy      871 ----- 871
Db      3405 TGCAAAAAACTGTGAATGCGCCGAAGAGTGCATTTACAGAGCTCACAAGTTAGTG 3464
Qy      871 ----- 871
Db      3465 ATCTATCATGATGGAGTACGAAAGATATGACATTTGGAGTTCCTGTTCTATATACA 3524
Qy      872 -----GluMetPhe-----LysSerLeuAlaAsn 879
Db      3525 AGACTTGAGGATTTATATCTGATTAACATTAGACAGCCAACTCCAAAGCTCACCCTCT 3584
Qy      880 LeuLysTyrlLeuAsnIleSerPheTyrgPheAsnLeuLysGluLeuPro----- 895
Db      3585 CTTCATATCATGATGATGAT-----GGTAAATTATCTCGAATTCAGTCAACAAGCCAG 3638
Qy      896 ---ThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrgAla 914
Db      3639 ATTTCTCTCTCTTCTCACTCTGCTTCACTTCTCAAACTTCAAACTTGGAAATTTCCATAT 3698
Qy      915 LeuGlnSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIle 934
Db      3699 CTCCATATCATTTTCAAGATAGCACTGCCCCCTC-----TCCCTCTCTCAGCTGAGATC 3752
Qy      935 ThrTyrgCysGluMetLeuGlnCysLeuPro---GluGlyLeuGlnHisLeuThrAlaLeu 953
Db      3753 TTCATTTGCCCTTAATTCCTCAATTCCTTCCATTAAGCGGATGCC-----TCTTCCCTC 3806
Qy      954 ThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIleGly 973
Db      3807 TCTAACTATTGATTTGAGATGTGCTCATGTCTCACACCACTACTTAATTTGACAAGGGG 3866
Qy      974 GluAspTrpTyrgLysIleAlaHisIleProArgValPheIle 987
Db      3867 GAATATCTGGCCCAAAATTTGCTCATATCCCACTACTGATC 3908

```

RESULT 2
 US-08-930-996A-1
 Sequence 1, Application US/08930996A
 Patent No. 6100449
 GENERAL INFORMATION:
 APPLICANT: FLUHR, Robert
 APPLICANT: ESHED, Yuval
 APPLICANT: ORI, Naomi
 APPLICANT: PARAN, Ilan
 APPLICANT: ZAMIR, Daniel
 TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
 TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
 TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROMDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.

```

1 COUNTRY: USA
2 ZIP: 20004
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patent In Release #1.0, V
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/930,996A
12 FILING DATE: 09-DEC-1997
13
14 PRIOR APPLICATION DATA:
15 PRIOR APPLICATION NUMBER: PCT/US96/05272
16 FILING DATE: 15-APR-1996
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: IL 113,373
20 FILING DATE: 13-APR-1995
21
22 INFORMATION FOR SEQ ID NO: 1:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 4946 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: cDNA
29 FEATURE:
30 NAME/KEY: CDS
31 LOCATION: 299..3958
32
33 US-08-930-996A-1

```

QY 506 MetSerIleGly-----PheThrIysValIleSerSerTySerIleSerHis 521
Db 1904 TATTCATATAGAGCAGATGAGTGTGAGTGTGAGAAATTTGAATCATCTCTTAATCAGACGAG 1963
QY 522 LeuGlnIysPheVal----- 526
Db 1964 CTGAGGACATTACTTCCAAATGATATTCAGTTCCTTAATCTCAAAAACTAAGCAAGAG 2023
QY 527 -----SerIleArgValIleAsnIleSerAspIle 536
Db 2024 GTGTTCATACATATGCTGCTACATTAAGATCTTGAGGGCAGCTATCTGTCTATTAC 2083
QY 537 LysIleuIysGlnIleuProSerSerIleGly--AspIleValHisIleuArgTyIleuAsn 555
Db 2084 CAGATGTAGGCTGTCCAAATGACTGTGTATCAAAATTAAGCTCTCAGATTTTGGAC 2143
QY 556 LeuSerGlyAsnThrSerIleArgSerIleuProAsnGlnIleuCyIysLeuGlnAsnIleu 575
Db 2144 CTCTCT---GAGACATTCATTACAAAGTTCGCGGATTCATTTTGTGTGTATTAATTA 2200
QY 576 GlnThrIleuAspLeuHisIleGlyCyHisIleSerIleuCyIysLeuProIysGlnThrSerIys 595
Db 2201 GAGACATCTTCCTCTCATCTTGTAATATCTTGAGAGGCTACGCTGCAGATGGAGAG 2260
QY 596 LeuGlySerIleuArgAsnIleuIleuIleuAspGlyCyIysGlyIleuThrCyMetProPro 615
Db 2261 TTGATTAATCTTGCGTCATCTTGACATTAAGCAACACTGGCGGCTTGAAG---ATCCCACTA 2317
QY 616 ArgIleGlySerIleuThrCyIleuIysThrIleu-----SerArgPheValIleGlyIle 633
Db 2318 CATCTGACGACAGTGTGAAAAGCTCCCAAGTGTGGTGAGGACAAAGTTCTTGATAGTGT 2377
QY 634 GlnIysIysSerCyIysGlnIleuGlyIleuIleuArgAsnIleuIleuTyGlySerIleuIle 653
Db 2378 TGGAGATGGA---TATTTGGGTAAACACACC-----AACTTAATATGATCTCTCA 2428
QY 654 IleThrHisIleuGlnIysValIleuAsnIleuAspIleAspIleValIleAsnIleuSerIle 673
Db 2429 ATTCTAGAGCTTGAAAATGCTGTGTTGATGAAGGAAAGCTGTGAAGGCAAAAGTGAAGGAG 2488
QY 674 LysGlnIleuIleuHisSerIleuSerMetIysThrAspAspAspGlyIysArgIleTyx 693
Db 2489 AAGATCATCTGTTGACATTTATTCATTGAGTGAAGTGAAGCAATTAGTGTGACATTTCA 2548
QY 694 GluSerGlyIysValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 713
Db 2549 CAACACAGAAAAG---GACATACCTTGATGAGCTACGCCCAATMAAAACATTAAAGCACTT 2605
QY 714 ThrIleArgGlyPheArgGlyIleArgIleuProAspIleProMetAsnHisSerValIleuIys 733
Db 2606 GAATTCATCTGATATTAAGGAGCAAACTTTCCAACTGGGTAGCTGATCTTTGTGT 2665
QY 734 AsnValIleSerIleGlnIleIleSerCyIysIysAsnCyIysSerCyIysLeuProProPheGly 753
Db 2666 AAGCTGGGATTTGATCTTAAGAACTGCAAGGACTGTACTCTCTCCAGCACTAGGA 2725
QY 754 GlnIleuProCyIysIleuIysSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 773
Db 2726 CAATCTCCCTTTTGGATTCCTTTCCAT---AGAGGATGCAATGGGATTAAGAGTGTGT 2782
QY 774 AspSerGlyPheProThrArg----- 780
Db 2783 ACAAGAGAGTTCTATGAGCAGATTTGCTCCAAAAAGCTTTTAATCTCTTGTGAAGTT 2842
QY 781 -----ArgArgPhePro 784
Db 2843 AGATTTGAAGATATGCTGAATGGAAGCAATGGCACACATAGAAATTTGAGAGATTCCT 2902
QY 785 SerIleuArgIysIleuAsnIleArg-----Gln 793
Db 2903 ACACCTTGAGAACTTTCCATTAAAAATTTGCCCTGAGCTCAGTTGGAGATACCCATCCAA 2962
QY 794 PheGlyAsnIleuIysGlyIleu----- 800

Db 2963 TTTCAAGTTAAAAAGGTAGATATATGATTTGTAAGTGTGTATCTCTCTTTCTTTT 3022
QY 801 -----LeuIysIys 803
Db 3023 AGCATACTGCCACTACTCTTGAGAGAAATTAAGATATCTGTGTGCCAAAAATTAAGATTG 3082
QY 804 Gln-----GlyGln----- 806
Db 3083 GAGGCGCCAGTTGGTGGAGATTTGTGGAGATTTGAGTGTGATTTGATTTGGTTGTGA 3142
QY 807 -----GlnIleuCyAspValIleuGlnIleGlnIleIysCyIys--- 820
Db 3143 GATGATATATCAGCTGAGTTCTCCCAACAGCAGCTCAATTAAGATTAAGAAATTCAC 3202
QY 821 -----PrometPheValIleProThr----- 827
Db 3203 AACGTTACTAGTTTGTGATTTCTTACTGCACTGAAGTCTCCATATTCGAATTTGAA 3262
QY 827 ----- 827
Db 3263 AAATCTCGATGCGATGTGAGAGAGCGGCCAGCTGACGTCAATATTTGGGAGAT 3322
QY 828 -----LeuSerSerValIysIysIleu----- 834
Db 3323 AAGAAAGTCAGATGTCTTCCAGAACTCCTTCATCTCTCAAGAAAGTCCGACTGATTAT 3382
QY 834 ----- 834
Db 3383 TGTCAGAAATAGAGAGAAATTCGCTCAATTAACAAATATCGATATGATATTC 3442
QY 835 -----ValIleSerGlyAspIysSerAspIleIleGlyPheSerSerIleSerAsnIleu 852
Db 3443 AAGAACTGTGTGAATGGCCGAAGAG---TGGCATTTA 3478
QY 853 MetAlaIleuThrSerIleuGlnIleArgTyxAsnIysGlnIleu----- 866
Db 3479 CAGAGACTCAGAGATTATGATCAAAATGATGAGAGTGAAGCAATTTGAACATTGG 3538
QY 867 -----AlaSerIleuProGlnIleu 872
Db 3539 GAGTTCCTTCCTATTCAGAGACTATTCATATTCATTCGAAACATTAAGCAGCCAA 3598
QY 873 MetPheIysSerIleuAlaAsnIleuIysTyIleu-----AsnIleSerPheTyx 888
Db 3599 CATCTCAAAAGCTCAGCTCTCTTAATTTCTACGATTTGTTGGTATTTATTCAGATT 3658
QY 889 PheAsnIleuIysGlnIleuProThrSerIleuAlaSerIleuAsnAlaIleuIleuIleuIleu 908
Db 3659 CAGTCACAGGCCCACTT---TCTCTCTTTCTCAGCTCACTTGGCTTCAAACTCAACA 3715
QY 909 IleHisSerCyIysAlaIleuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 928
Db 3716 ATCTGGAATTTTCTTAATCTTCATCACTCACTCAATCAAGCAGCAGCTCC---TCC 3769
QY 929 LeuThrGlnIleuSerIleThrTyxGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 947
Db 3770 CTCTCTCACTGATCATCTCCAAATTCCTTAATTCCTTAATTCCTTCAATTAAAGGAGTG 3829
QY 948 GlnHisIleuThrAlaIleuThrAsnIleuSerValGlnIleuPheCyProThrIleuAlaIysArg 967
Db 3830 CCC-----TCTTCCTCTCTCAGCTATTCATTTCCAAATGTCCATGTCTCAGCAGCTA 3883
QY 968 CyGlnIysGlyIleGlyIleuAspTyIysIleAlaHisIleProAspValPheIle 987
Db 3884 CTAGAAATTTGACAGAGGGGAATACTGACAGAAATTTGCTCATATCCACCATACAGATC 3943

RESULT 3

US-09-004-838-1
; Sequence 1, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michémore, Richard W.

APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elnhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-07810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4208 base pairs
TYPE: nucleic acid
STRADENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4208
OTHER INFORMATION: /note= "RLG1A"
US-09-004-838-1
US-10-647-268-2 (1-988) x US-09-004-838-1 (1-4208)
Alignment Scores:
Pred. No.: 1.66e-102 Length: 4208
Score: 1028.50 Matches: 321
Percent Similarity: 47.49% Conservative: 181
Best Local Similarity: 30.37% Mismatches: 389
Query Match: 20.06% Indels: 169
Gaps: 29
DB: 3
1 MetAlaGlu-----AlaPheLeuGlnValIleuLeuAspAsnIleuThrCysPhe 16
1099 ATGGCTGAATATGCTTCTTCTGCTCTTCTTGACACGCGTCTTGAAAGCTGCACATYTGAA 1158
17 IlegIngluLeuLeuGlyLeuIleuGlyPheLysAspGluPheGluLysLeuGlnSer 36
1159 GCCTTGAAGAAGATGCTGCTCCAAAAGAAATTGAATCTGAAGCTTAAGAAATTGAAGAG 1218
37 ThrPheThrIleGlnAlaValLeuGluAspAlaGlnLysGluLeuLysAspLys 56
1219 ACATTAGACCAATCCAGATCTGCTTAACGATGCTTCCACAGAGAGAACTAATATGAA 1278
57 AlaIleGluAsnTriPheGlnLysLeuAsnAlaAlaIleTyGlnAlaAspAlleu 76
1279 GCCGTTAAAGATGGCTGAATGATCTCCCAACATTTGCTTAAGACATGACGACCTACTT 1338
77 AspGluCysLysThrGluAlaProIleArgGlnLysLysAsnLysTyGlyCysTyHis 96
1339 GATGATTTTGCAACTGAAGCTGTCACGATGTTGACCGAGAGGAGTGAAGCTTCCTCC 1398

97 ProAsnVal-----IleThrPheArgHisLysIle 106
1399 AGATGTGTAAGAAAACCTAATCCCAAGTGTGCAACAAGTTCTCCACAAGATATGATGATG 1458
107 GlyLysArgWetLysLysIleMetGluLysLeuAspValIleAlaAlaGluAlaGlyLys 126
1459 CATGCCAAGTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1518
127 PheHisLeuAspGluArgThrIleGluArgGlnValAlaThrArgGlnThrGlyPheVal 146
1519 CTGCTTTAAGTGTATGATACATATGAAAGCCAAATTGAAAGCTATGAGGCTCTTG 1578
147 LeuAsnGluProGlnValTyGlyArgAspLysGluLysAspGluIleValLysIleLeu 166
1579 GTATGATAAAGCGGTACTGTCGCGAGCAAGATGATGATAAAGATGATGATAAAGATGATG 1638
167 Ile-----AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
1639 TTGGGGGATGAAGTGAATCAGGAGTCAAAACTTCAGCTCGGCCCATATGATGATGATG 1698
185 GlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlu 204
1699 GGTGAGTGTGTAAACAACTGATGCTAGCTGATCTTTGATGATGATAAAGAAAGTAAAGAT 1758
205 HisPheHisProLysIleTyPheLysValSerGluAspPheAsnGluLysArgLeuIle 224
1759 CACTTCAAGCTCAAGCGCTGGGCTTGTGTTCTGATGATGATGATGATGATGATGATGATG 1818
225 LysGluIleValGluSerIleGluGluLysSerLeuGlyLysMetAspLeuAlaProLeu 244
1819 AGAGTTATTTATCATCTGATGCTGAGCTGGGAAAAGAGAGTTTGAAAGCTTAATCTGCT 1878
245 GlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyLeuLeuValIleAspAspVal 264
1879 CAAAGAGCTCTTAAGAGAAACCTTAGAAGACGATATTTCTAATAGTTTGGATGATGATG 1928
265 TrpAsnGluAspGlnAspLysIleValLysLeuArgGlnValLeuLysValGlyAlaSer 284
1939 TGCTCTGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1998
285 GlyAlaSerValLeuThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeu 304
1999 GGAAGTAGAATTAATCATGACAACTCGAAGAGCAATTCACAGAAAGCTGGGCTTTTCT 2058
305 GlnProTyGlnLysSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArg 324
2059 CATCAAGACCTCTGAGAGGCTTATCACAAGATGATGCTTGTCTTGTGCTCAACAC 2118
325 AlaPheGlyHisGlnGlu-----GluIleAsnLeuAsnLeuValAlaIleGlyLysGluIle 343
2119 GCATTTGGTGAACAACTTGAATTCATCACTCAAGGCCACATGAGGAAGCTGTTT 2178
344 ValLysLysCysGlyGlyValProLeuAlaAlaSerThrLeuGlyLysIleLeuArgPhe 363
2179 GTGAAGAATGTGATGCTTACCTTACCTTGAACAACTTGAAGAGCTTATTAAGACACA 2228
364 LysArgGluGluAspGlnTrpGluHisValArgAspSerGluIleTrpLysLeuProGln 383
2229 AAAACAGACGAGAAACATGGAAGAGCTGTGATGATGATGATGATGATGATGATGATGATG 2298
384 GluLysSerIleLeuProAlaLeuArgLeuSerTyHisHisLeuProLeuAspLeu 403
2299 AGCGAT---GAGATGTTCCGCGCTTGAAGCTAAGCTAAGTATGATCTTCTGCCWCTTTG 2355
404 ArgGlnCysPheThrTyCysAlaValPheProLysAspThrGluMetGlyLysGlyAsn 423
2356 AAGCTRTTTRTGTGATATGCTCTCTGTTCCAAAGCATATGATGATGATGATGATGATGATG 2415
424 LeuIleSerLeuTrpMetAlaHisGlyPheIle---LeuSerLysGlyAsnLeuGluLeu 442
2416 TTGATTTATTTGTGATGCGAAGAGGTTTTCACCAACCAACTATVAAACAGTCAAG 2475


```

QY 443 GluAenValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPheGlnGluLeu 462
DB 2476 CAACGKTGGGCTTGAATATTTTAAAGAGTTRTGTCAAGTCTTTTTCAA----- 2529
QY 463 GluValIysSerGlyGlnThrTyrPheIysMetHisAspLeuIleHisAspLeuIleThr 482
DB 2530 CATGCTCCCAATRCAAAATCSFTGTTGTGATGACATGACCTTAATGATATTTGGCTCA 2589
QY 483 SerLeuPheSerAlaSerThrSerSerSerAlaIle-----ArgIu 496
DB 2590 TTTGTGCTGGAGAAATTTTTCAGGCTTACATAGATGAGATGAGAGAAATTTAGATG 2649
QY 497 IleIleValGluAsnTyrIleHisMet----- 505
DB 2650 SAATCTTTGAGAAAGACCCGACATATGTCATTTGATGAGATATACATAGTACAA 2709
QY 506 -----MetSerIleGly 509
DB 2710 ARGTTGAGCCATTTAGAGAGCTAAATTTAGAACATTTTTCAGATTTGTCTGTGG 2769
QY 510 PheThrIysValIleValSerSerTyrSerLeuSerHis-----IleGln 523
DB 2770 GTGTAGAGATTTGAGAGATGTTTACTTATCAACAGAGCTTTAATGACATCTTCA 2829
QY 524 LysPheValSerLeuArgValLeuAsnLeuSerAspIleIleLeuIleGlnLeuProSer 543
DB 2830 GATTACCATTTCTTAAGGCTCTTAACTTTGATTTTCTTAAATATTAATAGTACCAAA 2889
QY 544 SerIleGlyAspLeuValIleLeuArgTyrLeuAsnLeuSerGlyAsnThrSerIleArg 563
DB 2890 KTCGSGGAGATATGAAACACTTGGCGTACTTAATCTATCTW---GRAACTTAAATCA 2946
QY 554 SerLeuProAsnGlnLeuCysIleValLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCys 583
DB 2947 CATTTACCGGAATWATKCTCGCAATCTTATATTAATTAACAACTTATTTGTCTGTG 3006
QY 584 HisSerLeuCysCysLeuProIysGluThrSerIleGlySerLeuArgAsnLeuLeu 603
DB 3007 GATTTATTTAGTTAAATTTGCCCAARACCTTCTCAAACTTTAAATTTGASACATTTT 3066
QY 604 LeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySerLeuThrCysLeu 623
DB 3067 ATGAGGGRATCTCCAAATTTTAAABAACATGCCCTTARAGGATGTGATGAAATCTCA 3126
QY 624 LysThrLeuSerArgPheValValGlyIleGlnIlySerCysGlnLeuGlyLeu 643
DB 3127 CAATCTCTCTTY---GTAAACATTTGCATA-----GCAATTAACCGAGCTT 3168
QY 644 ArgAsnLeu---AsnLeuTyrGlySerIleGluIleThrHisLeuGluArgValIysAsn 662
DB 3169 AAGAACTTGCAAAATCTTCATGGAATTTTGTATTTGGCGGCTGGGAAAAATGAAAT 3228
QY 663 AspMet-AspAlaIysGluIleAsnLeuSerAlaIysGlu----- 675
DB 3229 GCMGTGKATGACGTTAAGCACTTGTCTCAAAAAGGTTWATGARTTANAAACTGG 3288
QY 676 -----AsnLeuHisSerLeuSerMetIlyStrPheAspArgGluArgProArgIle 692
DB 3289 RWTGKGGGGTGATRAATTAATTTTCTT---CCGAAATGGGAACTT---GAAA----- 3338
QY 692 eTyrGluSerGluValGluValLeuGluIleLeuIysProHisSerAsnLeuThrCys 712
DB 3339 -----GAGTCTCTCAATGAAGTATGCTCTCAATGATGACTTANA 3379
QY 712 eLeuThr-----IleArgGlyPheArgGlyIleArgLeuProAspTyrPheAsn 728
DB 3380 AAAAACCCCAATATATGCTTATAGGGGGATAGAGTTTCCAAATG---GGTGTGTTCA 3436
QY 728 HisSerValLeuIysAsnValIleSerIleGluIleIleSer---CysIysAsnCysSe 747
DB 3437 CTAAAGGTTTCTGAAA-----CTAGAGATGTGTTCTATGATGATGAAAA---GA 3483
QY 747 rCysLeuProPheGlyGluLeuProCysLeuIysSerLeu----- 761

```

```

DB 3484 NTGTTTACGTAGTTTCATCATCAACCAAGTGGGAAATAGATATTTTCAGGCGTAC 3543
QY 762 -----GluLeuThrPheArgIysSerAla----- 768
DB 3544 TGATGATGTGGAGAGGTATGATAGGTTTCTTGGGCGGTAGAGAAATATAGCATCA 3603
QY 769 -----GluValGluTyrVal---AspSerGlyPheProThrArgArgPhePr 784
DB 3604 TTCTTGTAATGAATATATATTTGTGGATTCAGAACAGAGCAATAGTTCTTAT 3663
QY 784 oSerLeuArgIysLeuAsnIleArgGluPheGlyAsnLeuIysGlyLeuLeuIysGly 804
DB 3664 GAATTTAAAGAAATGATTTAGGATGATGCAAAATTTGCTGATTTAGGCGGAGAAAA 3723
QY 804 uGlyGluIu----- 807
DB 3724 GAGAGATATATATATATATATAGGAGAGAGCACTTAACATCTTTTAGAGGTGAAATGT 3783
QY 808 -----GlnCysProValLeuGluGluIleGluIleIleCysCysPro----- 821
DB 3784 ATGAGATGTAAACAGCTTGGAGCATTTGAGG-----TGTCCAGATAGCATGAGAA 3834
QY 822 -----MetPheValIleProThrLeuSerSerValIleIysLeuValIleSerGlyAs 839
DB 3835 TTTGATATATGACATGTGTGATCATATACATCCGCTCTCTCCCAACAGAGAGAGACA 3894
QY 839 pLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuG 859
DB 3895 GAG-----ATCAAGCACTTATCACTACATCACTGA 3921
QY 859 nIleArgTyrAsnIysGluAspAlaSerLeuProGluIleMetPheIysSerLeuAlaAs 879
DB 3922 TTGCAAGAGCTTTCGAAAGAGAGTTGGAGAGAGAGAGAGCAAGAGTCTTATAAA 3981
QY 879 n-----IleuIysTyrLeuAsnIleSerPheTyrPheAsnLeuIysGluLe 894
DB 3982 CTCAAAATATGAGATGCTTGAATCAATGATATATGTAATTTGATGCAATCTGAAATCTAT 4041
QY 894 uProThrSerLeuAlaSerLeuAsnAlaLeuIleHisLeuGluIleHisSerCysTyrAl 914
DB 4042 C---AGTAAATTTGGTCTTCATTCACATGACAGATATATATATCAAACTGTCCGAG 4098
QY 914 aLeuGluSerLeuProGluIleGluIleValIysGlyLeuIleSerLeuThr 930
DB 4099 TRTGAGATCTTCTTGACATGAGTTGCCAAATCTCACTCTTAAACA 4147

RESULT 4
US-09-004-838-70
; Sequence 70, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; CONFERRING PEST RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998

```

```
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 4163 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4163
OTHER INFORMATION: /note= "RLG1-E169"
US-09-004-838-70
```

```
Alignment Scores:
Pred. No.: 2.68e-100 Length: 4163
Score: 1008.50 Matches: 311
Percent Similarity: 46.52% Conservative: 177
Best Local Similarity: 29.65% Mismatches: 395
Query Match: 19.67% Indels: 166
Gaps: 27
```

US-10-647-268-2 (1-988) x US-09-004-838-70 (1-4163)

```
QY 1 MetAlaGlu-----AlaPheLeuGlnValLeuAspAsnLeuThrCysPhe 16
Db 1099 ATGGCTGAATTCGTCCTTCTGCTCTTCTTGACAGCGTGTTGAAAGCTGGCATTTGAA 1158
QY 17 ILeGlnGlyLeuLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 36
Db 1159 GCCTTGAAGAGATGCTTCCTCCAAAAGATTGATCTGACCTTAAGAAATTGAAAGAG 1218
QY 37 ThrPheThrThrIleGlnAlaValLeuGlnAspAlaGlnIleValLeuLeuLeuLeuLeu 56
Db 1219 ACATTAGACCAAAATCCAGATGCTGCTTAACATGCTCCAGAGAGAGATTAATATGAA 1278
QY 57 AlaIleGlnAsnTrpLeuGlnIleValLeuAsnAlaAlaIleValLeuLeuLeuLeuLeu 76
Db 1279 GCCGTTAAAGATGCTGATGATGATCTCCAAACATTTGGCTTATGACATGACGACCTACTT 1338
QY 77 AspGlnCysValThrGlnAlaProIleArgGlnIleValLeuLeuLeuLeuLeuLeuLeu 96
Db 1339 GATGATTTTGGCACTGAAGCTCTTCAACGCTGAGTTGACCGAGAGGCTGAGCTCTCC 1398
QY 97 ProAsnVal-----IleThrPheArgIleValLeu 106
Db 1399 AGTATGTAAGAAACTAATCCCAAGTTGTCACAAAGTTTCTCAAAAGTATATGAGATG 1458
QY 107 GlyIleValGlnMetIleValLeuValLeuValLeuValLeuValLeuValLeuValLeu 126
Db 1459 CATGCAAGTTAGATGATTTGCCACAGGTTACAGAACTGATGAGGCAAAAATATAT 1518
QY 127 PheIleLeuAspGlnArgThrIleGlnArgGlnValAlaThrArgGlnThrGlyPheVal 146
Db 1519 CTGCTTTTAAGTGTATACATATATATAAGCCAAAATTGAAAGGTATGAGCGCTTTTG 1578
QY 147 LeuAsnGlnProGlnValIleValLeuValLeuValLeuValLeuValLeuValLeuVal 166
Db 1579 GTAGATGAAGCGGATCTGCGACGTGAAGATGATATGAAATAATTTGCTGGAAGAGCTG 1638
QY 167 Ile-----AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
Db 1639 TTGGGGGATTAAGATCAATCAAGGAGTCAAAAATTTCAGCATCTGCTCCCATAGTTGGTATG 1698
```

```
QY 185 GlyIleLeuGlnIleValLeuAlaGlnMetValPheAsnAspGlnArgValIleGln 204
Db 1699 GTGGAGTGTGTAAACAACACTCTAGACTTTGTATGATGAAAGAAAGTGAAGAT 1758
QY 205 HisPheHisProIleIleTrpIleCysValSerLeuAspPheAsnGlnIleValLeuLeu 224
Db 1759 CACTTCGAACCTACAGGCTGTGGGTTGTGTCTCATAGTTCAGTGTCCCAATATTAAGC 1818
QY 225 LysGlnIleValGlnSerIleGlnIleValSerLeuGlnIleValMetAspLeuAlaProLeu 244
Db 1819 AGAGTTATTTATCAATCTGTACCTGGGAAAGAGAGATTGAAAGCTTAATCTGCTT 1878
QY 245 GlnIleValLeuAspLeuLeuAsnGlnIleValLeuValLeuValLeuValLeuValLeuVal 264
Db 1879 CAAGAGCTCTTAAGAGAACTTAGAACACAGATATTTCAATATGTTTGTGATGATGTG 1938
QY 265 TrpAsnGlnAspGlnAspIleTrpAlaValLeuArgGlnValIleValValSer 284
Db 1939 TGGTCTGAAGCTATGCTATGCTATGGAGAAATTAAGTGGCCCATTCCTTGGCGGCTCTCT 1998
QY 285 GlyAlaSerValLeuThrThrThrArgLeuGlnIleValGlnSerIleMetGlyThrLeu 304
Db 1999 GGAAGTGAATTAATCATGACCAACTCGAAGAGCAATTCCTCAGAAAGCTGGCTTTTCT 2058
QY 305 GlnProIleValLeuSerAsnLeuSerGlnIleValAspCysTrpLeuLeuPheMetGlnArg 324
Db 2059 CATCAAGACCTCTCGAGAGGCTATCAACAGATGATGCTTGTCTTGTGCTCAACAC 2118
QY 325 AlaPheGlnIleGlnGlnIleGlnIleAsnLeuValAlaIleGlyLeuGlnIle 343
Db 2119 GCATTTGGTGTACAAACTTGTGATTCACATCCAAACATGAGCCACATGGAGAACTGTTT 2178
QY 344 ValIleValCysGlnIleValIleProLeuAlaAlaIleValThrLeuGlnIleLeuArgPhe 363
Db 2179 GTGAAGAAATGTATGCTTACCTTCTAGCTTTAAGAACACTTGAAGGTTATTAAGACA 2238
QY 364 LysArgGlnIleValArgGlnIleValArgAspSerGlnIleTrpIleValProGln 383
Db 2239 AAAACAGACGAGAAACATGAGAGAGCTGTGATAGTGAATGAGGTTTGAAGAG 2298
QY 384 GlnIleSerSerIleLeuProAlaLeuArgLeuSerGlnIleValSerProLeuAspLeu 403
Db 2299 AGCGAT--GAGATGTTGCTGGCTCTTGAAGTAAAGCTTAACATGATCTTTCGCKCTTTG 2355
QY 404 ArgGlnCysPheThrIleValAlaPheProIleAspTrpGlnMetGlnIleValAsn 423
Db 2356 AAGCTRTTGTGATATATGCTCTGTTTCCAAAGACTATGATGATGACAGAGAGAG 2415
QY 424 LeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerIleValAsnLeuGlnIle 442
Db 2416 TTGATTTATTTGTGATGAGTGCAGAAAGGTTTTTGACCAACCACTATVAAACAGTCAAG 2475
QY 443 GlnAsnValGlnAsnGlnValIleTrpAsnGlnIleValLeuArgSerPhePheGlnIle 462
Db 2476 CAAGCTTGGGTCTTGAATATTTTAAGATGTTTGTTCGAARCTKTTTTCATCA----- 2529
QY 463 GlnValIleValSerGlnIleThrThrPheIleValMetIleValAspLeuAlaThr 482
Db 2530 CATGCTCTTAATRCAAAATCTGTTTGTGATGATGATGATGATGATGATGATGATGATGAT 2589
QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIle-----ArgGln 496
Db 2590 TTTGTGCTGAGAAATTTTTCAGAGTTAGACATGATGATGATGATGATGATGATGATGATGAT 2649
QY 497 IleIleValGlnAsnIleValIleHisMet-----MetSerIleGly 509
Db 2650 SAATCTTTGARAAGCAACGACATATGATGATGATGATGATGATGATGATGATGATGATGAT 2709
QY 506 -----MetSerIleGly 509
Db 2710 ARGTTGAGCATTTAGAGAGCTTAAAAATTGAGAACATTTTATGACATTTGTCTGTTGG 2769
```



```

; LOCATION: 1..2353
; OTHER INFORMATION: /note= "RLGIB"
US-09-004-838-2

Alignment Scores:
Pred. No.: 4,38e-96 Length: 2353
Score: 966.50 Matches: 242
Percent Similarity: 53.52% Conservative: 131
Best Local Similarity: 34.72% Mismatches: 265
Query Match: 18.85% Indels: 59
DB: 3 Gaps: 12

US-10-647-268-2 (1-988) x US-09-004-838-2 (1-2353)

OY 1 MetalagluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlu 20
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 289 CTGGTTCGCGCTCTTTGCGGCTTTCTTGAAGAGCTTGTGAAGCCTTGAGAGG 348
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThr 40
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 349 GTTGCTCTCCAAAGTAATGACAGAGAGCTCGAGAAATGAATGCTCATGATCAT 408
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 41 IleglnAlaValLeuGlnAspAlaGlnLysGlnLeuLysAspLysAlaIleGln 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 409 ATAAAGCTGTGCTCAATGATGCTTCTCAGAGAGAAATAGTAAGAGAGCTGTAAAGAA 468
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 TTPLeuGlnLysLeuAsnAlaAlaIleTyrgluAlaAspAspIleLeuAspGluCys 80
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 469 TGGTTGAATGCTCTTCAACATTTGCTTACGACATGATGATCTTGGCGATTGGCA 528
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 81 ThrGluAlaProIleArgGlnLysAsnLysTyrgly----- 93
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 529 ACCAAAGCTATCCATCCTATAGTCTCTGAGAAATCGGGCCACCATCAACAAGSTAGCA 588
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 94 -----CysTyrlHisProAsnValIleThrPheArgHisLysIleGlyLys 108
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 589 AAGTTAATTCATCTTGTCTCTCTAGTTGTGCAAGTACT-----AAGATGCGCAAC 639
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 109 ArgMetLysLysIleMetGlnLysLeuAspValIleAlaIleGluArgLysPheHis 128
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 640 AAGATACATTAATATTACACAGAGTTACAGAACTATTAGAGAGAGAAATATATCTTGGCA 699
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 129 LeuAspGluArgThrIleGluArgGlnValAlaThrArgGlnThrGlyPheValLeuAsn 148
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 700 TTAATGTGAATTTGGTGAAGCCGAAACTGTGAATATAGAAATCAGAACCTCTTTGTGTA 759
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 149 GluPro---GlnValTyrglyArgAspLysGlnLysAspGluIleValLysIleLeu 167
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 760 GATCATCTAGATATTGTGACGACAGATGATTAAGAAAGCGTGTCTTCAAGCTATAT 819
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 168 AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyGlyLeu 187
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 820 GAACCATGTGAT-----AGAAACTTTAGCATCTTGCCNATAGTGGATGGGTTA 873
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 188 GlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHis 207
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 874 GATAAGACACATTTAGTATGACTTTGTATATGATTAAGCAAGTAAAGATACACTTGGAA 933
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 208 ProLysIleTTPLeuCysValSerGluAspPheAsnGlnLysArgLeuIleLysGlu 227
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 934 CTCAAGGCGGTGGTGTGTCTGATGATTTGATCTTCGTGATTAAGCAAAACCAATT 993
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 228 ValGlnSerIleGlnGlnLysSerLeuGlyMetAspLeuAlaProLeuGlnLysLys 247
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 994 TTCGATCGATAGAGAGGAGAAACCAAGAGTTTAAAGATTTAAATCTGCTTCAGGTGCT 1053
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 248 LeuArgAspLeuLeuAsnGlyLysLysTyrglyLeuLeuValLeuAspAspValTTPAsnGlu 267
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1054 TTTAAAGCAAAATATCTCAAGAAAGATTTCTGTGTTCTTGATGATGATGAGCGAG 1113
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 268 AspGlnAspLysTTPAlaLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSer 287
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1114 AGCTATACTGATTTGGAAATCTTGAAGAGTTCATTTCTAGCAGAGACCGAGAAAGTAAA 1173

```

```

OY 288 ValLeuThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeuGlnProLys 307
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1174 GTATTCATTCACACACCCGCAAGTCTCGTGTGAACCAATTTGGTCTCATGATCAACCATAC 1233
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 308 GluLeuSerAsnLeuSerGlnGlnAspCysTTPLeuLeuPheMetGlnAlaPheGly 327
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1234 CAATTTGTGATTTGTGCATGACATGCAATGCTATCTTATTTTGTCAACGCGATTTGGT 1293
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 328 ---HisGlnGlnGlnIleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLysLys 346
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1294 GTAAATGCTTTGATTCACATCCGATCTTAACACATGCTGAAGGATTTGTGAAAAA 1353
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 347 CysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlu 366
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1354 TGTGATGCTTTGCCATTTGGCTTTGATGACCTTGGAGGTTATGAGCAAAAAGAGAT 1413
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 367 GluArgGlnTTPGlnHisValArgAspSerGluIleTTPLysLeuProGlnGlnGlnSer 386
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1414 GAGGAGAAATGAGAGAACTATTGAATATGATGATGAGGTTAGAGAAAGAGAT--- 1470
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 387 SerIleLeuProAlaLeuArgLeuSerTyrlHisIleLeuProLeuAspLeuArgGlnCys 406
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1471 GAGATTAATTCGGYTCTTACCTAAGCTATATATATCTTCTGCTCTTGAAGCAGTTG 1530
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 407 PheThrTyrglyAlaValPheProLysAspThrGlnMetGlyLysAsnLeuIleSer 426
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1531 TTTGCATATATGCTCTCTTGTCCCAAGACATATGTTCAACAAGAGAGATGATTTTA 1590
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 427 LeuTTPMetAlaHisGlyPheIleLeuSerLysGly---AsnLeuGlnLeuGlnAsnVal 445
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1591 TTATGATATGGCAGAGAGGTTTGTGCACATGAAATCAACAAGTCAATGAAGCGCTTA 1650
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 446 GlyAsnGlnValTTPAsnGlnLysLeuTyrlLeuArgSerPhePheGlnGlnIleGlnValLys 465
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1651 GNTCTTGAAATATTGTGACGACTTTGTGCAGAGTCATTTTTCAA-----CATGCATCT 1704
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 466 SerGlyGlnThrTyrlPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPhe 485
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1705 GATGACAAATGCTGTTGTGGTGCACGACCTCATGATGACTTGGCCACATCTGTGCT 1764
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 486 SerAlaSerThrSerSerSerAsnIle-----ArgGlnIleIleValGlnAsnTyrlLe 503
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1765 GAGATTAATTTTAAAGATTAGACATTGAATGAATGAAGAAAGCTTTGGAAAAAATACCGA 1824
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 504 HisMet----- 505
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1825 CATATGTCATTTGTTGTGAGAGTTACATGCTTTACAAAAGTTCCGAACCTTTAAAGCA 1884
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 506 -----MetSerIleGlyPheThrLysValIleSerSer 516
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1885 GCTAAAAAATTGAGAACCTTTCTAGCAATGCTGTGGAGATGAATAAAAGTTGAGCAACA 1944
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 517 TyrlSerLeuSerHis-----LeuGlnLysPheValSerLeuVal 530
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1945 TTTTATCTTAAATTAAGTCTTGAATGACTTATCTTACGATTAACCATTTGTAGAGTT 2004
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 531 LeuAsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHis 550
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2005 CTAAAGTTTGAATTATCTTGAATCAAGAGGTACTGAAATTAATAGCAATTTGAAACAC 2064
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 551 LeuArgTyrlLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCys 570
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2065 TTGGCGTATCTTAATTTATCA---CACACGAGTATCACACATTTAACGAAAAAGTCTGC 2121
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 571 LysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuPro 590
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2122 AATCTTTTAAACCTTAACAAACATTAATCTTGTGTGCTGTGTGTTTATTAACCAAGTTTCC 2181
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 591 LysGlnThrSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrglyLeu 610
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2182 AACCACTTCTTAAAGCTTGAATTAATTAACGATTTGACATTTAGCGATACCTCCGGTTTG 2241
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


DB 1261 AATGATCTCTGCTCTTTGAAGAAGTTGTCATCTGCTCTTCCCAAAAGAC 1320
QY 417 ThrgluMetGluYsglyAsnLeuIleSerLeuTrpMetAlaHisglyPheIle--Leu 435
DB 1221 TATGTTGTCATTAAGAGAGAGCTTGATTTGTTGATGATGACGAAGGGTTTTCACACCA 1380
QY 436 SerlysglyAsnLeuLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeu 455
DB 1381 TCAACCAACAGCAAGTCBAGTGAACGCTTGAGHCAATGAAGTTTGGATGAATGTGTCTCA 1440
QY 456 ArgSerPhePheGlnGluIleGluValIysSerGlyGlnThrTyrPheIleMetHisAsp 475
DB 1441 AGATCATTTTTCAA-----CATGCCCTGATGCCAATGATGTTTGTGATGATGATC 1494
QY 476 LeuIleHisAspLeuAlaThrSerLeu 484
DB 1495 CTGATGATGATGACTTGGCAATCTGT 1521

RESULT 7
US-08-947-823-2
; Sequence 2, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kalooshian, Isgouhi
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Molligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Confering
; TITLE OF INVENTION: Pect Resistance in Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..3852 /note= "Copy 1 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
; US-08-947-823-2

Alignment Scores:
Pred. No.: 3,916-56 Length: 3997
Score: 609.50 Matches: 257
Percent Similarity: 41.64% Conservative: 144
Best Local Similarity: 26.69% Mismatches: 383
Query Match: 11.89% Indels: 179
DB: 3 Gaps: 37

US-10-647-268-2 (1-988) x US-08-947-823-2 (1-3997)

QY 5 PheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGluLeuGlyLeuIle 24
DB 1252 TTCATGATCTCTTACACATACATTAATGATTTGTAATCTTAATGCTTATTCATT 1311
QY 25 LeuGlyPheIleAspGluPheGluIleGluLeuSerThrPheThrThrIleGlnAlaVal 44
DB 1312 GCTTTGATTAAGAGAAATCGAGCTGTGAAGCAACCTGAAATTCATTAAGATCTTC 1371
QY 45 LeuGluAspAlaGlnIleGluIleLeuIleAspLysAlaIleGluAsnTrpLeuGlnLys 64
DB 1372 TTTCGATGATCTTACAGCAAGATTTGTATAAAGATCTC-----TGCGACACGTT 1419
QY 65 LeuAsnAlaAlaIleAlaIleGluIleAspAlaIleLeuAspGluCysIleThrGluAlaPro 84
DB 1420 CTAGAT---GTGGCTTATGAGGCAAGATGATCATGATTCAC----- 1458
QY 85 IleArgGlnLysLysAsnLysTyrGlyCysTyrHis-----ProAsnVal 99
DB 1459 ATTATTTGCTGACGATTAAT-----GATCTTACATCTTATTTTCACCTCCATTCACC 1512
QY 100 IleThrPheArgHisIleGlyLysArgMetLysLysIleMetGlyLysLeuAspVal 119
DB 1513 ATA-----AAGAAGATCAAACTTATCAAGAAAGATCTCGCT 1551
QY 120 -----IleAlaIleGluArg-----IleLysPheHisLeuAspGluArgThr 133
DB 1552 TTAGATGAGAACATTTCCCAAGACAGAGCTTATATCTTGTGGAACCTCCCAAGAACCA 1611
QY 134 IleGluArgGlnValAlaThrArgGlnThrGlyPheValIleAsnGluProGlnValTyr 153
DB 1612 GTTGAAGAAAGTCAATTGACA-----ACTGATTAATAATTAAGTGA 1650
QY 154 GlyArgAspLysGluYsglyAspGluIleValIleLysIleLeuIleAsnValSerAsnAla 173
DB 1651 GATTTTGAAGAGAAACAACCTTGAATTAAGAAAGCTC-----ACCAAGGATGCT 1701
QY 174 GlnThrLeuProValIleLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAla 193
DB 1702 GCAGATCTAAGTGCATTTTCATCATCTGATGCGGCGGATTCAGGTAACTACTTTGGCA 1761
QY 194 GlnMetValPheAsnAspGlnArgValIleGluHisPheHisProLysIleTrpIleCys 213
DB 1762 TACAAAGTATACATGATTAATCATGATTCAGCGGTTTCGACCTTCGATGATGATGACG 1821
QY 214 ValSerGluAspPheAsnGluLysArgLeuIleLysGluIleValIleGluSerIleGluGlu 233
DB 1822 GTCCACCAAGGATGTGATGAAGAAAGTTGTTGAATCAAAATTTTCAGTCAAGTAAAGTGC 1881
QY 224 LysSerLeuGlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsn 253
DB 1882 TCAGATTCAAAATTTGAGTGAAGATATTGATGTGCTGATTAATTAATTCGAAACCACTGTT 1941
QY 254 GlyLysLysTyrLeuLeuValLeuAspAspValTrpAsnGluAspGlnAspLysTrpAla 273
DB 1942 GGAAGAGGATATCTTATGTCTTGAATGACGTGCG-----GATTACTAATCAATGAGGAT 1995
QY 274 LysLeuArgGlnValLeuValIleValIleAlaSerGlyAlaSerValLeuThrThrThrArg 293
DB 1996 GAGTTTAACAAGACCTTTTCTGAATCTTAAGAAAGAGTAAAGATTAATTTTGAACAATCGG 2055
QY 294 LeuGluLysValGlySerIleMetGlyThrLeu-----GlnProTyrGluLeuSerAsn 311


```

Db 47882 -----TTCCAAATTCATGATCTTGCGATGACTTTGTTGATTAAGACAGAAAG 47732
Oy 480 -----LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAlaArgGluLe 497
Db 47733 GAAATTTGTTGATGATCAATGATCAATGCTCCATGATTTGTCCTCGTCAAAAT 47792
Oy 498 ILeVal-----GluAsnTyrIleHisMetMetSerIleGlyPheThrIleVal 513
Db 47793 ACCATTGATTTGATGAGAGAGACACTTGGGCTTAATTTTGTGATGTTGATTCAT 47852
Oy 514 ValSerSerTyrSerLeuSerHisLeuGlnIlePheValSerLeuArgValLeuAsnLeu 533
Db 47853 AAGAAAGGCAATTCGTGTAAACACCTC-----TATCTTTGAGATTAATGCA--- 47900
Oy 534 SerAspIleIleValLeuGlnLeuProSerSerIleGlyAspIleValHisIleAsnGly 553
Db 47901 -----GACCAGCTGGATGACAGATGTTGTTGATGACATTCACCTTAAGAC 47945
Oy 554 LeuAsn-----LeuSerGlyAsnThrSerIle-----ArgSerLeu 565
Db 47946 TTGAGGCTTCTTAAGAGTGTGACCTGACATGCTTTTATCATGCTGAAGATTTCTTG 48005
Oy 566 ProAsnGlnLeuCyLeuLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCyHisSer 585
Db 48006 CTGAATGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48059
Oy 586 LeuCySerLeuProIleGlnThrSerIleGlnIleGlnIleGlnIleGlnIleGlnIle 605
Db 48060 GTTAATATGCTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 48119
Oy 606 GlyCyArgIleLeuThrCyMetProProArgIleGlySerLeuThrCyLeuIleThr 625
Db 48120 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48179
Oy 626 LeuSerArgPheValIleGlyIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 645
Db 48180 CTGTCC-----GTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 48203
Oy 646 LeuAsnLeuTyrGlySerIleGlnIleThrHisIleGlnIleGlnIleGlnIleGln 665
Db 48204 -----TTTGAATATGAT 48215
Oy 666 AlaIleGlnIleAsnLeuSerAlaIle-----GluAsnLeuHisSerLeuSer 681
Db 48216 GCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 48275
Oy 682 MetIleTyrAspAspAspGluArgProArgIleTyrGlnSerGlnIleGlnIleGln 701
Db 48276 -----GACTGTTGATTTCTTAATGCAAGATTAACAAG 48308
Oy 702 GluAlaIleLeuTyrProHisSerAsnLeuThrCyLeuIleThrIleArgGlyPheArgGlyIle 721
Db 48309 AATATTTTCAAAAGGTTTCCCAATCTTCAGTTGCTTCA-----TTT 48350
Oy 722 ArgLeuProAspIleTyrMetAsnHisSerValLeuIleAsnValIleSerIleGlnIleIle 741
Db 48351 GAACCTCAAGAGCTGATGAGATTAATCAACAGCAACATTTG----- 48392
Oy 742 SerCyLeuAsnCySerSerCyLeuProProPheGlnIleProCyLeuIleSerLeu 761
Db 48393 -----TTCTCGGAATGATGATTTCTTAAGTCAACTA 48422
Oy 762 Glu--LeuTyrArgGlySerAlaGluValGluTyrValAspSerGlyPhe----- 777
Db 48423 GAAACACTCTCTGTAGTTTAAAGTTCAACACAAACGATAGAGGCTCTCTGTACG 48482
Oy 778 -----ProThrArgArgArgPheProSer--LeuArgIleLeuAsnIleArgGlu 793
Db 48483 ACAAAATCGCGCGGATTTTCACTTCCTTCAAAATTTGAAATATCTGTGTGTGATA 48542
Oy 794 PheGlyAsnLeuIleGlyLeuIleIleGlyLeuIleGlyLeuIleGlyLeuIleGlyLeu 813

```

```

Db 48543 TTTCGCTGATCCATCCATTCATCAACATACG-----AGACTGCCAACCTTGAA 48596
Oy 814 GluIleGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 833
Db 48597 GAGTTG----- 48614
Oy 834 LeuValValSerGlyAspIleSerAspAlaIleGlyPheSerSerIleSerAsnLeuMet 853
Db 48615 ACAATCATCCATGAGAAAGATGACATGAGGAGAGACACCTTTGACAAATCTCAAA 48674
Oy 854 AlaLeuThrSerLeuGlnIleArgTyrAsnIleGlnIleIleIleIleIleIleIle 873
Db 48675 TTTTGAACCTTCAATCAAGATGATGATTTCCAAAGTGGAGGCTTGA-----GAGGAATCC 48728
Oy 874 PheIleSerLeuAlaAsnLeuIleTyrLeuAsnIleSerPheTyrPheAsnLeuIleGlu 893
Db 48729 TTC-----CCCAATCTTGAGAAATTAATACTGGGGGATGCTCAATGAGAG 48779
Oy 894 LeuProThrSerLeuAlaSerLeuAsnAlaLeuIleIleIleIleIleIleIleIle 913
Db 48780 ATTCACCTAGTTTGGAGATATTATTCATGTAATCTATCAAAATGTGAAGATCCT 48839
Oy 914 AlaLeuGlu 916
Db 48840 CAACCTTGA 48848

RESULT 9
US-09-245-928A-15
; Sequence 15, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Mi resistance gene
US-09-245-928A-15

Alignment Scores:
Pred. No.: 1,13e-51 Length: 9870
Score: 575.50 Matches: 254
Percent Similarity: 41.07% Conservative: 144
Best Local Similarity: 26.21% Mismatches: 382
Query Match: 11.22% Indels: 189
DB: 4 Gaps: 40

US-10-647-268-2 (1-988) x US-09-245-928A-15 (1-9870)
Oy 5 PheLeuGlnValIleLeuAspAsnLeuThrCyAspIleGlnIleGlnIleGlnIle 24
Db 4505 TTTCATGATCTTCTACACATGACACTTAATGATTTGCTAGATTTGATGCTTATTCAT 4564
Oy 25 LeuGlyPheIleAspGluPheGlnIleIleLeuGlnSerThrPheThrThrIleGlnAlaVal 44
Db 4565 TCTTGAATTAAGAAAGAAATGAGATGCTGAGTCAGCAAGATCGAATTCATTAAGATTC 4624
Oy 45 LeuGlnIlePheIleGlnIleIleGlnIleIleIleIleIleIleIleIleIleIle 63
Db 4625 TTTCGGGATCTGCTGAGCAAGATTTGATTAAGAT-----ATCTGGGACGCT 4672
Oy 64 LysLeuAsnAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 83

```

```
Db      4673 GTTCTAGT---GTGGCTTATGAGCCAAAGATGTCATAGATCA----- 4714
QY      84 ProilearglnlysllysasnlystyglyCysTyrhis-----Proasn 98
Db      4715 ---ATTATGTTCCAGATTAAT-----GGTCTTATCATCTTAATTTCTCACTTCCCAT 4765
QY      99 ValllethrpheahgnlyellleglylsarhmetlyslsilemeGlnlyleuasp 118
Db      4766 ACCATA-----AAGAAGATCAAACTTATCAAGAAAGAGATCTCT 4804
QY      119 Val-----llealalagluarg-----llelysrhehileuaspduarg 132
Db      4805 GCTTAGTAGAGAAACATTTCCCAAGACAGAGCTTAATCTGTGTAACCTCCCAAGAA 4864
QY      133 ThrileguatrglnvalAlathrarglnthrglyphevalleuasngluProglInal 152
Db      4865 CCAGTTGAGAGAAAGTCATTCACA-----ACTGATTAATAATTT 4903
QY      153 TyrglyatgsarplysGlnlysharpolullevalylsileleuileasnvalSerasn 172
Db      4904 GTAGGTTTTGAGAGAGACAAACTTGATTAAGTAAAGCTC-----ACCAAGTGA 4954
QY      173 AlaGlnthrlleuProvalleuProilleuuglyMetglyleuGlyleuGlyThrleu 192
Db      4955 CCCCAGATTATGATGTCATTTCCATCCAGTATCCGGGTTCAGGTAAACATCTTTG 5014
QY      193 AlaGlnMetValPheasnarpGlnargValileglnhisrhehisprolyslleTrrle 212
Db      5015 GCATCAAAAGTATACATGATTAAGTCAGTTCTTACATTTGACCTTCGTGCAAGTGC 5074
QY      213 CysValserGlnaspPheasnGlnlyshargleuileysGlnullevalGlnSerleGlu 232
Db      5075 ACGGTGCATCAAGATATGACACAGAAAGTTGGTGAATACATTTTCAAGTCACTAGT 5134
QY      233 GlnlysserleuGlylyMetaspLeuAlaProleuGlnlysllysleuargshreleu 252
Db      5135 GCCTCAGATTCAAATTTGAGTGAAGAAATATGATGTTGCTGATTAATTCGGGAAACA 5194
QY      253 AsnGlylyslsTyrleuLeuValleuaspArValTrrPasnGlnaspGlnaspIlystr 272
Db      5195 TTTGAAAGAGGTATCTTATGTTCTTAAATGATGATGTGG-----GATTACTACATG 5248
QY      273 AlaIlyleuargGlnValleuIlyslValGlyAlaSerGlyAlaSerValleuThrThr 292
Db      5249 GATGAGTTGACAAAGACCTTTTCTGAAGCTAAAGAAAGAGATTAATTTTGAACA 5308
QY      293 ArgLeuGlnlyValGlySerileMetGlyThrleu-----GlnProIyrgIleuSer 310
Db      5309 CCA---GAAGAGAAAGGTGCTTTCATGAGAAAGCTGAACATGATCTCTTGAACCTTGA 5365
QY      311 AsnleuSerGlnGlnaspCysTrrPleuLeuPheMetGlnargAlaPheGlyhisGlnGlu 330
Db      5366 TTGCTTAAGACACAGAAAGTTGGGAACTTTTGAAGAAAGACATTTGGTAAAT---GAG 5422
QY      331 GlnIleasnleuasnleuValAlaleglylsGlnullevalIlyslsCysGlyVal 350
Db      5423 AGTTGCCCTGATGAATATTAATGATGCGGTAAAGAAATAGCCGAATTTGTAAGGGCTT 5482
QY      351 ProleuAlaAlaIythrleuGlylyleuArgPheIysargGlnGlnGlnargln--- 369
Db      5483 CTTTGTGGTGGCTGATGATGATCTGCGAGTCATTTGCTGGAGGAAAGAAAGAGATGG 5542
QY      370 TrrGlnhisValArgaspSerGlnIleTrrPlyslleuProGlnGlnGlnSerIleleu 389
Db      5543 TGGCTTGAAGTTCAAGATTTGAGTTGAGTTCTTTTATTAATTAACAGTGAAGTGAAG 5602
QY      390 ProAlaIleuargLeuSerTyrhisIleuProleuaspLeuargGlnCysPheThrTyr 409
Db      5603 AAAGTTATGAATTAAGTATGACCATTTACCAATCACCCTCAAGCAAGCATGCTTGC 5662
QY      410 CysAlaValPheProIyaspPheThrGlnMetGlnlyslsGlnleuIleSerleuTrrMet 429

Db      5663 TTTCAGATTTGGCCGAAGACACTCTTTCAGATCAATCTAATTTGTTGACCTGTAATTTGGGT 5722
QY      430 AlahileglyPheIleleuSerlyslsIyasnleuGlnleuGlnasnValGlyasnGlnVal 449
Db      5723 GCTGAAGATTTGGGAAAGACCGAGATGAAGGATATAGAAAGAGTGGGAAGATTTAT 5782
QY      450 TrrasnGlnleuTyrIleuargSerPhe-----PheGlnGlnIleGlnValIySer 466
Db      5783 ATGATGATTTAATTTCCAGTACCTTGTATATTTGTTCAATGAGATA-----GGT 5833
QY      467 GlyGlnthTrrPheIysMetHisaspLeuIleHisaspLeuAla----- 481
Db      5834 GATTAAGTGAATTTCCAAATTCATGATCTTGATGATACCTTTGTTGTTGAATAAAGCA 5893
QY      482 ---ThrserleuPhe-----SerAlaSerThrsSerSerSerAsnIleargGlu 496
Db      5894 AAGAAATATTTGTTTTCATCCGATTAAGTCAAGTCTCCATCATTTGTTGCCCTCGTCA 5953
QY      497 IleIleVal-----GluasnTrrIleHisMetMetSerIleGlyPheThr 511
Db      5954 ATTACCATTTGATTAATGATGAGAGAGAGACACTTGGCTTAATTTGTCATGTTGCAT 6013
QY      512 IysValIalSerSerTyrSerleuSerHisleuGlnIlysrPheValSerleuargValleu 531
Db      6014 TCAATTAAGAAAGGACATCTCTGTAAACACCTC-----TATTTTGGAGS----- 6058
QY      532 AsnleuSeraspIlelyslleuIyGlnleuProSerSerIleGlyaspLeuValHisleu 551
Db      6059 -----ATTAATGAGAGACCACTGATGACAGTGTGTTGTGATGCACTTACCTTA 6106
QY      552 ArgTrrleuasnleuSerGlyasnThrSerIlearg----- 563
Db      6107 AGACACTTGAAGCTTATTAAGTGTGAGCTTGACCTGAACCTCTTAAATCATGTGAATGAT 6166
QY      564 SerleuProasnGlnleuCysIyaslleuGlnasnleuGlnthrlleuaspLeuHisGlyCys 583
Db      6167 TCTTTGCTGAATGAATATGATGATGATTAATCATTTAGGTACTTAAGAAATTCGG----- 6220
QY      584 HisSerleuCysIyaslleuProIyGlnThrSerIyaslleuGlySerleuargAsnleu 603
Db      6221 ACACAAAGTTAAATTTCTGCTTCTTCTTCAAACTCTGGAATCTTAAGAAAGCTGTTT 6280
QY      604 LeuaspGlyCysTrrGlyleuThrCysMetProProargIleGlySerleuThrCysleu 623
Db      6281 GTGTCTAACAAGATCAATCTTGTGACTATTAACCGAAGATTTTGGATCTTGAAGATGG 6340
QY      624 IythrIleuSerIargPheValValGlyIleGlnIlysserCysGlnleuGlyleu 643
Db      6341 CGAGTGCCTGCC-----GTGGGT-----GCTTGTCTTTC----- 6370
QY      644 ArgasnleuasnleuTrrGlySerIleGlnIleThrhisleuGlnargValIyasnasp 663
Db      6371 -----TTTGAT 6376
QY      664 MetaspAlaIyGlnAlaasnleuSerAlaIys-----GluasnleuHisSer 679
Db      6377 ATGATGCAATGATCAATATATGATAGCAAGACACAAAGTTAGAGAACTTGAAGATA 6436
QY      680 LeuSerMetIystrPaspaspGlnargProargIleTrrGlnSerGlnlyValGlu 699
Db      6437 TTAGGG-----GAAGCTTGATTTCTTATTCGAAGAAAT 6469
QY      700 ValleuGlnAlaIleuIyProHisSerasnleuThrCysleuThrIleargGlyPhearg 719
Db      6470 ACAATGAATATTTCCAAAGTTTCCCAATCTTCAAGTCTTCAG----- 6514
QY      720 GlyIleargleuProaspTrrMetAsnHisSerValleuIyasnValIalSerIleGlu 739
Db      6515 ---TTTGAACCAAGAGTCAATGATTAATTAACAAGCAACATTCG----- 6559
QY      740 IleIleSerCysIyasnCysSerCysleuProProPheGlyGlnleuProCysleuIy 759
Db      6560 -----TTCCGGAATTTGGATTTGCTTA 6563
```

```

Qy 760 SerleuGlu---LeuTrpArgGly-----SerAlaGluValGluTrp-ValAspSerGly 776
Db 6584 GAACTAGAAACACTCTGTGTAGTGTAAAGTTAAACAAACAACTGGGCTCT 6643
Qy 777 PheProThrArgArg-----ArgPheProSerLeuArgLysLeuAsnIleArg 792
Db 6644 GTTGGCAAAATCCGCCCTGGGATTTTCACTCCCTCA----- 6682
Qy 793 GluPheGluAsnLeuLysGlyLeuLeuLysGluGluGluCysProValLeu 812
Db 6683 -----AATTGAAAGAACTGTTG-----TTG 6703
Qy 813 GluGluIleGluIleLysCysAspMetPheValIleProThrLeuSerValLys 832
Db 6704 TATGACTTCTCTGACATCCGATTCACATACAAATAGAGACTGCCAAGCTTGA 6763
Qy 833 LysLeu-----ValValSerGlyAspLysSerAspAlaIleGlyPheSer 847
Db 6764 AATTGTCCTTATGATACATCATCCAGGAGAAATGACATGCGGAGGAAAC 6823
Qy 848 SerIleSerAsnLeuMetAlaLeuThrSerLeuGluIleArgTrpAsnLysGluAspAla 867
Db 6824 ACTTTGAGAAATCTCAATTTTGAACCTTCCGCTACTGACTTTTCCAAAGTGGAGGTT 6883
Qy 868 SerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTrpLeuAsnIleSerPhe 887
Db 6884 GGA-----GAGCAATCCTTCCCAATCTTGAGAAATTTAACTGAGAAATGCTGCT--- 6934
Qy 888 TyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysIleLeu 907
Db 6935 -----AAGCTTGGAGGATTCACCTAGTTTGGAGATATTATTATTTGAAATTTATC 6988
Qy 908 GluIleHisSerCysTrpAlaLeuGlu 916
Db 6989 AAAATTGTAAGAGCTCTCAACTGAA 7015

RESULT 10
US-08-947-823-4
; Sequence 4, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kalooshian, Isouhni
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Conferring
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..3860
; OTHER INFORMATION: /note= "Copy 2 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
; US-08-947-823-4

Alignment Scores:
Pred. No.: 6,286-52 Length: 3982
Score: 571.50 Matches: 255
Percent Similarity: 41.44% Conservative: 147
Best Local Similarity: 26.29% Mismatches: 378
Query Match: 11.15% Indels: 191
DB: 3 Gaps: 40

US-10-647-268-2 (1-988) x US-08-947-823-4 (1-3982)
Qy 5 PheLeuGluValIleLeuAspAsnLeuThrCysPheIleGluGluLeuGlyLeuIle 24
Db 1254 TTCAATGATCTTCTACACATGCACTTAATGATTGGTACAGATTCAATGCTATTCAATT 1313
Qy 25 LeuGlyPheLysAspGluPheGluLysLeuGluSerThrPheThrIleGluAlaVal 44
Db 1314 TCTTGATTAAGGAAGAAATCGAGTGTGTGTCAGCAAGAACTGAATTCATTAAGTCAATC 1373
Qy 45 LeuGluAspAlaGluLysLysGluLeu---LysAspLysAlaIleGluAsnTrpLeuGln 63
Db 1374 TTGGGGAGTGTCTGTGAGCAAGATTTGATTAAGAT---ATCTGGGACAGT 1421
Qy 64 LysLeuAsnAlaAlaIleTrpGluAlaAspAspIleLeuAspGluCysLysThrGluAla 83
Db 1422 GTTCTAGAT---GTGGCTTANAGCGCAAGATCTCATAGTTCA----- 1463
Qy 84 ProIleArgLysLysAsnLysTrpGlyCysTrpHis-----ProAsn 98
Db 1464 ---ATTATTGTTCCAGATTAAT---GGTCTTACATCTTATTCTCATTCCCATTT 1514
Qy 99 ValIleThrPheAsnGlyLysIleGlyLysArgMetLysLysIleMetGluLysLeuAsp 118
Db 1515 ACCATA-----AAGAAATCAAACTTATCAAGAAAGAGATCTT 1553
Qy 119 Val-----IleAlaAlaGluArg-----IleLysPheHisLysAspGluArg 132
Db 1554 GCTTAGATGAGACATTTCCCAAGACAGAGCTTAATCGTTGAACTCCCAAGAA 1613
Qy 133 ThrIleGluArgLysValAlaThrArgGlnThrGlyPheValLeuAsnGluProGlnVal 152
Db 1614 CCAGTTGAGAGAAAGTCAATGACA-----ACGATMAAATATTT 1652
Qy 153 TyrGlyArgAspLysGluLysAspGluIleValLysIleLeuIleAsnValSerAsn 172
Db 1653 GTAGGTTTGAAGAGACAAACTTAATCTTGAAGCTC-----ACCAAGTGA 1703
Qy 173 AlaGlnThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLysThrThrLeu 192
Db 1704 CCGCAGATTTAGATGATTCATTTGCATCAGCGTATGCGGTTGAGGTTAAACTACTTG 1763
Qy 193 AlaGlnMetValPheAsnAspGlnArgValIleGluHisPheHisProLysIleTrpIle 212
Db 1764 GCATCAAAAGTATCATATGAATGAAGTCACTTTCTAGACATTTTGAACCTTCGTCAGTGGTC 1823

```

[illegible]

QY	551	UAGTGTLeuAsnLeuSerGlyAsnThrSerIleArg-----	563
DB	2855	AAGCACTTTTAAAGGTGTGAACCTGTAACCTTTTAATCAATGGGAATGA	2914
QY	564	-SerLeuProAsnGlnLeuCysIleValAsnIleGlnThrLeuAspLeuHISglYCy	583
DB	2915	TTCTTTCTGAAATGAATTAATGAACTGTAATTCATTTGAGACTTAAGAAATTCGG-----	2969
QY	583	shISerLeuCysCysLeuProIlysgIuThrSerIyLeuGlySerLeuHrghAsnLeuLe	603
DB	2970	-ACACAAGTTAAATATGTGCTTTCTTTCTCAACCTGCGAATCTAGAAATCTGTT	3028
QY	603	uLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySerLeuThrCysIle	623
DB	3029	TGTGTCTAACAAAGATCAATCTTGAGACATATTACCGAAGATTTTGGATCTTGAAGATTG	3088
QY	623	uIySerThrLeuSerArgPheValValGlyIleGlnIlyLeuSerCysGlnLeuGlyIule	643
DB	3089	GGCAGTGTCTTC-----GTGGGT-----GCTTGTCTTTC-----	3119
QY	643	uArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHISLeuGlnIlyValIyAsnAs	663
DB	3120	-----TTTGA	3124
QY	663	pMetAspAlaIysgIuIaAsnLeuSerAlaIys-----GluAsnLeuHISe	679
DB	3125	TATGGATGCAATGATGATCAATATGATGATAGCAAGACACAAAGTTAGAGAACTTGAAGAT	3184
QY	679	rLeuSerMetIystrPheAspAspArgGluArgProArgIleTyrGlySerGlyIyValGI	699
DB	3185	ATTAGG-----GAATCTTGAAATTCCTATTGGAAGA	3217
QY	699	uValLeuGlnIaLeuIyProHISerAsnLeuThrCysLeuThrIleArgIlyPheAr	719
DB	3218	TACATGAATATTTCCAAAGGTTTCCAACTTTCAGTGGCTTCAG-----	3263
QY	719	gGlyIleArgLeuProArgTrpMetAsnHISerValLeuIyAsnValIalSerIleGI	739
DB	3264	-----TTTGAACCTCAGAGATCAGATGGAATATTCAACAGCAACACTTGG-----	3308
QY	739	uIleIleSerCysIyAsnCysSerCysLeuProProPheGlyIuleuProCysLeuIy	759
DB	3309	-----TTCCGAAATTGGATTGGCTTAAC	3331
QY	759	sSerLeuGlu--LeuTrpArgGly-----SerAlaGluValGluTyrValAspSerGI	776
DB	3332	TGAACCTAGAAACACTGTGTGATGGTTTAAAGTTCAACACAAACCACTGTGGCTTC	3399
QY	776	yPheProHrArgArg-----ArgPheProSerLeuArgIyIyLeuAsnIleAr	792
DB	3392	TGTTGTGACAAATCCGCCGTGGGATTTTCACATTCCTTCA-----	3431
QY	792	gGluPheGlyAsnLeuIyGlyIleuLeuIyIyGluGlyGluGluGlnCysProValLe	812
DB	3432	-----AATTGAAAGAACTGTG-----TT	3455
QY	812	uGluGluIleGluIleIyIyCysCysProMetPheValIleProThrLeuSerSerValIy	832
DB	3452	GTATGACTTTCCTGTGACATCCGATTCACATTAACAATGAGAACTGCCAACCTTGA	3511
QY	832	sIyIyLeu-----ValValSerGIyAspIySerAspAlaIleGlyPheSe	847
DB	3512	AAATTTGTCCCTTATGATACAAATCATCCAGGAGAAATGAACATGGCGAGAGAGA	3573
QY	847	rSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgIyPAsnIyGluAspAl	867
DB	3572	CACCTTTGAGAAATCTCAAAATTTTGAATCTGGCTACACTCTTTCCAAATGGGAGGT	3633
QY	867	AserLeuProGluGluMetPheIySerLeuAlaAsnLeuIyTyrIyLeuAsnIleSerPh	887
DB	3632	TGGA-----GAGGAATCTCTTCCCAATCTTGAAGAAATTAACATGACAGAAATGTGCT--	3683
QY	887	eTyrPheAsnLeuIyGluLeuProThrSerIleuAlaSerLeuAsnAlaLeuIyHISle	907

Db 3684 -----AACCTTGAGAGATTCCACCTAGTTTGAGATATTTATTCATTGAATTTAT 3736
Qy 907 uGUUleHisSerCySTYrAlaLeuGlu 916
Db 3737 CAAAATGTGTAAGAGTCTCTCAACTTGAA 3764

RESULT 11
US-09-360-186-2
Sequence 2, Application US/09360186
Patent No. 6262343
GENERAL INFORMATION:
APPLICANT: Staekawicz, et al.
TITLE OF INVENTION: Bsd Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
EARLIER FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3099
TYPE: DNA
ORGANISM: Capesicum annum
FEATURE:
NAME/KEY: CDS
LOCATION: (93)..(2810)
US-09-360-186-2

Alignment Scores:
Pred. No.: 3,97e-50 Length: 3099
Score: 553.50 Matches: 245
Percent Similarity: 38.93% Conservative: 170
Best Local Similarity: 22.98% Mismatches: 376
Query Match: 10.80% Indels: 275
Gaps: 40

US-10-647-268-2 (1-988) x US-09-360-186-2 (1-3099)

Qy 4 AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGluLeuGlyLeu 23
Db 111 GCTTCTTATGAGAACATAGAAATCTCTTGACATTCATTCGCCGATGCAATCTCTA 170
Qy 24 IleLeuGlyPheIlyAspGluPheGluIlyLeuGlnSerThrPheThrThIleGlnAla 43
Db 171 TCCTGTGATCACAGAGAACTTTGCGCTCTTGAAAAAGTTAGTCCCTGGAACTA 230
Qy 44 ValLeuGluAspAlaGlnIlyLeuS-----GlnLeuIlyAspIlyAlaIleGlu 59
Db 231 TTGTGCAAGAACTTTGAGAAAAACAATGTTTTGGGAAATGACGGAATTTGAAGTAG 290
Qy 60 AsnTrpLeuGlnIlyLeuAsnAlaAlaIlyTyrGlu-----AlaAspAsp 74
Db 291 ---GTAAGAGAAAGTTGCAAGTGTCTGATATACAAATTCACAGACTAAGAGAACT 347
Qy 75 IleLeuAspGluCysIlyThrGlnAlaProIleAspGlnIlyIlyAsnIlyTyrGlyCys 94
Db 348 GTACTGGGAGAAATTAAGC-----CAGAAAAAAAAGCG----- 383
Qy 95 TyrHisProAsnValIleThrPheArgHisIlySerIleGlyIlyAspMetIlySerIleMet 114
Db 384 -----CGTCGAAGCTTTCGTCGAAGCTTCGAACCTGCAACAGATACCA 419
Qy 115 GluIlyIleAspValIleAlaAlaGlnArgIleIlyPheHisIleuAspGluArgThrIle 134
Db 420 GAGGACATGATCATATCTGGAAGAGTCGACAAAGATCCAAAGATTAAGAAAAACAAGTA 479
Qy 135 GluArgGlnValAlaIleThrArgGlnThrGlyPheValIleAsnGlu----- 149
Db 480 TCAAGGAGATCATGTTTCATGATTTTCAAGTTCAACAAAGATATTTTGAAGTTAAG 539
Qy 150 ProGlnValTyrGlyArgAspIlyGluIlyAspGlnIleValIleIleuIleAsn 169

Db 540 AACAAATGTGTGACGATGATCAAGAAAGAGTTGTAGAGATCTAGTAGAAGC 599
Qy 170 ValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyIlyLeuGlyIly 189
Db 600 TACTCTGGGAGACC-----AAAGTCATCCCGATGTGCGAGATGGGAGATAGGTAA 653
Qy 190 ThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProIly 209
Db 654 ACAACCTTAGCAAAAAGAGTTTACATATGATCAATTCATTCATGCCGTTTGATTTGAT 713
Qy 210 IleTrpIleCysValSerGluAspPheAsnGluIlyAspArgIleIlySerGlnIleValGlu 229
Db 714 GCTGGGCTCAATATCTCAACACACACAAAGAAATTTGCTGGGCTTCTGCAT 773
Qy 230 SerIle-----GlnGlnIlySerIleuGlyIlyMetAspLeuAlaPro--- 243
Db 774 TCCCAATCAAAATGATGACAGGGTTAAGATGTGTGAAGCAGAGCTTAGCAGACATG 833
Qy 244 LeuGlnIlyIlyLeuArgAspLeuLeuAsnGlyIlyIlySerIlyLeuValIleuAspAsp 263
Db 834 TTACGAAAAAGTTTAAAG-----AGAAAGAGTACTTATTTGCTTGGATGAT 881
Qy 264 ValTrpAsnGluAspGlnAspIlyTrpAlaIlyLeuArgGlnValIleuIlyVal---Gly 282
Db 882 ATCTGAGAT-----TGTGAAGTGTGGATGGCGTGAGACGATGCTTCCAACTGAAGAC 935
Qy 283 AlaSerGlyAlaSerValIleuThrThrThrArgLeuGlnIlyIlySerIleMetGly 302
Db 936 AATCGAGGAGTCCAAATCTGTGATCCGCTAATGATGAAGATCTTGTATGCTGCT 995
Qy 303 ThrLeuGln---ProTyrGluLeuSerAsnLeuSerGlnGluIlyAspCysTrpLeuPhe 321
Db 996 GTAGAGATTTTCTTTCGGATGATGCTTCATGATCAAGATGACAGTGTGATTTTC 1055
Qy 322 MetGlnArgAlaPheGlyHisGlnGlnIlyLeuAsnLeuValAlaIleGlyIly 341
Db 1056 AAAAGTCAGCATTTTCA---AGTGAAGCATTACCATATGATGATTCGAGACTTTGGAAG 1112
Qy 342 GluIleValIlyIlyCysGlyIlyValProLeuAlaAlaIlySerThrLeuGlyIlyLeu 361
Db 1113 CAAATCGCAATGATGATGACAGGGGTTCACCTAATTCATTCGTTGACAGGGCTTCTC 1172
Qy 362 ArgPheIlyAspGlnGluArgIleTrpGlnHisValArg-----AspSerGluIle 378
Db 1173 AAATCTAAAGACAAATGAAAGATTCGAAAATGTTGCTTAAGATGTCAAATCTCTC 1232
Qy 379 TrpIlyIleuProGlnGlnIlySerSerIleLeuProAlaLeuArgIlySerThrHis 398
Db 1233 ACAATGATCTGTGAAACGATGTTCA-----CGTGTCTTGGGTTGAGTTACGATCAC 1286
Qy 399 LeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProIlyAspThrGlu 418
Db 1287 TTGCAAGCGGATCTTAATAACATGCTTCCTGATTTCCGAAATTTTCCGAAAGACAGTAT 1346
Qy 419 MetGlnIlySerIleLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerIlyGly 438
Db 1347 ATTCAGTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
Qy 439 AsnLeuGlnLeuGlnAsnValGlyAsnGlnValTrpAsnGlnLeuTyrLeuArgSerPhe 458
Db 1407 GATTGGAGAGAGG-----GTTGAGAGAGTCT 1433
Qy 459 PheGlnGluIle----- 462
Db 1434 TTGCAAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
Qy 463 GluValIlySerGlyGlnThrTyrPheIlyMetHisAspLeuIleHisAspLeuAlaThr 482
Db 1494 AAAATTTAGATCA-----TGTAAAGTTTCAATATATATATAGACTGTGC--- 1538
Qy 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlnIleIleValGluAsnTyr 502

[illegible]

QY	769	GlhValaGlutryValAspSerGlyPheProThrArgArgPheProSerLeuArgLys	788
Db	2565	-----ACAAATGACAAATTTCTGTCCTTGAGCCG	2594
QY	789	LeuAsn1LeArgGluPheGlyAsnLeuLysGlyLeuLeuLysGluGluGlu	808
Db	2595	CTCATGATTGGAAGCTGCCAAAATTTCAAA-----GAG	2627
QY	809	CysProVal-----LeuGluGluLeuLeuLysCysCysPro	821
Db	2628	ATACCCCTTCAGTTTGACATATACACACACTACAGCTGATGATTGAAGAGAGTCTCT	2667
QY	822	MetPheVal1LeProThrLeuSerSerValLysLysLeuVal1SerGlyAspLysSer	841
Db	2688	CCCAAACTTGGGGAATTCGTGCACGAATTCAGAAA-----GAACAA	2729
QY	842	AspAla1LeGlyPheSer-----Ser1LeSerAsnLeuMetAlaLeuThrSer	857
Db	2730	GAAGACCTCGGAACCAACCTCTGATGATGTTCTGATTCCAATCCATTGGAAGAGAGATGAT	2789
QY	858	LeuGln1LeArgTryrAsnLysGluAspAlaSerLeuProGluGluMet-----	873
Db	2790	TCTGATTCAAGAAACAATTAGAAAGATCTCAAGGCCAAGAGCATTGAATCTTGGAT	2849
QY	874	-----PheLysSerLeuAlaAsn	879
Db	2850	TTGATTTTGGCCCTCTATACAAATAATACCAATAATTATGCGTTTCAAGCAATGTGTGAC	2909
QY	880	LeuLysTryrLeuAsn1LeSerPhe-----TyrPheAsnLeuLysGluLeuPro	895
Db	2910	TTTCCAAGAGATGTGAATATCTTTGTGTGTGTACATATTTTGTGAGTTGTACTGATTCCT	2969
QY	896	ThrSerLeuAlaSerLeu	901
Db	2970	TCTTCCTTCTCTTTTA	2987
RESULT 12			
US-09-864-680A-2			
Sequence 2, Application US/09864680A			
Patent No. 6762285			
GENERAL INFORMATION:			
APPLICANT: Staakawicz, Brian J			
APPLICANT: Dahlbeck, Douglas			
APPLICANT: Tai, Thomas H			
TITLE OF INVENTION: B62 RESISTANCE GENE			
FILE REFERENCE: 42250/234021 (5830-4A)			
CURRENT APPLICATION NUMBER: US/09/864,680A			
CURRENT FILING DATE: 2001-05-24			
PRIOR APPLICATION NUMBER: US 09/360,186			
PRIOR FILING DATE: 1999-07-23			
PRIOR APPLICATION NUMBER: US 60/093,957			
PRIOR FILING DATE: 1998-07-23			
NUMBER OF SEQ ID NOS: 14			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 2			
LENGTH: 3099			
TYPE: DNA			
ORGANISM: Capsicum annuum			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (93)..(2810)			
OTHER INFORMATION:			
US-09-864-680A-2			
Alignment Scores:			
Pred. No.: 3.97e-50 Length: 3099			
Score: 553.50 Matches: 245			
Percent Similarity: 38.93% Conservative: 170			
Best Local Similarity: 22.98% Mismatches: 376			
Query Match: 10.80% Indels: 275			
DB: 4 Gaps: 40			

US-10-647-268-2 (1-988) x US-09-864-680A-2 (1-3099)
QY 4 AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyIleuLeu 23
Db 111 GCTTCTCTTAAGAGACATAGAAATCTCTTTCATTCATTCATTCGCGCATGCAATCTCTA 170
QY 24 IleuGlnPheLeuAspGlnPheGlnIleuLeuGlnSerThrPheThrIleGlnA 43
Db 171 TCCTGTGATCACAGAGAAACTTTCGCTCTTCGTGAAAAAGTAGTCCCTGGAGATA 230
QY 44 ValLeuGlnAspAlaGlnIleuLeuS-----GlnLeuLeuAspAlaIleu 59
Db 231 TTGTGCAAGAACTTTGCAAAAAACAATGTTTGGGAAATGACCGAATTTTGAATTAAG 290
QY 60 AsnTrpLeuGlnIleuAsnAlaIleuValLeuGln-----AlaAsp 74
Db 291 ---GTAGAGAAAGTTGCAAGTCTCTGAAATACAAATTCAACTGAGACTAACGAACT 347
QY 75 IleuLeuAspGlnCysLeuThrGlnIleuAspIleuArgGlnIleuLeuAsnLeuTyrlCys 94
Db 348 GTACTGGGAGAAAATTAAGC-----CAGAAAAAAAGGCG----- 383
QY 95 TyrIleAspAsnValIleThrPheArgIleuValIleGlyLeuAspMetCysIleuMet 114
Db 384 -----CGTCAAGGTTTCGTCAAAAGCTTCAACAGCTCAACAGTACCA 419
QY 115 GluIleuLeuAspValIleAlaIleuGlnArgIleuLeuPheIleuAspGlnArgThrIle 134
Db 420 GAGGACATGAGATCATATGTCGAAAGATGCAAAAGATTCAAAGATTAAGAAACAGATA 479
QY 135 GluArgIleuValAlaThrArgGlnThrGlyPheValLeuAsnGlu----- 149
Db 480 TCAAGAGAAATCATGTTGATGATTTTCAAGTTCAACAAACAAATTTTGAAGTTAG 539
QY 150 ProGlnValTyrlGlyArgAspLeuGlyLeuAspIleuValIleuValIleuAsn 169
Db 540 AACATATAGCTTGGACGTGATGATCAAAAGAAACAGTTTGAAGATGATGATGATGAGC 599
QY 170 ValSerAsnAlaGlnThrLeuProValLeuProIleuGlnIleuMetGlyIleuGlyLeu 189
Db 600 TACTCTGGGAAACC-----AAAGTCAATCCCGATGTCGGATGAGGATGAGTAA 653
QY 190 ThrIleuAlaGlnMetValPheAsnAspGlnArgValIleGlnIleuPheIleuProLeu 209
Db 654 ACAACCTTAGCAAAAGAGTTTACATGATGATGATGATGATGATGATGATGATGATGAT 713
QY 210 IleTrpIleCysValSerGlnAspPheAsnGlnIleuValGlnIleuValGln 229
Db 714 GCCTGGGCTACCATATCTCAACAGCACAAAAGAAATTTGCTGGGCTTCGAT 773
QY 230 SerIle-----GlnIleuLeuSerIleuGlyGlyMetAspLeuAlaPro--- 243
Db 774 TCCCAATCAAAATGATGATGACAGGGTTAAAGATGATGATGATGATGATGATGATGATG 833
QY 244 LeuGlnIleuValLeuArgAspLeuLeuAsnGlyLeuValTyrlLeuValIleuAsp 263
Db 834 TTACAGAAAATTTAAAG-----AGAAAAGCTTAAATGCTTTCGATGAT 881
QY 264 ValTrpAsnGlnAspGlnAspLeuTyrlAlaIleuValGlnValIleuValIleu 282
Db 882 ATCTGAGAT-----TGTGAAGTGGGATGCGGTGAGACGATGCTTCCAACTGAAGAC 935
QY 283 AlaSerGlyAlaSerValLeuThrThrArgLeuGlnIleuValGlySerIleuMetGly 302
Db 936 AATCAGAGAGATCAATATCTGTGATCTACCCGTAATGATGAAAGTCTTGTATGCTGCT 995
QY 303 ThrLeuGln---ProTyrlLeuSerAsnLeuSerGlnIleuAspCysTrpLeuLeuPhe 321
Db 996 GTAGAGATTTTCTTTCGCGATGATGCTTCAATGATGATGATGATGATGATGATGATG 1055
QY 322 MetGlnArgAlaPheGlyIleGlnGlnIleuLeuAsnLeuValAlaIleGlyLeu 341
Db 1056 AAAAGTCAGCATTTTCA---AGTGAAGCATTTACCATATGATGATGATGATGATGATG 1112

QY 342 GluIleuValIleuLeuCysGlyGlyValProLeuAlaIleuValThrLeuGlyIleu 361
Db 1113 CAATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1172
QY 362 ArgPheLeuValGlnGlnIleuValGlnIleuValArg-----AspSerGlnIle 378
Db 1173 AAATCTAAAGAGCAATAGAAATGGAACCTGCTGTAAGATGTCACATTCCTC 1232
QY 379 TrpIleuLeuProGlnGlnIleuSerSerIleuProAlaLeuArgLeuSerThrIle 398
Db 1233 ACAATGATCTGATGAGACATGTTCA-----CGTGTCTGGGATGATGATGATGATG 1286
QY 399 LeuProLeuAspLeuArgGlnCysPheThrTyrlCysAlaValPheProLeuAspThrGln 418
Db 1287 TTGACAAACGATCTTAAACATGCTCTTCGATTTTCGAAATTTTCCAGAAACATGAT 1346
QY 419 MetGlnIleuValLeuLeuIleSerLeuTrpMetAlaIleuGlyPheIleuSerIleu 438
Db 1347 ATTCACAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
QY 439 AsnLeuGlnIleuGlnAsnValGlyAsnGlnValTrpAsnGlnIleuTyrlLeuArgSerPhe 458
Db 1407 GATTGGAAGGAG-----GTTGAGAAAGTGT 1433
QY 459 PheGlnGlnIle----- 462
Db 1434 TTGCAGAGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1493
QY 463 GluValIleuSerGlyGlnThrTyrlPheLeuMetIleAspLeuIleIleAspLeuAlaThr 482
Db 1494 AAAATTTGATCA-----TGTAGGTCATGATCTTAATATATGACCTGTC--- 1538
QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlnIleIleValGlnAsnTyrl 502
Db 1539 -----GTGAGAGAAAGTTCAAAAGGAGAAACATT 1565
QY 503 IleIleuMetSerIleGlyPhe----- 510
Db 1566 TTTATCATGAACGACATTTGTTCTTGACGTATCATATCCAGATGTCATATCTCTATG 1625
QY 510 ----- 510
Db 1626 TATAAATGACGCCCTTAAGCGCGTACGTGATGAATTAATTAATTAATTAATTAATTA 1685
QY 510 ----- 510
Db 1686 CTTTATAGGCTCTTCTTAACCCCTGTAATCGTACGTGAGATCATGACAAACAAAT 1745
QY 511 -----ThrIleValIleSerSerIleu----- 519
Db 1746 CTTTGAAGACAAACCATCTGTTTCTCTTTTATCTTGAAGCTTTTATATTAATTAATTA 1805
QY 520 ---SerIleuGlnIleuPheValSerLeuArgValIleuAsnLeuSerAspIleuLeu 538
Db 1806 AAATCAGAGGTTGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1865
QY 539 LeuGlnLeuProSerSerIleGlyAspLeuValIleuValGlyIleuAsnLeu----- 556
Db 1866 GATGTTTCCCTCAGAGATACATAAGCTCATGCTGTTGAGTACATATCTTTCAGC 1925
QY 557 SerGlnIleuThrSerIleuArgSerLeuProAsnGlnIleuCysIleuGlnIleuGln 576
Db 1926 TATGGAAATTTCCATGTA-----CTTCAGAAATTTGACAGTTATGAAATCTGCAG 1976
QY 577 ThrLeuAspLeuIleuGlyCysIleuSer---LeuCysCysLeuProTyrlGlnThrSerIle 595
Db 1977 ACATTCATTTGTTCAAGCGTTTCATGATGATGATGATGATGATGATGATGATGATGATG 2036
QY 596 LeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysIleuTyrlGlyLeuThrCysMetProPro 615
Db 2037 CTATGCAATTAAGCATCTTAACCTGCAAGATTTTATTTGTCAGATGTCGCCAAAGTGA 2096

```

QY 616 Arg116Iegly-----Ser1euthrCysleuylsThrLeuSer----- 627
Db 2097 TCTGTGTGACAAAGAGAGGAGCTTGATTTTCAAACTTACAACTTATTTCTTACTGTCT 2156
QY 628 -----ArgPheVal1Gly11IeglnlySylsSerCys6IleuGly 641
Db 2157 CCAGGTTGTGCACAGAGAGAGGATTATTATGGGAGATTGAGAAATGCAAA--AAATTAGCA 2213
QY 642 GluLeuArgAnleuAnleuThyGlySer11IeglnleThrH1sleuGluArgValys 661
Db 2214 ATCAGTGAATAAGATGAGTACTATAAAAGTTTCGGAGCTTGAGCTTCCCAAC----- 2267
QY 662 AsnAspMetAspAla1Ala1sleuSerAla1sleuSerAla1sleuSer1euser 681
Db 2268 -----AsnCTTGTCTATCTGCAGCAACTTGAATAATATGAGT 2303
QY 682 Met---LysTrpAspAspAspGluArgProArg11eThyrgIuSerGlu1sVal1GluVal 700
Db 2304 CTTATATCTGTGATTATAGCTTTTGGCCAGTATCATTCAGTGAAGTCAAAAGCTTTTCCA 2363
QY 701 LeuGlu1Ala1eulysProH1sSerAnleuThrCysleuThr11eArgGlyPheArgGly 720
Db 2364 GCACGCTCAAGAGTTGAAGTTGAGAAAGAACTTATCTTACAGC----- 2405
QY 721 IleArgLeuProAspTrpMetAsnH1sSerVal1eulysAsnVal1Ser11eGlu1le 740
Db 2406 -----TGGTCACTACTTGACATCATAGCTGAGTTCCTACCTTGAGGTG 2450
QY 741 IleSerCys1sAsnCySerCys-----LeuProProPhe 752
Db 2451 CTGAAGCTGATGATGAGAGCTGTGTGTGAGAAAGATGCATCCAAATTTGATAGGATTT 2510
QY 753 Gly1GluLeuProCysLeu-----LysSer1eGluLeuThrArgGly1Ser1a 768
Db 2511 AATCATTTGAAGCTTTGTCTATTAATATAGTCTTTCAAGTTCTGGAAGCC----- 2564
QY 769 GluVal1Glu1sVal1AspSerGlyPheProThrArgArgPheProSer1eulys 788
Db 2565 -----ACAATGACAAATTTCCGTCTCTTGAAGGC 2594
QY 789 LeuAnleu1eArgGluPheGlyAsnleu1sGlyLeu1eulysGly1Glu1Glu1n 808
Db 2595 CTCATGATTTAGAAAGTTGCAAAATTTGAAA-----GAG 2627
QY 809 CysProVal-----LeuGlu1Glu1Iegln1eulysCysCysPro 821
Db 2628 ATACCATTTGAGTTGTCAGATATACACACACTACAGCTGATTGAGTAAAGAGTGTCT 2687
QY 822 MetPheVal11eProThrLeuSerSerVal1sleuVal1ValSerGly1sAsp1sSer 841
Db 2688 CCCAAACTTGGGAGATCTGCTGCACGAATTCAGAAA-----GACAA 2729
QY 842 AspAla11eGlyPheSer-----Ser11eSerAsnleuMetAla1eulysSer 857
Db 2730 GAAAGACTGGAACAAACCTGTGATGTTGCTATCTCAATCCATTTGAAGAGAGTGTAT 2789
QY 858 LeuGln11eArgTrpAsn1sleuGluAspAla1Ser1eulysProGlu1Glu1Met 873
Db 2790 TCTGATTCAGAGAAACATTAGAAAGATCTCAAGGCCGAGAGAGATGAAGCTTTGGGAT 2849
QY 874 -----Phe1sSer1eulysAsn 879
Db 2850 TTGATTTTGGCCCTCTATACAAATATCACTAAATATATCGGTTTCAACAAATGTGTAC 2909
QY 880 Leu1sTrp1sLeuAsn11eSerPhe-----TyrPheAsnleu1sGlu1eulysPro 895
Db 2910 TTCCAAGAGATGTGATATCTTTTGTGTGTAAACATATTTTGAAGTTGTATGATTCCT 2969
QY 896 ThrSer1eulys1eulys 901
Db 2970 TCTTCTCTCTCTCTTTTAA 2987

```

```

US-09-360-186-4
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Stakavicz, et al.
; TITLE OF INVENTION: B62 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capesicum annum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2718)
US-09-360-186-4

Alignment Scores:
Pred. No.: 6.77e-50 Length: 2718
Score: 550.50 Matches: 226
Percent Similarity: 39.27% Conservative: 151
Best Local Similarity: 23.54% Mismatches: 340
Query Match: 10.74% Indels: 243
Gaps: 36

US-10-647-268-2 (1-988) x US-09-360-186-4 (1-2718)
QY 4 AlaPheLeuGluVal1eulysAsnleuThrCysPhe11eGln1sGly1Glu1eulys 23
Db 19 GCTTCTCTTATGAGAAACATATGATCTCTCTTGCATTCATATCCGATGCAATCTCTA 78
QY 24 11eulysGlyPhe1sAspGluPheGlu1sleuGln1eSerThrPheThr11eGln1a 43
Db 79 TCTGTGTATCAGAGAGAACTTTGGCTCTGTGTGAAAAAGTTAGTTCCTGGAAGTA 138
QY 44 Val1eulysAsp1sAla11eGlu1 59
Db 139 TTGTGCAAGAACTTTGAGAAACAAATGTTTGGGGAATGACGATTTTGAAGTAGAG 198
QY 60 AsnTrpLeuGln1sleuAsn1a1a1a1eThyGlu 74
Db 199 ---GTAAGAGAAAGTTGCAAGGTCTGTGAATATACAAATTCAGTGAAGTAAAGAGT 255
QY 75 11eulysAspGluCys1sThrGlu1a1a1eArgGln1sleuAsn1sThyGlyCys 94
Db 256 GTACTGGGAGAAATTAAGC-----CAGAAAAAAGGCG----- 291
QY 95 TyrH1sProAnVal11eThrPheArgH1s1sleu1sleu1sleu1sleu1sleu1sleu1 114
Db 292 -----CGTGAAGTTTGTCTCAAGCGTTCACAAAGTATTAAG 327
QY 115 Glu1sleuAspVal11eAla1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 134
Db 328 GAGACATGATCATATATGTGAAAGAGTGCACAAAGATCAAGATTAAGAAAAACAAGTA 387
QY 135 GluArg1nVal1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 149
Db 388 TCAAGAGATCATTTGTTATGATTTTCAAGTTTCAACAAAGATTTTGAAGTTAAG 447
QY 150 ProGln1sTrp1sArgAsp1sleu1sAsp1sleu1sleu1sleu1sleu1sleu1sleu1 169
Db 448 AACAAATATGTTGAGCGTATGATCAAGAAACAGTTGTTAAGAAAGATCTGATGAAGC 507
QY 170 Val1sSerAsn1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 189
Db 508 TACTCTGGGGAAGC-----AAAGTATCCGATTTGTGGGATGGAGGATAGTAA 561
QY 190 ThrThr1eulys1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 209

```

```

Db 562 ACAACCTTAGCAAAAGAGATTACATGATGATCAATTCATGCGCTTTGATGATTCAT 621
Qy 210 ILeTrrpIeCyvIsSerGluAspPheAangIuIySArGluIleIySgluIleValu 229
Db 622 GCGTGGCTACCATTCATCTCAACAGACAACAAAAGAAATTTGCTGGCGCTTCGAT 681
Qy 230 SerIle-----GluGluIySerLeuGlyGlyMetAspLeuAlaPro--- 243
Db 682 TCCCAATCAAAATGATGATGACAGCGTTAAAGATGATGCTGAAGCAGACTGACAGACTG 741
Qy 244 LeuGluIySlySLeuAxApLeuLeuAangIyIySlySlyrLeuLeuValLeuAspAsp 263
Db 742 TTACAGAAAAGTTTAAAG-----AGAAAAGAGTACTTAATGCTTGGATGAT 789
Qy 264 ValTrrpAangIuAspGluAspIyTrrpAlaIySleuAangIuValLeuIyVal---Gly 282
Db 790 ATCTGGAGT-----TGTAAGTGTGGAGTGGCGCTGACAGATGCTTCAACTGAAGAC 843
Qy 283 AlaSerGlyAlaSerValLeuThrThrArGleuGluIyValGlySerIleMetGly 302
Db 844 AATCGAGGAGTCCGAATCTGTGATCCCGCTAATGATGAAGTACGTTGATTCGTGT 903
Qy 303 ThrLeuGln---ProTyrGluLeuSerAenLeuSerGluIyAspCysTrrpLeuLeuPhe 321
Db 904 GTAGAGAAATTTTCTTTCGCGATGAGCTTCATGATCAAGATGAGATGGAGTCTTTTC 963
Qy 322 MetGluAargAlaPheGlyIleGluGluIuIleAenLeuAenValAlaIleGlyIyS 341
Db 964 AAAAGTCAGAGATTTTCA--AGTGAAGCATTTACCATATGATGATTCGAGACTGTGGAAG 1020
Qy 342 GluIleValIySlySLeuGlyIyValProleuAlaIySlyrLeuGlyIyIleLeu 361
Db 1021 CAATTCGAGATGATGATGACGGGTTCACCTAATGATTCGCGTTCGAGCGCTTTC 1080
Qy 362 ArgPheIySArGluIyAargIuIyTrrpIuIleValAarg-----AspSerGluIle 378
Db 1081 AAATCTAAAAGCAATGAGATTTGAAACTGTGCTAAAGATGTCAGATTCATTCGTC 1140
Qy 379 TrrpIySLeuProGluIyGluIySerSerIleLeuProAlaLeuAargLeuSerTyrHis 398
Db 1141 ACAAAATGATCTGTGAACAGATGTTCA-----CGTGTGCTGGGTGATGATGATCAC 1194
Qy 399 LeuProleuAspLeuAargGluIyCysPheThrTyrCysAlaValPheProIyAspTrrpIu 418
Db 1195 TTGCAAGCCATCTAAAACATGCTTCTGCAATTTCCGAATTTTCCAGAAAGACGTGAT 1254
Qy 419 MetGluIySgluAenLeuIleSerLeuTrrpMetAlaHisGlyPheIleLeuSerIySgl 438
Db 1255 ATTCAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
Qy 439 AenLeuGluIyGluAenValGlyAenGluValTrrpAangIuLeuTyrLeuAysSerPhe 458
Db 1315 GATTTGAGAGAGAG-----GTTGAGAGAGTGT 1341
Qy 459 PheGluGluIle----- 462
Db 1342 TTGCAAGAGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401
Qy 463 GluValIySserGlyGluIyThrTrrpPheIySmetHisAspLeuIleHisAspLeuAlaThr 482
Db 1402 AAAATTTGATCA-----TGTAAGTTCATGATCTTAATATGATGATCTGTGC--- 1446
Qy 483 SerLeuPheSerAlaSerThrSerSerSerAenIleArgGluIleIleValGluAenTyr 502
Db 1447 -----GTGAGAGAAAGTTCAAAAGGAGAAACATT 1473
Qy 503 IleHisMetSerIleGlyPhe----- 510
Db 1474 TTTATCATGAACGACATTTGCTTTCGACGTATCATATCCAGATGTTCAATATCTGTATG 1533
Qy 510 ----- 510

```

```

Db 1534 TATAAAATGCAGCCCTTTAAGCGGTGACGTGGTGAATTAATTAATTTGCTCCATAGT 1593
Qy 510 ----- 510
Db 1594 CTTTATAGGGCTCTTTTACCCCTGTAAATGTCAGTTGAGAGATCATGACAAACAAT 1653
Qy 511 -----ThrIySValIySerSerTyrSerLeu----- 519
Db 1654 CTTTGAAGACACCATTCGTTTCTTTCCTTTCATCTTGAGCCCTTAATATATGTTCTC 1713
Qy 520 ---SerHisLeuGluIySLeuValSerLeuAargValLeuAenLeuSerAspIleIySleu 538
Db 1714 AAATCAGAGGTTGTTCAATTTCAATTTCAATTTCAATTTGAGTGGAGACAGACAGATT 1773
Qy 539 IySgluIyProSerSerIleGlyAspLeuValHisLeuAargTyrLeuAenLeu----- 556
Db 1774 GATGTTTCCCTCGAGAGATCTAGGCTCATCGTGGAGGATCTTATCATCTTTCAGC 1833
Qy 557 SerGlyAenThrSerIleArgSerLeuProAangIuLeuCySlySLeuGluAenLeuGln 576
Db 1834 TATGGAAATTTGCATGTA-----CTCCAGAAAATTTGCAGATTATGGAATCTGCAG 1884
Qy 577 ThrLeuAspLeuHisGlyCyHisSer---LeuCySlyLeuProIySgluIyThrSerIyS 595
Db 1885 ACATTCATTTGTTCAACGGTTTCGATCAGATTAATTAATTTTGGCTGAGAAATTTGGGA 1944
Qy 596 LeuGlySerLeuAargAenLeuLeuAspIyCySlyrGlyLeuThrCysMetProPro 615
Db 1945 CTAAATGCAATTTAAGCATCTTAAACCTGCCAGATTTTATTTGGCCAGATTCGCCAAGTGA 2004
Qy 616 ArgIleGly-----SerLeuThrCysLeuSlyrThrLeuSer----- 627
Db 2005 TCTGTGACAAAGAGAGGACTGATTTTCAAACTTACAAACTATTTCTTACTGTCT 2064
Qy 628 -----ArgPheValIyGlyIleGluIySlySLeuGlyIySgluIyS 641
Db 2065 CCAGCTTTGTCAGAAAGAGGAGTATGATGAGGATGAGGATGAGATGTCMAA---AAATTTGA 2121
Qy 642 GluLeuAargAenLeuAenLeuTyrGlySerIleGluIleThrHisLeuGluAargValIyS 661
Db 2122 ATCAGTGAATTAAGATGATCTAATAAGTTTTCGAGCTCTGGGCTCCCAAC----- 2175
Qy 662 AsnAspMetAspAlaIySgluAlaAenLeuSerAlaIySgluAenLeuHisSerLeuSer 681
Db 2176 -----AATCTGTCTATCTGACGAACTTGAATATGAGT 2211
Qy 682 Met---LysTrrpAspAspAspGluAargProAargIleTyrGluSerGluIyValGluVal 700
Db 2212 CTTTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271
Qy 701 LeuGluAlaLeuIySProHisSerAenLeuThrCysIleThrIleAargGlyPheAargGly 720
Db 2272 GCAAGCTCAAGAAAGTTGAAGTTGAAAGAACTTATCTTAAGC----- 2313
Qy 721 IleArgLeuProAspTrrpMetAenHisSerValLeuIySValIleSerIleGluIle 740
Db 2314 -----TGTCTATCTTGGACATCATCTACTAGTTGCTTAACCTTGAAGTG 2358
Qy 741 IleSerCysIySAsnCySserCys-----LeuProProPhe 752
Db 2359 CTGAAGCTGATGATGACGCTGTTGTGTAAGATGACATCCAAATTTGATGGGATTT 2418
Qy 753 GlyIyLeuIyProCysLeu-----LysSerLeuGluIyLeuTrrpAargGlySerAla 768
Db 2419 AATCGATTTGAAGCTTTGCTTAATTAATTAATTAATTTTCAAGTTCTGAAAGCC----- 2472
Qy 769 GluValGluIyValaSerSerGlyPheProThrAargAargPheProSerLeuAargIyS 788
Db 2473 -----ACAAATGACAAATTTCTGTCTGACGCC 2502
Qy 789 LeuAenIleAargIyPheGlyAenLeuIySgluIyLeuLeuIySgluIyGluGluGln 808
Db 2503 CTCATGATTAAGATGTCAAAATTTGAAA-----GAG 2535

```

QY 809 CysProVal-----LeuGluIuIleGluIleLysCysCysPro 821
Db 2536 ATACCATTAGATTTCAGATATACACACTACGCTGATTGATTAAAGAGTTCCT 2595
RESULT 14
US-09-864-680A-4
Sequence 4, Application US/09864680A
Patent No. 6762285
GENERAL INFORMATION:
APPLICANT: Staekawicz, Brian J
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: B2 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/360,186
PRIOR FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent version 3.1
SEQ ID NO 4
LENGTH: 2718
TYPE: DNA
ORGANISM: Capsicum annuum
US-09-864-680A-4
Alignment Scores:
Pred. No.: 6,77e-50 Length: 2718
Score: 550.50 Matches: 226
Percent Similarity: 39.27% Conservative: 151
Best Local Similarity: 23.54% Mismatches: 340
Query Match: 10.74% Indels: 243
Gaps: 36
US-10-647-268-2 (1-988) x US-09-864-680A-4 (1-2718)
QY 4 AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyLeuGlyLeu 23
Db 19 GCTTCTCTTATGAGAACATGATCTCTTGCATTCATTCGCCGATGCATCTCTA 78
QY 24 IleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThrIleGlnAla 43
Db 79 TCCTGTGATCACAAGAGAACCTTGGCGCTTTCGGAAGAAAGTTAGTTCCTGGAAGA 138
QY 44 ValLeuGluAspAlaGlnLysLys-----GlnLeuLysAspLysAlaIleGlu 59
Db 139 TTGTTCAGAGAACCTTGGAGAAAACAATGTTTTGGGAAATGACGGATTTGAGATAGAG 198
QY 60 AsnTrpLeuGlnLysLeuAsnAlaAlaIleLysGlu-----AlaAspAsp 74
Db 199 ---GTAAAGAAAGTTGCAAGTCTGCTGTAATCACAAATTCAACTGAGACTAAACAGAACT 255
QY 75 IleLeuAspGluCysLeuThrGlnAlaProIleArgGlnLysLysAsnLysTrpGlyCys 94
Db 256 GTACTGGGAGAAATTAAGC-----CAGAAAATAAGCG----- 291
QY 95 TyrHisProAsnValIleThrPheArgHisLysIleGlyLysArgMetLysLysIleMet 114
Db 292 -----CGTCGAGAGTTTCGTCAAAGCTTCGCAACAGCTGCAACAGATAGCA 327
QY 115 GluLysLeuAspValIleAlaIleGluArgIleLysPheHisLeuAspGluArgThrIle 134
Db 328 GAGGAGCATGATCATATCTGGAAGAGTGCACAAAATCCAAAGATTAAGAAAACAAGTA 387
QY 135 GluArgGlnValAlaThrArgGlnThrGlyPheValLeuAsnGlu----- 149
Db 388 TCAAAGGAATCATGTTGATGATTTTTCAGAGTTCAACAAACATATTTTGAAGTTAG 447
QY 150 ProGlnValTyrGlyArgAspLysGluLysAspGlnIleValLysIleLeuIleAsnAsn 169

Db 448 ACAATATGTTGACGTGATGATCAAGAGAAACAGTTGTTAGAGATCTGACTAGAAC 507
QY 170 ValSerAsnAlaGlnThrLeuProValIleLeuGlyMetGlyLysLeuGlyLys 189
Db 508 TACTCTGGGAGAACCC-----AAAGTCATCCCATATGTCGGGATGGGAGCATAGGTAA 561
QY 190 ThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProLys 209
Db 562 ACAACCTTACCAAAAGAAAGTTTACATGATGATCAATCTTACCCGCTTTGATGTTTCAT 621
QY 210 IleTrpIleCysValSerGluAspPheAsnGlnLysArgLeuIleLysGluIleValGlu 229
Db 622 GCCTGGCTACATATCTCAACAGCACACAAAGAAATTTTGCTGGCGCTTTCAT 681
QY 230 SerIle-----GluGlnLysSerLeuGlyLysMetAspLeuAlaPro--- 243
Db 682 TCACCAATCAAAATGATGACAGGCTTAAGATGATGTAAGACAGAGCTAGACAGCATG 741
QY 244 LeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTrpLeuLeuValLeuAspAsp 263
Db 742 TTACAGAAAAGTTTAAAG-----AGAAAGAGTACTTAATATGCTTGGATGAT 789
QY 264 ValTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysVal---Gly 282
Db 790 ATCTGAGT-----TGTGAAGTGTGGATGGCGTGAGACAGTCTTCCAACTGAAGAC 843
QY 283 AlaSerGlyAlaSerValLeuThrThrArgLeuGlnLysValGlySerIleMetGly 302
Db 844 AATGACAGGAGTCGAATACCTGTTGATCCCGTAAATGATGAAGTGTGATGCTGT 903
QY 303 ThrLeuGln---ProTyrGluLeuSerAsnLeuSerGlnLysAspCysTrpLeuLeuPhe 321
Db 904 GTAGAGATTTTCTTGGCGATGAGCTTCATGATGATGAAGTGAAGTGGAGCTTTTC 963
QY 322 MetGlnArgAlaPheGlnHisGlnGluGlnLeuAsnLeuValAlaIleGlyLys 341
Db 964 AAAAGTCAGCATTTTCA---AGTGAAGCATTACCATATGATTCGAGACGCTTGGAAAG 1020
QY 342 GluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyLysLeu 361
Db 1021 CAATTCGAGATGATGATGACGGGTTACCTACTATTTGTCGTTGGACGGGCTTCTC 1080
QY 362 ArgPheLysArgGluGluArgGlnTrpGlnHisValArg-----AspSerGlnIle 378
Db 1081 AAATCTAAAGACAAATAGAGATTTGAAAACCTTGTCTAAAGATGTCMAATCTTGTTC 1140
QY 379 TrpLysLeuProGlnGluLysSerSerIleuProAlaLeuArgLysSerTyrHis 398
Db 1141 ACAATGATCTGATGAACATGTTCA-----CGTGTCTTGGGTTGATGATGATGATC 1194
QY 399 LeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGlu 418
Db 1195 TTGACAGCGATCTTAAACAATGCTTCTGATCTCGAATTTTCCGAAAGACAGATGAT 1254
QY 419 MetGluLysGlyAsnLeuIleSerLeuThrMetLysHisGlyPheIleLeuSerLysGly 438
Db 1255 ATTCAGTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
QY 439 AsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhe 458
Db 1315 GATTTGGAGAGAGAG-----GTTGAGAGAGTGT 1341
QY 459 PheGlnGluIle----- 462
Db 1342 TTGCAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401
QY 463 GluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThr 482
Db 1402 AAAATTTAGATCA-----TGTAAAGTCTGATGATCAATATGATGATGATGATGAT 1446
QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyr 502
Db 1447 -----GTGAGAGAGAGTTCAAGGAGAGACATTT 1473

QY 503 ILeHMeMetSerIleGlyPhe----- 510
DB 1474 TTTATCATGAGACGATTTGTTGACGATCATATCCAGATGTTTCAATCTGTATG 1533
QY 510 ----- 510
DB 1534 TATAAATGACGCCCTTTAAGCGGTGATGTAATTAATTAATGTCCTATGCT 1593
QY 510 ----- 510
DB 1594 CTTTATAGGGCTCTTCTTAACCCCTGTAATGCTGATGAGATCATGACAACAAT 1653
QY 511 -----ThlyeValValSerSerTySerLeu----- 519
DB 1654 CTTTGAAGACGACCATTTGTTTCTTTTCACTTTGAGCCCTTATATATGTTCTC 1713
QY 520 ---SerHleuGlnLysPheValSerLeuArgValLeuAenLeuSerApIleLysLeu 538
DB 1714 AAATCGAGGTGTTTCATTTCATTAATTAATTAATTAATTAATTAATTAATTA 1773
QY 539 LysGlnLeuProSerSerIleGlyAspLeuValHleuArgTyLeuAenLeu----- 556
DB 1774 GATGGTTTCCCTCGAGATTAAGCTTCATCTGCTGAGGTACCTATCATTTGTTGAC 1833
QY 557 SerGlyAenThrSerIleArgSerLeuProAenGlnLeuCyLysLeuGlnAenLeuGln 576
DB 1834 TATGGGAATTTGCAATGTA-----CCTCGAAGAAATTTGCAAGTTTATGCAATCTGCAG 1884
QY 577 ThrLeuAenLeuHleGlyCyHleSer---LeuCyCyLysLeuProLysGlnThrSerLys 595
DB 1885 ACATTCATGTTTCAACGGTTTCGATCGATTAATTAATTAATTAATTAATTAATTA 1944
QY 596 LeuGlySerLeuArgAenLeuLeuAenArgLysTyArgLysLeuThrCyMetProPro 615
DB 1945 CTAATGCAATTAAGCATTTAACTGAGATTTCATTTGTCAGATTCGCCAAGTGA 2004
QY 616 ArgIleGly-----SerLeuThrCyLysLeuThrLeuSer----- 627
DB 2005 TCTGTGACAAAGAGACCTGATTTTTCAACTTTCACAACTTATTTCTTACTGTC 2064
QY 628 -----ArgPheValValGlyIleGlnLysLysSerCyGlnLeuGly 641
DB 2065 CCAGCTTTGTCACGAGAGGATTTATGAGGATTCAGAAATGTCAAA---AAATTAAGA 2121
QY 642 GlnLeuAenArgAenLeuLeuThrIleGlyIleThrHleuGlnArgValLys 661
DB 2122 ATCAGTGAATTAAGATGACTTAAAGTTTCGGGACTCTGGGCTTCCCAAC----- 2175
QY 662 AenAenMetAenAlaLysGlnAenLeuSerAlaLysAenLeuHleSerLeuSer 681
DB 2176 -----AATCTTGTCTATCTGCGACCACTTGAATATTGAGT 2211
QY 682 Met---LysTPAAspAenArgLysProArgLysLeuTyArgLysLeuValGlnVal 700
DB 2212 CTTATATCTGTGATTAAGCTTTTGCCAGTGCATTTCAAGTGAAGAAAGCTTTTCA 2271
QY 701 LeuGlnAlaLysLysProHleSerAenLeuThrCyLysLeuThrIleArgGlyPheArgGly 720
DB 2272 GCAACGCTCAAGAGTTGAGTGAAGAAAGAACTTATCTAAGC----- 2313
QY 721 IleArgLeuProAenThrMetAenHleSerValLeuLysAenValSerIleGlnLeu 740
DB 2314 -----TGGTCACTTCTGACATCACTGAGTTCAGTTCCTAAGCTTGAAGGTG 2358
QY 741 IleSerCyLysAenCySerCyS-----LeuProProPhe 752
DB 2359 CTGAAGCATGATGATGACGCTTGTGTGTAAGAAATGCAATTCATTTATGAGGATTT 2418
QY 753 GlnLysLeuProCyLysLeu-----LysSerLeuGlnLeuThrArgGlySerAla 768
DB 2419 AATGATTAAGAGCTTTGCTTAATTAATTAATTAATTAATTAATTAATTAATTA 2472

QY 769 GlnValGlnTyValAspSerGlyPheProThrArgArgPheProSerLeuArgLys 788
DB 2473 -----ACAATGACAAATTTCTGCTCCTGACGCG 2502
QY 789 LeuAenIleArgGlnPheGlyAenLeuLysGlyLeuLeuLysGlnGln 808
DB 2503 CTCATGATTAAGAGTTGCAAAATTTGAAA-----GAG 2535
QY 809 CysProVal-----LeuGlnGlnIleGlnIleLysCyCysPro 821
DB 2536 ATACCATTAAGTTTGCAGATTAATACACACTTACAGCTGATTAAGAGAGTGTCT 2595

RESULT 15
US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staakawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capricorn annuum
US-09-360-186-1

Alignment Scores:

Pred. No.: 5 186-48 Length: 31491
Score: 550.50 Matches: 226
Percent Similarity: 39.27% Conservative: 151
Best Local Similarity: 23.54% Mismatches: 340
Query Match: 10.74% Indels: 243
DB: 3 Gaps: 36

US-10-647-268-2 (1-988) x US-09-360-186-1 (1-31491)

QY 4 AlaPheLeuGlnValLeuLeuAenLeuThrCySphIleGlnGlyLeu 23
DB 1498 GCTTCTCTTAAGACATTAAGATCTCTTTCATTTGCGGATGCAATCTCTA 1557
QY 24 IleLeuGlyPheLysAenGlnPheGlnLysLeuGlnSerThrPheThrIleGlnAla 43
DB 1558 TCTGTGATCACAGAGAACTTTCGCTCTGTGAAAAGTTAGTTCCTGGAAGTA 1617
QY 44 ValLeuGlnAenAlaGlnLysLys-----GlnLeuLysAenLysAlaIleGln 59
DB 1618 TTTGTCAAGAACTTTGAGAAAACAAATGTTTGGGAAATGACGATTTTGAAGTGA 1677
QY 60 AenThrPheGlnLysLeuAenAlaAlaLysGln-----AlaAenAen 74
DB 1678 ---GTAAGAGAAAGTTGCAAGCTGCTGATTAACATTCACCTGAGACTAAGCAACT 1734
QY 75 IleLeuAenGlnCyLysLysGlnAlaProIleArgGlnLysAenLysTyArgLys 94
DB 1735 GTACTGGGAGAAATTAAGC-----CAGAAAAAAAAGGCG----- 1770
QY 95 TyHleProAenValIleThrPheArgHleLysIleGlyLysAenMetLysLysIleMet 114
DB 1771 -----CTGCAAGGTTTGTGCAACCTGCAACCAAGTGA 1806
QY 115 GlnLysLeuAenValIleAlaAlaGlnArgIleLysPheHleLysAenGlnArgThrIle 134
DB 1807 GAGACATGATCTATCTGGAAGAGTGCAGAAAGTCAAGTAAAGAAAAACAAGTA 1866
QY 135 GlnArgGlnValAlaThrArgGlnThrGlyPheValLeuAenGln----- 149
DB 1867 TCAAGAAATCATGTTGATGATTTTCAAGTTCAACAAACGATATTTGAAGTTAAG 1926

QY 150 ProGlnValTyrGlyArgAspLysGluLysAspGluLeuValLysIleLeuIleAsnAsn 169
 Db 1927 AACAAATATGTTGGACGTGATGATCAAGAAACAGTTGTAGAAAGATGACTAGTAAGC 1986
 QY 170 ValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLys 189
 Db 1987 TACTCTGGGGAACCC-----AAAGTCATCCCGATTTGCGGATGGGAGCTAGGTA 2040
 QY 190 ThrThrIleuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPheHisProLys 209
 Db 2041 ACAACCTTAGCAAAAGAAAGTTACATGATGATGATCAATTCATATGCCGTTTGATGCTTCAT 2100
 QY 210 IleTrpIleCysValSerGluAspPheAsnGluLysArgLeuIleLysGluIleValGlu 229
 Db 2101 GCCTGGGCTACCATATCTCAACAGACAAACAAAGAAATTTTGCTGGGCTTCGTCAT 2160
 QY 230 SerIle-----GluGluLysSerLeuGlyGlyMetAspLeuAlaPro--- 243
 Db 2161 TCCACAAATCAAAATGATGACAGGGTTAAGATGATGTGTGAAGACAGACTAGCAGCATG 2220
 QY 244 LeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeuValLeuAspAsp 263
 Db 2221 TTACGAAAGAGTTTAAAG-----AGAAAGAGGTACTTAATTGTCTTGATGAT 2268
 QY 264 ValTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysVal---Gly 282
 Db 2269 ATCTGGAGT-----TGTAAGGTGGGATGCGTGGAGACGATGCTTCCAACTGAAGAC 2322
 QY 283 AlaSerGlyAlaSerValLeuThrThrArgLeuGluLysValGlySerIleMetGly 302
 Db 2323 AATGCAAGGAGTCAATCTGTTGACTGACCTACCCGTAATGATGAAGTACGTTGTAATCTG 2382
 QY 303 ThrLeuGln---ProLysIleLeuSerAsnLeuSerGlnLysAspCysTrpLeuPhe 321
 Db 2383 GTAGAGAAATTTTCTTGGCGATGAGCTTCATGATCAAGATGAGTGGAGTCTTTTC 2442
 QY 322 MetGlnArgAlaPheGlyHisGlnGluIleAsnLeuAsnLeuValAlaIleGlyLys 341
 Db 2443 AAAAGTGCAGCATTTTCA---AGTGAAGCATTAACATATGATGATGACGATGCTGGAAG 2499
 QY 342 GluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyLysIleLeu 361
 Db 2500 CAATTCGACATGATGATGACAGGTTACCACTAACATATGTCGTGTCACAGGCTTCGC 2559
 QY 362 ArgPheLysArgGluGluArgGlnTrpGluHisValArg-----AspSerGluIle 378
 Db 2560 AATCTAAAAGGCAATGAAGATGGAAACGTGTGTAAGATGTCMAAGTCATTCGTC 2619
 QY 379 TrpLysLeuProGlnGluLeuSerSerIleLeuProAlaLeuArgLeuSerTyrHis 398
 Db 2620 ACMAATGATCTGATTAACAGATGTTCA-----CGTGTCTGGGTGAGTTACAGATC 2673
 QY 399 LeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGlu 418
 Db 2674 TTGACAAAGCATTAATAACATCTCTTCGCAATTCGGAATTTTCCAAAGACAGTAT 2733
 QY 419 MetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGly 438
 Db 2734 ATTCCAGTGAAGAAATTTGATGATGATGATGCTGAGGGGTTCTCGAAAGTTGGA 2793
 QY 439 AsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhe 458
 Db 2794 GATTGGAAAGGAGAG-----GTTGAGAAAGTGT 2820
 QY 459 PheGlnGluIle----- 462
 Db 2821 TTGCAAGAGCTTTCATAGATGTCAGTCTGTCAGCAAGAGAGTGAAGTGAACA 2880
 QY 463 GluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThr 482
 Db 2881 AAAATATGATCA-----TGTAAGGTTTCATGATCTATATATGACCTGTGC--- 2925

QY 483 SerLeuPheSerAlaSerThrSerSerAsnIleArgGluIleIleValGluAsnTyr 502
 Db 2926 -----GTAGAGAAAGTTCAAAAGGAGAACATT 2952
 QY 503 IleHisMetSerIleGlyPhe----- 510
 Db 2953 TTTATCATGAACAGCATTTGTTCTTGACGTATCATATCCAGAAATGTCATATCTGTATG 3012
 QY 510 ----- 510
 Db 3013 TATTAATAAGACCCCTTAAACCGGTGACGTGTGATGAATTAATTATTTCCCTAATGT 3072
 QY 510 ----- 510
 Db 3073 CTTTATAGGCTCTTCTTACCCCTGTAATGTCAGTTGAGATCATGACAAACAAT 3132
 QY 511 -----ThrLysValIleSerSerTyrSerLeu----- 519
 Db 3133 CTTTGAACGAAACCCATCTGTTTCTCTTTTCATCTTGAGCCTTATATATGTTCTC 3192
 QY 520 ---SerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeu 538
 Db 3193 AAATCAGAGGTTGTCATTTCAATTAATCAAGCTTTCGAGCTGAGACACAGACAAAT 3252
 QY 539 LysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu----- 556
 Db 3253 GATGCTTCCCTCGAGAGATATCTAAGCCTCATCGTTGAGGTACATATGATTTGTCAGC 3312
 QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
 Db 3313 TATGGAAATTCGATGTA-----CTTCACAAAAATTTGACGGTTATGGAATCTCGAC 3363
 QY 577 ThrLeuAspLeuHisGlyCysHisSer---LeuCysCysLeuProLysGluThrSerLys 595
 Db 3364 ACATTCATGTTGCAACGGTTTCGATCAGATATATATATTTTGTGTAGGAAATTTGGGAA 3423
 QY 596 LeuGlySerLeuArgAsnLeuAsnLeuLeuAspGlyCysTyrGlyLeuThrCysMetProPro 615
 Db 3424 CTAAATGCAATTAAGCATCTTAACCTGACCATTTATTTGATGTCAGATGTCGCAAGTGA 3483
 QY 616 ArgIleGly-----SerLeuThrCysLeuLysThrLeuSer----- 627
 Db 3484 TCTGTTCACAAAGAGGACCTTGATTTTCAACCTTACCAACCTATTTCTTACTGTCT 3543
 QY 628 -----ArgPheValValGlyIleGlnLysLysSerCysGlnLeuGly 641
 Db 3544 CCAGCTGTTGCAAGAGAGGATTAATATGCGGATTCAGATGTCAA---AAATTAGA 3600
 QY 642 GluLeuArgAsnLeuAsnLeuLysGlySerIleGluIleThrHisLeuGluArgValLys 661
 Db 3601 ATCAGTGGAAATTAAGGATGACTATTAAGATTTTGGGAGCTGGGCTTCCCAAC----- 3654
 QY 662 AsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSer 681
 Db 3655 -----AATCTGTCTATCTGCGACGCAACTTGAATAATGAGT 3690
 QY 682 Met---LysTrpAspAspGluArgProArgIleTyrGluSerGlyLysValGluVal 700
 Db 3691 CTATATCTGTGATTAAGCTTTTGGCAGTGCATCATTCAGAGCAAAAGCTTTTCCA 3750
 QY 701 LeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
 Db 3751 GCACGCTCAAGAGTTGAAGTTGGAAGAACTTATCTTAAC----- 3792
 QY 721 IleArgLeuProAspTrpMetAsnHisSerValLeuLysAsnValIleSerIleGluIle 740
 Db 3793 -----TGGTCATPACTTGGACATCATAGCTGAGTTCCTTAACCTTGAGGTG 3837
 QY 741 IleSerCysLysAsnCysSerCys-----LeuProProPhe 752
 Db 3838 CTGAAGCTGATGAGATGAGAGCTGTTGTGTGTAAGAAATGCGCATCCAAATGTTATGAGGATTT 3897
 QY 753 GlyGluLeuProCysLeu-----LysSerLeuGluLeuTrpArgGlySerAla 768

```
Db      3898 AATCGATTGAAGCTTTGCTAATTAATAATAGTTTCTTCAGTCTGGAAGCC----- 3951
Qy      769 GluValGluTyValAspSerGlyPheProThrArgArgPheProSerLeuArgLys 788
Db      3952 -----ACAAATGACAAATTTCTCTCTCTTGAGCGC 3981
Qy      789 LeuAenIleArgGluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGln 808
Db      3982 CTCATGATTAGAAAGTTCGCAAAATTTGAAA-----GAG 4014
Qy      809 CysProVal-----LeuGluGluIleGluIleLysCysCysPro 821
Db      4015 ATACCCATTGAGTTTGACAGATATACACACACTGAGTTCGATTGAGTTAAGAGTCTCT 4074
```

Search completed: April 17, 2005, 04:53:27
Job time : 568 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 17, 2005, 03:01:49 ; Search time 1176 Seconds

(without alignments)
5096.863 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFLOVLNLTCTFIQGE.....EKIGEDWYKIAHPRVFY 988

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 562541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USFNO_spool_p/US10647268/runat_15042005_154722_26608/app_query.fasta_1.1159
-DB=Published Applications NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRN=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plo -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAILEN=200000000 -USER=US10647268 @CGN 1.1 723 @runat_15042005_154722_26608
-NCPU=6 -ICPU=3 -NO MMAP -LARGEJURY -NEG_SCORES=0 -WAIT -DSPELOCK=100
-MINLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5127	100.0	3193	18	US-10-647-268-1
2	5028.5	98.1	3595	18	US-10-647-268-3
3	5028.5	98.1	5028	18	US-10-647-268-9
4	4475	87.3	3347	18	US-10-647-268-5
5	3766.5	73.5	2913	17	US-10-360-522-48
6	3648	71.2	3260	17	US-10-360-522-51
7	3638.5	71.0	3592	17	US-10-360-522-49
8	3638.5	71.0	5191	17	US-10-360-522-50
9	3606.5	70.3	3971	17	US-10-360-522-52
10	3400	66.3	3899	17	US-10-360-522-53
11	3342	65.2	3222	18	US-10-647-268-7
12	1517	29.6	3333	18	US-10-437-963-79971
13	1516	29.6	3669	18	US-10-437-963-51007
14	1477.5	28.8	3852	18	US-10-437-963-33659
15	1442.5	28.1	4206	18	US-10-437-963-96637
16	1362	26.6	3759	17	US-10-425-114-29667
17	1355.5	26.4	3633	18	US-10-437-963-29281
18	1339	26.1	3858	18	US-10-437-963-52795
19	1333.5	26.0	4372	18	US-10-437-963-87934
20	1312.5	25.6	3825	18	US-10-437-963-93682
21	1310.5	25.6	3969	18	US-10-437-963-5769
22	1283	25.0	3615	18	US-10-437-963-33626
23	1278.5	24.9	3822	18	US-10-437-963-100477
24	1272.5	24.8	6779	18	US-10-437-963-29812
25	1264.5	24.7	5498	18	US-10-437-963-29817
26	1256	24.5	2949	18	US-10-437-963-79939
27	1200	23.4	3366	18	US-10-437-963-57476
28	1168	22.8	3497	17	US-10-424-599-24663
29	1129	22.0	2883	18	US-10-437-963-26578
30	1122	21.9	3213	18	US-10-437-963-51005
31	1119.5	21.8	5403	17	US-10-424-599-24667
32	1113.5	21.7	3369	18	US-10-437-963-40347
33	1108	21.6	2565	18	US-10-437-963-56879
34	1104.5	21.5	3273	18	US-10-437-963-19647
35	1093	21.3	3177	18	US-10-437-963-28789
36	1080	21.1	4008	18	US-10-437-963-47465
37	1075.5	21.0	4248	18	US-10-437-963-62624
38	1070.5	20.9	2415	18	US-10-437-963-24753
39	1066	20.8	2985	18	US-10-437-963-26581
40	1065	20.8	2887	18	US-10-437-963-61107
41	1059	20.7	4468	18	US-10-437-963-99527
42	1054	20.6	2409	18	US-10-437-963-67879
43	1041.5	20.3	3172	18	US-10-437-963-10860
44	1040.5	20.3	3954	18	US-10-437-963-29358
45	1035	20.2	2961	18	US-10-437-963-101390

ALIGNMENTS

RESULT 1
US-10-647-268-1
Sequence 1, Application US/10647268
Publication No. US20040237137A1
GENERAL INFORMATION:
APPLICANT: Oosumi et al., Teruko
TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
FILE REFERENCE: 0155_02
CURRENT APPLICATION NUMBER: US/10/647, 268
PRIOR FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 60/407, 100
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 3193
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: CDS

LOCATION: (52) .. (3018)
US-10-647-268-1

Alignment Scores:

Pred. No.:	0	Length:	3193
Score:	5127.00	Matches:	988
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-10-647-268-2 (1-988) x US-10-647-268-1 (1-3193)

```
QY      1 MetAlaGluAlaPheLeuGluValLeuLeuAspLeuThrCysPheIleGlnGlyGlu 20
DB      52 ATGGCTGAAGCTTCTTCCTTCAAGTTCTGTAGACAACTGACTGTGTTTCATCCAAAGGGA 111
QY      21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThrThr 40
DB      112 CTGGATTGATTCTTGCTTTTAAGATGAGTTCCGAAAAGCTTCAAGCACGTTTACTCA 171
QY      41 ILeuGlnAlaValLeuGluAspAlaGlnLeuGlnLeuLeuAspLeuAlaIleGln 60
DB      172 ATCCAAAGCTGTGCTGAGATGCTCAGAAAGCAATTGAAGGACAAAGCAATGACAAAT 231
QY      61 ThrLeuGlnLeuLeuAspAlaAlaAlaTyrGluAlaAspAspIleLeuAspGluCys 80
DB      232 TGGTTGCAAGAACTCAATGCTGCTGCATATGAGCTGATGACATCTTGACGAAATGTA 291
QY      81 ThrGluAlaProIleArgGlnLeuLeuAspLeuTyrGlyCysTyrHisProAsnValIle 100
DB      292 ACTGAGGACCAATTTAGACAGAGAAAGCAAAATATGGGTGTTATCATCCAAAGCTTATC 351
QY      101 ThrPheArgHisLeuIleGlyLeuAspGlyLeuIleMetGlnLeuLeuAspValIle 120
DB      352 ACTTTTCTCTCAAAATGCGGAAAGATGAAAGAAAGATTATGAGAAACTGATGTAAT 411
QY      121 AlaAlaGluArgIleLeuPheHisLeuAspGluArgThrIleGluArgGluValAlaThr 140
DB      412 GCAAGGGAACGAAATTAAGTTTCATTTGATGAAAGACATATAGACAGCAAGTTCTTCA 471
QY      141 ArgGlnThrGlyPheValLeuAsnGluProGlnValTyrGlyArgAspLeuGlnLeuAsp 160
DB      472 CGCCAAACAGGTTTGTGTTGATGAACCAAGTTTATGGAAGAGACAAAGAAAGAAC 531
QY      161 GluIleValIleLeuIleLeuAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
DB      532 GAGATAGTGAAGAAATCTGATTAACAAATGTAGCAATGCCCAACCTTCCAGTCTCCCA 591
QY      181 ILeuLeuGlyMetGlyGlyLeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGln 200
DB      592 ATACTTGGTATGGGGGAGCTAGGAAAGACGACTCTTGCCCAATGGTCTTCAATATCAG 651
QY      201 ArgValIleGlnHisPheHisProLeuIleTyrIleCysValSerGlnAspPheAsnGlu 220
DB      652 AGAGTAATTTAGACATTTCCATCCAAAATATGATTTGTGCTCGGAAGATTATATGAG 711
QY      221 LysAspGluLeuIleGlyGluIleValGlnSerIleGlnGluLeuSerLeuGlyGlyMetAsp 240
DB      712 AAGAGGTGATTAAGAAATGTGTAGAACTTATTTGAAGAAAGTCACTTGGTGGCATGAGC 771
QY      241 LeuAlaProLeuGlnLeuLeuLeuAspLeuLeuAsnGlyLeuLeuGlyTyrLeuLeuVal 260
DB      772 TTGGCTCCACTTCAAAAGAGCTTGGGAGCTTGCGAATGGAAGAAAATATTTGCTGCTG 831
QY      261 LeuAspAspValTyrAsnGlnAspGlnAspLeuTyrAlaLeuLeuArgGlnValLeuLeu 280
DB      832 TTAGATGATGTTTGGAAATGAAGATCAAGTAAATGAGTGAAGTAAACAAGCTTGAAG 891
QY      281 ValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlnLeuValGlySerIle 300
DB      892 GTTGAAGCAAGTGGCGCTTCTGTCTTAACCACTACTCGTCTTGAAAAGGTGTGATCAAT 951
```

```
QY      301 MetGlyThrLeuGlnProTyrGlnLeuSerAsnLeuSerGlnGluAspCysTyrLeuLeu 320
DB      952 ATGGGAACATTTGCAACCATATGAATGTGCAAAATTTGCTCAAGAAAGATTTGTTGCTGTTG 1011
QY      321 PheMetGlnArgAlaPheGlyHisGlnGlnGluIleAsnLeuAsnLeuValAlaIleGly 340
DB      1012 TTCAATGCAACCTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGGGCTATGCGGA 1071
QY      341 LysGlnIleValIleLeuLeuCysGlyGlyValProLeuAlaAlaTyrThrLeuGlyGlyIle 360
DB      1072 AAGGAGATTTGAAAATATGAGTGTGTGCTGCTGCTTACAGCTTAAACCTTTGGAGATAT 1131
QY      361 LeuArgPheLeuArgGlnGluArgIleTyrGlnHisValArgAspSerGluIleTyrLys 380
DB      1132 TTGGCGCTTTAAGACAGAAAGAAAGACAGTGGGAACATGTGAGAGATGAGATTTGGAAA 1191
QY      381 LeuProGlnGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTyrHisIleLeuPro 400
DB      1192 TTGCTCAAGAAAGAAAGTCTTATTTCTGCTGCTGAGACTTAATGTTACCATCACCTTCCA 1251
QY      401 LeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMetGlu 420
DB      1252 CTGATTTTGAACAATGCTTTTACATATTTGTGCAATATTTCCAAAGATACCGAAATGGA 1311
QY      421 LysGlnAsnLeuIleSerLeuTyrMetAlaHisGlyPheIleLeuSerLysGlyAsnLeu 440
DB      1312 AAGGAAATCTAATCTCTCTGATGACACATGCTTTATTTATGCAAAAGAAACTTG 1371
QY      441 GluLeuGlnAsnValGlyAsnGlnValTyrAsnGlnLeuTyrLeuAspSerPhePheGln 460
DB      1372 GAGCTAGAGATGAGTGAATGAAGATGAGATGAATTAATTAATTAATTAATTAATTAATTA 1431
QY      461 GluIleGlnValLysSerGlyGlnThrTyrPheLeuMetHisAspLeuIleHisAspLeu 480
DB      1432 GAGATTGAGTAAATCTGTCGCAACATTTATTTCAAGATGATGATTCATTCATGATCTG 1491
QY      481 AlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlnIleIleValGln 500
DB      1492 GCAACATCTTATTTTGGGCAAGACATCAAGCAGCAATATCCAGAAATATGTGAGAA 1551
QY      501 AsnTyrIleHisMetMetSerIleGlyPheThrLysValIleSerSerTyrSerLeuSer 520
DB      1552 AATTACATACATTAATGATGCTCATTTGCTTCACTAAAGGTATCTTCACTCTTCTCC 1611
QY      521 HisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLysGln 540
DB      1612 CACTTGCAGAAAGTTTGTCTCTTGAAGGCTCTTAATCTTAATGACATTAACCTTAAGCAG 1671
QY      541 LeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThr 560
DB      1672 TTACCGTCTTCAATTTGAGATCTAGTACATTTAAGATCTTAACCTTGTCTGGCAATACT 1731
QY      561 SerIleAspSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeu 580
DB      1732 AGTATGCTATGATCTTCCAAACAGTATGCAAGCTTCAAAATCTGACAGACTCTTGATGTA 1791
QY      581 HisGlyCysHisSerLeuCysCysLeuProLysGlnThrSerLysLeuGlySerLeuArg 600
DB      1792 CATGGCTCATTTCACTTTGTGTTGTCGCAAAAGAAACAAACCAACTGTGATGCTTGA 1851
QY      601 AsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySerLeu 620
DB      1852 AATCTTTTACTTGAATGTTGCTATGATGATGACTTGTATGCAACCAAGATAGGATCTTTG 1911
QY      621 ThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLysSerCysGlnLeu 640
DB      1912 ACATGGCTTAAAGACTTAAAGTGAATTTGTGGTGGAAATTCGAAGAAAGTTGTCACTT 1971
QY      641 GlyGlnLeuArgAsnLeuAsnLeuTyrGlySerIleGlnIleThrHisLeuGlnArgVal 660
DB      1972 GGTGAATTAACAAACCTGAAATCTCTATGGCTCAATTTGAATCAAGCAATCTTGAAGAGTGT 2031
QY      661 LysAsnAspMetAspAlaLysGlnAlaAsnLeuSerAlaLysGlnAsnLeuHisSerLeu 680
```

```

Db      2032 AAGATGATATGAGCAAAAGAACCCATTTATCTGCAAAAGAAATCTGCATCTTTA 2091
Oy      681  SermetLysTPASpASpAAspGluArgProArgIleTyrgLysSerGluValGluVal 700
Db      2092 AGCATGAATGGAGATGACGATGACGTCACCTATATATGATTCAGAAAAGCTTAAAGTG 2151
Oy      701  LeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
Db      2152 CTTGAAGCTCTCAAAACCACTCCCATCTGACTTTTAAACAATCAGGGGCTTCAGAGGA 2211
Oy      721  IleArgLeuProArgTTPMeCasnHisSerValLeuLysAsnValValSerIleGluIle 740
Db      2212 ATCCCTCTCCAGACTGATGATCATCTACGACTTTGGAAGAAATGTGTCTTATGAAATC 2271
Oy      741  ILeSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuProCysLeuLysSer 760
Db      2272 ATCAGTTCCAAAACCTGCTCATGCTTACCACTTGTGAGCTGCTGTCTTAAAGAT 2331
Oy      761  LeuGluLeuTPArgGlySerAlaGluValGluTyrgValAspSerGlyPheProThrArg 780
Db      2332 CTAGAGTTGTGAGAGGGGCTTCGGAAGTGAAGTATGTTGATTCGATTCCTTCAAGA 2391
Oy      781  ArgArgPheProSerLeuArgLysLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeu 800
Db      2392 AGAAGTTTCCATCTCTGAGAAAACCTTAATATACGCAATTTGGTAATCTGAAGATTTG 2451
Oy      801  LeuLysLysGluGlyGluGluGlnCysProValLeuGluGluIleGluIleLysCysCys 820
Db      2452 CTGAAAAAGGAGGAGAGAGCAATGCCCTGTGCTTGAAGAAATVTAAGATTTAAAGTTGC 2511
Oy      821  PrometPheValIleProThrLeuSerSerValLysLysLeuValValSerGlyAspLys 840
Db      2512 CCTATGTTGTTTATTCACACCTTTCTTCTGTCAAGAAATTTGTAAGTGGGACAAAG 2571
Oy      841  SerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIle 860
Db      2572 TCAGATGCAATAGGTTTCAGTTCCATATCTAATCTCATGGCTTACTTCCCTCAAAAT 2631
Oy      861  ArgTyrgAsnLysGluAspAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeu 880
Db      2632 CGCTATACCAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCTTGCACAAATCTC 2691
Oy      881  LysTyrgLeuAsnIleSerPheTyrgPheAsnLeuLysGluLeuProThrSerLeuAlaSer 900
Db      2692 AAATCTTGATATATCTTTTACTTCAATCTTAAAGAGCTGCTTACCAAGCTTGCCTAGT 2751
Oy      901  LeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrgAlaLeuGluSerLeuProGlu 920
Db      2752 CTCAATGCTTGAACATCTGGAATTCATAGTTGTTATGCACTAGAGAGTCTCCCGAG 2811
Oy      921  GluGlyValLysGlyLeuLysSerLeuThrGlnLeuSerIleThrTyrgSerGluMetLeu 940
Db      2812 GAAGGCTGGAAGGTTTATTTACCTCACTCACAGTTATCATTAACACTGCTGAATAATGCTA 2871
Oy      941  GlnCysLeuProGluGlyLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPhe 960
Db      2872 CAATCTTACCGAGAGATTCAGACACTTAACAGCTTCAAAATTTATCACTTAAAGTTT 2931
Oy      961  CysProThrLeuAlaLysArgCysGluLysGlyIleGlyGluAspTTPTyrgLysIleAla 980
Db      2932 TGTCCAAACACTGGCCAGCGGTGTGAGAAAGGAATAGGAAGAAGCTGGTACAAATTTCT 2991
Oy      981  HisIleProArgValPheIleTyrg 988
Db      2992 CACATTCCTCGTGTGTTATTTAT 3015

```

```

RESULT 2
US-10-647-268-3
; Sequence 3, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko

```

```

; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3595
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(487)
; OTHER INFORMATION: Spu11 protein
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (488)..(899)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (900)..(3432)
; US-10-647-268-3

Alignment Scores:
Pred. No.: 0 Length: 3595
Score: 5028.50 Matches: 987
Percent Similarity: 87.66% Conservative: 0
Best Local Similarity: 87.66% Mismatch: 1
Query Match: 98.08% Indels: 138
DB: 18 Gaps: 1

US-10-647-268-2 (1-988) x US-10-647-268-3 (1-3595)

Oy      1  MetaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db      57  ATGGGTGAAGCTTTCCTTCAAGTTCTGTAGACAAATCTGACTTGTTCATCCAGGGGA 116
Oy      21  LeuGlyLeuIleLeuGlyPheLysAspGluPheGlyLysLeuGlnSerThrPheThrThr 40
Db      117  CTGGATTGATTTCTTGTTTAAAGATGATTCGAAAAGCTTCAAAAGACGCTTTACTTCA 176
Oy      41  IleGlnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsn 60
Db      177  ATCCAGCTGTGCTAGAAAGATGCTCAGAAAGCAATTGAAGGACAAAGCATAGAAAT 236
Oy      61  TrpLeuGlnLysLeuAsnAlaAlaTyrgLysAlaAspAspIleLeuAspGluCysLys 80
Db      237  TGGTTGCAGAAACTCAATGCTGTCATATAGAGCTGATGACATCTTGAGCAATGTAAA 296
Oy      81  ThrGluAlaProIleArgGlnLysAsnLysTyrgLysCysTyrgHisProAsnValIle 100
Db      297  ACTGAGCACAATTAAGACAGAAAGAAATATGAGGTATTCATCCAAACCTTATC 356
Oy      101  ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
Db      357  ACTTTTCTCACAAGATTGGGAAAAAGATGAAAAAGATTATGAGAAACTGATATTT 416
Oy      121  AlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
Db      417  GCAGCGGAACAAATTAAGTTTCATTTGATGAAAGACTATATAGAGACAAAGTTGCTACA 476
Oy      141  ArgGlnThr 143
Db      477  CGCCAAACAGGTGCTCATCTTAATATTTTCTGAAAAAACAGCTTTATATCATCAAAATT 536
Oy      143  ----- 143
Db      537  CATGTGCTTTTGGGAATTCGCTAATCTAATGTTGCTCAAGTCTAAGTAGTAAGT 596
Oy      143  ----- 143
Db      597  GCATCCAGCTTTGATTTATTAATCTAATCTAATCTGTTTAAAGTGAAGTTTAAACAT 656

```

143 ----- 143
QY
Db 657 ATATNACTCAGATTAATCCATAGCTTACTCATAGATTAGATAGGCCCAAGCTTAA 716
QY 143 ----- 143
Db 717 ATGACAGATTAAGCCAGAGTTGTTTACCTCTTAATAATTACATGATAATATATGTA 776
QY 143 ----- 143
Db 777 ATTCAAAAAGTCATTTTTTTTAAATTGAAATATTTCTGCTGCTTCTCAAGCTTATCAT 836
QY 143 ----- 143
Db 837 GTCTTTTACTGTGCAAAATCTACTTGTGATTTTGTCTGACTCTACCGAGCTTGGCC 896
QY 144 -GLYPheValLeuAenGluProGlnValTyrgIyArGAspLysGluLysAspGluIleVal 163
Db 897 AGGTTTGTGTTGAATGAACCAAGTTTATGGAAGAGCAAGAAAAGAGAGATAGT 956
QY 163 ILYsIleLeuIleAenAenValSerAsnAglInThrLeuProValLeuProIleLeuGI 183
Db 957 GAAATATCCGTGATTAACAATGTAGCAATGCCCAACACTTCCAGTCTCCCAATCTTGG 1016
QY 183 YMeGlyGlyLeuGIYlySerThrThrLeuAglImetValPheAenAspGlnArGValII 203
Db 1017 TATGGGGGACTAGGAAGACACTCTTGGCCAAATGGCTTCAATGATCAGAGATANT 1076
QY 203 eGIuHisPheHisProLYsIleTrpIleCYsValSerGIuAspPheAsnGluLYsArgLe 223
Db 1077 TGAGCATTTCCATCCCAAAATATGATTTTGTCCTCGGAAGATTTTAAATGAGAAGAGTT 1136
QY 223 uIleLYsGIuIleValGIuSerIleGIuGIuLYsSerLeuGIYGIYMeTAspLeuAlaPr 243
Db 1137 GATTAAGCAAAATTTGATGATCTATTGAGAAAAGCACTTGGTGCACTGGACTGCTCC 1196
QY 243 oLeuGIuLYsLYsLeuArGAspLeuLeuAsnGIYLYsLYsTYrLeuLeuValLeuAspAs 263
Db 1197 ACTTCAAAAAGACTTGGGACTGCTGTGATGAGAAAATATTTGCTGCTCTTGAATCA 1256
QY 263 pValITrPAenGIuAspGlnAspLYsITrPAIleLYsLeuArGlnValLeuLYsValGIYAl 283
Db 1257 TCTTTGGATGAAGATCAAGATTAAGTGGCTTAAGACAAAGCTTGAAGTTGGAGC 1316
QY 283 aSerGIYAlaSerValLeuThrThrThrArGLeuGIuLYsValGIYSerIleMeGIYTh 303
Db 1317 AAGTGCGCTCTCTGTTCTTACACTACTGCTTGAAGAGTTGATCAATATATGGGAAC 1376
QY 303 rLeuGIuProTYrGIuLeuSerAsnLeuSerGlnIuAspCYsITrPLeuLeuPheMeGI 323
Db 1377 ATTTGACCAATATGAATTTGTCAAAATTTGTCTCAAGAGATTTGTGTTGTCTTACGA 1436
QY 323 nArGAlaPheGIYHisGlnGIuGIuIleAsnLeuAenValAlaIleGIYLYsGIuI 343
Db 1437 AGGTGATTTGGGCAACAAGAAATTAATCTTAATCTTGTGGCTATCGGAAGAGAGAT 1496
QY 343 eValLYsLYsCYsGIYGIYValProLeuAlaAlaLYsThrLeuGIYGIYIleLeuArGh 363
Db 1497 TGTGAAAAATGTGGGTGTGTGCTTACACTTAACCTTGGAGGTATTTTGGCTT 1556
QY 363 eLYsArGGIuGIuArGlnITrPGLuHisValArGAspSerGIuIleITrPLeuLeuProGI 383
Db 1557 TTAG 1616
QY 383 nGIuGIuSerSerIleLeuProAlaLeuArGLeuSerTYrHisHisLeuProLeuAspLe 403
Db 1617 AGAAGAAAGTTCTATTTCTGCTGCTCCCTGAGACTTATGATCACTCACTTCACTTATTT 1676
QY 403 uArGlnCYsPheThrTYrCYsAlaValaPheProLYsAspThrGluMeGIuLYsGIYAs 423
Db 1677 GAGACAAATGCTTTACATATTTGTGAGATTTCCAAAGAGATACCGAAATGAGAAAGGAAA 1736

QY 423 nLeuIleSerLeuITrPMeAlaHisGIYPheIleLeuSerLYsGIYAsnLeuGIuLeuGI 443
Db 1737 TCTATCTCTCTCGATGAGACATAGTTTATTTATTCAGAAAGAACTTGGAGCTAGA 1796
QY 443 uAenValGIYAsnGIuValITrPAenGIuLeuTYrLeuArGSerPhePheGlnGIleGI 463
Db 1797 GAATGTAGTAAATGAAATGAGATGAAATTAATCTTGAAGTCTTCTTCCAAAGAGATTGA 1856
QY 463 uValLYsSerGIYGIuThrTYrPheLYsMeHisAspLeuIleHisAspLeuAlaThrSe 483
Db 1857 AGTTAAATCTGTCAAACTTATTTCAAGAGCAGATCTCATTCATGATCTGGCAATCTC 1916
QY 483 rLeuPheSerAlaSerThrSerSerSerAsnIleArGluIleIleValGIuAenTYrII 503
Db 1917 TCTATTTTCGCAAGACATCAAGCAACAATATCCGAGAAATATATGAAAAATTTACAT 1976
QY 503 eHisMeMeSerIleGIYPheThrLYsValValSerSerTYrSerLeuSerHisLeuGI 523
Db 1977 ACATATGATGTCCTAGTGTTCACCTAAAGGTATCTTACTCTCTTCCCACTTGCA 2036
QY 523 nLYsPheValSerLeuArGValLeuAenLeuSerAspIleLYsLeuLYsGlnLeuProSe 543
Db 2037 GAAGTTGTCTCGTTGAGGGGTCTTAATCTAAGAGACATAAACTTAAGCAGTTACGCTC 2096
QY 543 rSerIleGIYAspLeuValHisLeuArGYrLeuAsnLeuSerGIYAsnThrSerIleAr 563
Db 2097 TTCCATTGAGATCTAGTACATTTAAGATVACTTAACCTTGTCTGCAATATCTATATTGC 2156
QY 563 gSerLeuProAsnGlnLeuCYsLYsLeuGlnAsnLeuGIuThrLeuAspLeuHisGIYCY 583
Db 2157 TAGCTTCCAAACCAAGTATGACAGCTTCAAAATCTGCAGACTTTGATCTACATGGCTG 2216
QY 583 sHisSerLeuCYsCYsLeuProLYsGIuThrSerLYsLeuGIYSerLeuArGAsnLeuLe 603
Db 2217 TCATTCATTTGTTGTTGGCCAAAAGAACAGCAAACTTGTAGTCTTCGAAATCTTTT 2276
QY 603 uLeuAspGIYCYsTYrGIYLeuThrCYsMeTProProArGIleGIYSerLeuThrCYsLe 623
Db 2277 ACTGATGTTGCTATGATGATGACTTGTATGCCAACAAAGATGAGATCTTGAACATGCT 2336
QY 623 uLYsThrLeuSerArGpPheValValGIYIleGIuLYsLYsSerCYsGlnLeuGIYGIuLe 643
Db 2337 TAAAGCTTAAGTATGATTTGTGTGGAGATTCAGAAAGAAAGTTGTCACTTGTGTGATTT 2396
QY 643 uArGAsnLeuAsnLeuTYrGIYSerIleGIuIleThrHisLeuGIuArGValLYsAsnAs 663
Db 2397 ACGAAACCTGATCTCTATGCTCAATGGAATCAGCATCTTGAGAGAGTGAAGAAATGA 2456
QY 663 pMeTAspAlaLYsGIuAlaAenLeuSerAlaLYsGIuAsnLeuHisSerLeuSerMeTY 683
Db 2457 TATGATCCAAAGAGCAATTTATCTGCAAAAAGAAATCTGCATTTCTTAAGCATGAA 2516
QY 683 eITrAspAspAspGIuArGProArGIleTYrGIuSerGIuLYsValGIuValLeuGIuAl 703
Db 2517 ATGGATGACATGAACTCCACGATATATGATCAGAAAAAGTTGAAAGTGGCTTGAAGC 2576
QY 703 aLeuLYsProHisSerAsnLeuThrCYsLeuThrIleArGIYPheArGIYIleArGLe 723
Db 2577 TCTCAACACACACTCATCTGACTTGTTAACAATCAGGGGCTTCAAGAGAAATCCGCTC 2636
QY 723 uProAspITrPMeTAsnHisSerValLeuLYsAsnValValSerIleGIuIleIleSerCY 743
Db 2637 CCCAGACTGAGATGATCTCACTGATTTAAAAAATGTCTCTATATGAAATCATCAGTTG 2696
QY 743 eLYsAsnCYsSerCYsLeuProProPheGIYGIuLeuProCYsLeuLYsSerLeuGIuLe 763
Db 2697 CAAAACTGCTCATCTTACCACTTTGTGTAGAGTGTGCTTGTAAAAAGTCTGAGATT 2756
QY 763 uITrArGIYSerAlaGIuValaGIYTYrValAspSerGIYPheProITrArGArGArGh 783
Db 2757 ATGAGAGGGGTCTCGGAGAGTGAATGATTGATTCTGATTCCTCAAGAGAAAGGTT 2816
QY 783 eProSerLeuArGIYLYsLeuAsnIleArGIuPheGIYAsnLeuLYsGIYLeuLeuLYsLY 803

```

Db      2817  TCCATCTCTGAGAAAACCTTAATATACGCGAATTATCATCATCGAAGATTGCTGAAAAA 2876
Qy      803   egluglglugluginCyseProvalleugluginleglunilleyCysePrometPh 823
Db      2877  GGAGGAGAGAGCAATGCCGTGCTTGAGAGATAGAGATTAATGTTGCTGATGTT 2936
Qy      823   eValleProThrLeuSerSerValylsleuValyserylYAspLysSerAspAl 843
Db      2937  TGTATTTCCAAACCTTTCTTCTGTCAGAAANTGGTAGTATGGGCAAGTCAAGATGC 2996
Qy      843   aileglyPheSerSerIleSerAsnleuMecAlaLeuThrSerleuglunilleyTyAs 863
Db      2997  AATAGGTTTCAGTTCCATATCTAATCTCATGCTCTTACTTCCCTCAAAATCGCTATTA 3056
Qy      863   nlygluAspAlaSerleuProgluGluMetPheLysSerleuAlaAsnleuLysTyle 883
Db      3057  CAAGAGAAATGCTTCTACTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTCAATACCT 3116
Qy      883   uAsnIleSerPheTyPheAsnleuLysgluLeuProThrSerleuAlaSerleuAsnAl 903
Db      3117  GAATATCTCTTTTATCTTCAATCTTAAGAGCTGCTACAGCCTGCTAGCTCAATGC 3176
Qy      903   aleuLysHileuglunilleyHileSerCyseTyAlaLeugluserleuProgluGlyVa 923
Db      3177  TTTGAGCATCTGGAATTCATAGTTGTTATGCACTAGAGAGTCCCGAGAGAGTGT 3236
Qy      923   llygluLysleuIleSerleuThrInleuSerIleThrTyCysegluMetleuglInCyle 943
Db      3237  GAAAGGTTTATTTCTACTCACACAGCTTATCCATTAACATGCTGAAATGCTACATGTTT 3296
Qy      943   uProgluLysleuglnHileuThrAlaLeuThrAsnleuSerValylsPheCyseProth 963
Db      3297  ACCGAGGAGATTGCGACACCTTACAGCCTTCAAAATTTATCAGTTGAGTTTGTCCAAAC 3356
Qy      963   rleuAlaLysArgCysegluLysglYilegluAspTyrTyrlsIleAlaHilePr 983
Db      3357  ACTGGCCAGGCGTGTGAGAGGAGATAGAGAGACGTACAAAAATGCTCAATCC 3416
Qy      983   carGValPheIleTyR 988
Db      3417  TCGTGTTGTTTATTTAT 3432

RESULT 3
US-10-647-268-9
; Sequence 9, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 5028
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(553)
; OTHER INFORMATION: Potato Ub13 promoter
; FEATURE:
; NAME/KEY: gene
; LOCATION: (973)..(4566)
; OTHER INFORMATION: Solanum bulbocastanum genomic Sbul1
; NAME/KEY: CDS
; LOCATION: (1029)..(1459)
; FEATURE:

```

```

; NAME/KEY: Intron
; LOCATION: (1460)..(1871)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1872)..(4404)
US-10-647-268-9

Alignment Scores:
Pred. No.: 0
Score: 5028.50
Percent Similarity: 87.66%
Best Local Similarity: 87.66%
Query Match: 98.08%
DB: 18

US-10-647-268-2 (1-988) x US-10-647-268-9 (1-5028)

Qy      1   MetAlaGluAlaPheLeuGlnValleuLeuAspAsnleuThrCysePheIleGlnGlyGlu 20
Db      1029  ATGCTGAAAGCTTCTTCAAGTTCTGTGACATCATCTGCTGTTTCATCCAAAGGAGAA 1088
Qy      21   LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysleuGlnserThrPheThrThr 40
Db      1089  CTTGATTTGATTTCTGTTTAAAGATGATTCGAAAGCTTCAAAGACGCTTATCACTACA 1148
Qy      41   lIleGlnAlaValleuGluAspAlaGlnLysLysGlnleuLysAspLysAlailegluAsn 60
Db      1149  ATCCAGCTGTGCTGAGAAATGCTCAGAGAGACATTTGAAGACAGCAATAGAAAAT 1208
Qy      61   TrpleuGlnLysleuAsnAlaAlaAlaTyrlsAlaAspAspIleleuAspGluCyLys 80
Db      1209  TGGTTGAGAAATCTCAATGCTGCTGCATATGAGGCTGATGACATCTTGAGCAATGTAA 1268
Qy      81   ThrGluAlaProIleArgGlnLysLysAsnLysTyrlsGlyCyseTyrlsPheAsnValIle 100
Db      1269  ACTAGGACCAATTTAGACAGAGAGAAACAATATGGGTGTTATCATCCAAAGCTTATC 1328
Qy      101  ThrPheArgHileLysIleGlyLysArgMetLysLysIleMetGlnLysleuAspValIle 120
Db      1329  ACTTTTGTCCAAAGATTTGGGAAAAGATGAAAAGATTAAGGAAACTAGATTAAT 1388
Qy      121  AlaAlaGluArgIleLysPheHileuAspGluArgThrIleGluArgGlnValAlaThr 140
Db      1389  GCAGCGAGACAAATTAAGTTTCATTTGGATGAAAGACTATATAGAGACAGATTGCTACA 1448
Qy      141  ArgGlnThr----- 143
Db      1449  CGCCAAACAGGTGCTCATTTAGATATTTTCTGAAAAACAGCTTATATCATCAAAATT 1508
Qy      143  ----- 143
Db      1509  CATGTGTTTGGGAATTCGTTAATCTTAATGTTGCTCAAGTCTTAAGTAGTAAGT 1568
Qy      143  ----- 143
Db      1569  GGATCCAGCTTTGATTTATTAATCTATAGCTAAATCTGTTAGTGAAGTTTAAACAT 1628
Qy      143  ----- 143
Db      1629  ATATTAACCTCAGATTAATTCATAGCTTACTATAGATTAAGATAGAGCCCAAGTCTTA 1688
Qy      143  ----- 143
Db      1689  ATGACAGATTAAGCCAGAGATTTTAAAGCTTATTAATTAACATATATATATGCA 1748
Qy      143  ----- 143
Db      1749  ATTCAAAAAGTGATTTTATTAATTAATTAATTTGCTGCTTCCAAAGCTTATCATTT 1808
Qy      143  ----- 143
Db      1809  GTCTTTTACTGTGCAAAATTTCTACTTTGATTTTGTGTAAGCTTACGAGCTTGAGCC 1868

```

144 -GlyPheValLeuAsnGluProGlnValTyrGlyArgAspLysGluLysAspGluIleVal 163
1869 AGGTTTGTCTTTGATGAAACCAAGTTTATGAAAGACAAAGAAAGGACGAGATAGT 1928
163 llyleuIleuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuG1 183
1929 GAAATTCCTGATTAACATGTTAGCAATGCCAAACACTTCACAGTCCCTCCCAATACCTGG 1988
183 yMeG1yG1LeuG1yLysThrThrLeuAlaGlnMeValPheAsnAspGlnArgValI1 203
1989 TATGGGGGACATAGAAAGACACTCTTGCCCAATGGCTTCATGATGATCAGAGATAT 2048
203 eGlnHisPheHisProLysIleTrpIleGysValSerGluAspPheAsnGluLysArgLe 223
2049 TGAGCATTTCCATCCCAAAATATGAGATTGTCCTCGAAGATTTTAAATGAGAAAGGTT 2108
223 uIleLysGluIleValIleGluSerIleGluLysSerLeuG1yG1yMeAspLeuAlaPr 243
2109 GATTAAGGAATTTGATGATATCTAATGAAAGAAAGTCACTGGTGGCATGGACTGGCTCC 2168
243 OLeuGluLysLysLeuArgAspLeuLeuAsnG1yLysLysTyrLeuLeuValLeuAspAs 263
2169 ACTTCAAAAGAAAGCTTCGGGACTTGCTGATGAAAGAAATATTTGCTGCTTAGATGA 2228
263 PValITrpAsnGluAspGluAspLysTrpAlaLysLeuArgGlnValLeuLysValIleG1 283
2229 TGTTTGGATGAAAGATCAAGATTAAGTGGCTTAAGTTAAGACAAGCTTGAAGTTGGAGC 2288
283 aSerG1yAlaSerValLeuThrThrThrArgLeuGluLysValG1ySerIleMeG1yTh 303
2289 AAGTGGCGTCTGTTCTTAACACACTACGCTCTTGAAGAAAGTTGGATCAATATATGGGAC 2348
303 rLeuGlnProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMeG1 323
2349 ATTGCAACCATATGATATGATGTCAAATTTGCTCAAGAGATTTGGTGTGTTATGCA 2408
323 nArgAlaPheGluYH1sGlnGluGluIleAsnLeuAsnLeuValAlaIleG1yLysGluI1 343
2409 AGGTGATTTGGGACCCAGAAAGAAATATATCTTAATCTTGGCTTAACCGAAAGAGAT 2468
343 eValIlyLysCysG1yG1yValProLeuAlaAlaLysThrLeuG1yG1yIleLeuArgPh 363
2469 TGTGAAAAATGTTGGTGGTGGCTCTACACACTAAACCTTGGAGGATTTTCCGCTT 2528
363 eLysArgGluGluArgGlnTrpGluIleAlaArgAspSerGluIleTrpLysLeuProG1 383
2529 TAAGAGAGAAAGAAACAGATGGAAACATGTGAGATGAGATTTGAAAATTCGCTCA 2588
383 nGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrH1sH1sLeuProLeuAspLe 403
2589 AAAAAAGATTTCTATTTCTGCTGCTGCTGACCTTAAGTTCACATCACCTTCCACTGATT 2648
403 uArgGlnCysPheThrTyrCysAlaValaPheProLysAspThrGluMeGluLysG1yAs 423
2649 GAGACAAATCTTATACATATTTGTCAGTATTTCCAAAGATACCGAAATGAAAAGGAAA 2708
423 nLeuIleSerLeuTrpMetAlaH1sG1yPheIleLeuSerLysGluAsnLeuGluLeuG1 443
2709 TCTAACTCTCTCTGATGGACATGCTTTATTTATTTATGAAAGAAACCTTGGAGCTTAA 2768
443 uAsnValIleAsnGluValITrpAsnGluLeuTyrLeuArgSerPhePheGlnGluIleG1 463
2769 GAATGAGATTAAGATTAAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTA 2828
463 uValIlySerG1yGlnThrTyrPheLysMeCh1sAspLeuIleH1sAspLeuAlaThrSe 483
2829 AGTTAAATCTGGTCAAACTTATTTCAAGATGATTCATTCATTCATTCATTCATTCATTC 2888
483 rLeuPheSerAlaSerThrSerSerSerSerSerSerSerSerSerSerSerSerSerSer 503
2889 TCTAATTTTGGGACAGACATCAAGGACGATATCCAGAAATATATGTAATTAATTAATTA 2948
503 eHisMetSerIleG1yPheThrLysValIleSerSerTyrSerLeuSerH1sLeuG1 523

2949 ACAATATGATGTCATGCTGTTCACTAAAGTGATATCTTACTCTCTTCCACTTGCA 3008
523 nLysPheValSerLeuArgValaLeuAsnLeuSerAspIleLysLeuLysG1nLeuProSe 543
3009 GAAGTTTGTCTGTGGGGTGTCTTAATCTAAGTACATTAACCTTAAGACATGATCCGTC 3068
543 rSerIleG1yAspLeuValH1sLeuArgTyrLeuAsnLeuSerG1yAsnThrSerIleAr 563
3069 TTCAATGAGAGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTCG 3128
563 gSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuH1sG1yCy 583
3129 TAGCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTGCAACCTTGTATCTACAGGCTG 3188
583 eHisSerLeuCysGysLeuProLysGluThrSerLysLeuG1ySerLeuArgAsnLeuLe 603
3189 TCATTCATCTTGTGTGTGTGCCAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 3248
603 uLeuAspG1yCysTyrG1yLeuThrCysMetProProArgIleG1ySerLeuThrCysLe 623
3249 ACTTGATGTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3308
623 uLysThrLeuSerArgPheValIleG1yIleGlnLysLysSerCysGlnLeuG1yGluLe 643
3309 TAAGACTTAAGTATGATTTGGTGGAAATTCAGAAAGAAAGAAAGAAAGAAAGAAAGAA 3368
643 uArgAsnLeuAsnLeuTyrG1ySerIleGluIleThCh1sLeuGluArgValaLysAsnAs 663
3369 ACGAAACCTGAATCTTATGCTCTCAATTTGAATACCCATCTTGAGAGAGTGAAGATGA 3428
3429 TATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTATTAACATGA 3488
663 pMeAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuH1sSerLeuSerMeLys 683
683 sTrpAspAspAspGluArgProArgIleTyrGluSerGluLysValIleGluVala 703
3489 ATGGAGTACCATTAACGTCACGATATATGATGATGATGATGATGATGATGATGATGATG 3548
703 aLeuLysProH1sSerAsnLeuThrCysLeuThrIleArgG1yPheArgG1yIleArgLe 723
3549 TCTCAACCAACATCTCCATCTGATCTGTTTAACATCAGGGGCTTCAGAGAAATCCGCT 3608
723 uProAspTrpMetAsnH1sSerValLeuLysAsnValaSerIleGluIleIleSerCy 743
3609 CCCAGACTGATGATCACTCACTGTTGAAAAATGTTGCTCTTGTGAATCAATCAAGTTG 3668
743 eLysAsnCysSerCysLeuProProPheGluGluLeuProCysLeuLysSerLeuGluLe 763
3669 CAAAACTGCTCATGCTTAACCACTTGTGTGAGCTGCTTGTCTTAAAAAGTCTTAGAGTT 3728
763 uTrpArgG1ySerAlaGluValaGluTyrValaAspSerG1yPheProThrArgArgArgPh 783
3729 ATGAGAGGGGCTCTGGGAAAGGAGTATGTTGATTCGATTCCTCAAGAAAGAGGTT 3788
783 eProSerLeuArgLysLeuAsnIleArgGluPheG1yAsnLeuLysG1yLeuLeuLysLys 803
3789 TCCATCTCTGAGAAAACTTAATATATACGGAATTTGATATGTAAGGATTTGCGAAAAA 3848
803 eGluGluGluGluGlnCysProValLeuGluGluIleGluIleLysCysCysProMetPh 823
3849 GGAAGAGAAAGGACATCCCTGCTGCTGAAGATTAAGATTAAGATTAAGATTAAGATTA 3908
823 eValIleProThrLeuSerSerValaLysLeuValaIleSerG1yAspLysSerAspAl 843
3909 TGTATTTCCAACTCTTCTTCTGTCAGAAATTTGTTAGTGGGCAAGTCAAGATGC 3968
843 aIleG1yPheSerSerIleSerAsnLeuMeCh1sLeuThrSerLeuGlnIleArgTyrAs 863
3969 AATAGTTTCAAGTTCCATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 4028
863 nLysGluAspAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLe 883

Db 4029 CAAAGAGATCTTCACTCCAGAGAGATGTTCAAAAGCCTTCGMAATCTCAATACTT 4088
Qy uAsn1eSerPheTyrPheAsnLeuIleuProThSerLeuAlaSerLeuAsnAl 903
Db 4089 GAATATCTCTTTTACTTCAATCTTTAAAGAGCTGCTTCAAGCCTGGGTAGTCTCAATGC 4148
Qy 903 aLeuIleHisLeuGluIleHisSerCysTyrAlaLeuGluSerLeuProGluGluIle 923
Db 4149 TTGGAAGCATCTGAAATTTCAATAGTTGTTATGCACTAGAGAGATCCCCGAGAAAGTGT 4208
Qy 923 llyGluIleuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCysLe 943
Db 4209 GAAAGTTTAAATTCACCTCACACAGTTATCCATTAACATGCTGAAATGCTACATATGTT 4268
Qy 943 uProGluIleuGlnHisLeuThrAlaLeuThrasnLeuSerValGluPheCysProTh 963
Db 4269 ACCGAGGAGATTGACACACCTTACACCCCTCAAAATTTATCAGTTGAGTTTGTCCAAC 4328
Qy 963 rLeuAlaIleAspArgCysGluIleGlyIleGluAspTyrTyrIleAlaHisIleP 983
Db 4329 ACTGGCCAAAGCGGTGTGAGAAAGGAAATAGAGAAAGATGTTACAAATTTGCTCACATTC 4388
Qy 983 cArgValPheIleTyr 988
Db 4389 TCGTGTGTTTATTTAT 4404

RESULT 4

US-10-647-268-5
; Sequence 5, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647, 268
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(509)
; NAME/KEY: Intron
; LOCATION: (510)..(788)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (789)..(3344)
US-10-647-268-5

Alignment Scores:

Pred. No.: 0 Length: 3347
Score: 4475.00 Matches: 883
Percent Similarity: 83.94% Conservative: 37
Best Local Similarity: 80.57% Mismatches: 66
Query Match: 87.28% Indels: 110
Gaps: 2

US-10-647-268-2 (1-988) x US-10-647-268-5 (1-3347)

Qy 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 57 ATGGCTGAAGCTTCTTCAAGTCTGTAGCAATCTGACTGTTTTCATCCAAAGGGGAA 116
Qy 21 LeuGlyLeuIleLeuGlyPheIleAspGluPheGluIleLeuGlnSerThrPheThrThr 40
Db 117 GTTGATTTGATTTCTTGTGTTTAAAGATGATTCGAAAGACTTCAAAAGCACATTTACTACA 176

Qy 41 lIeGlnAlaValLeuGluAspAlaGlnIleIleGlnLeuIleAspIleIleGln 60
Db 177 ATCCAGCTGTGTAGAAAGATGCTCAGAAAGAAAGCAATTAAGAGCAACAGCATATAGAAAT 236
Qy 61 TTPLeuGlnIleLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysIle 80
Db 237 TGGTTGCAGAAACCTCAAGTGTGTATATAGCTGACGACATCTGGAGCAAGTAA 296
Qy 81 ThrGluAlaProIleArgGlnIleIleAspIleTyrGlyCysTyrHisProAsnValIle 100
Db 297 ACTAGGACCAATTAAGACAGAAAGAAACAAATTAAGGCTTTATCATCCAAAGCTTATC 356
Qy 101 ThrPheArgHisIleIleGlyIleArgMetCysIleIleMetGluIleAspValIle 120
Db 357 GCTTTCGCTCAAGATTTGGGAAAAAGATGAAAAAGATTATGGAAGAACTAGATTAAT 416
Qy 121 AlaAlaGluAlaGlyIleIlePheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
Db 417 GCACCGGAAACGAATTAAGTTTCATTTGGCTGAAAGACTACAGAGAGCAAGTTGCTACA 476
Qy 141 ArgGlnThr 143
Db 477 CGCCAAACAGGTGCTCATCTTAGATATTTTCTAATAAAACAGCTTATATCATGAAT 536
Qy 143 143
Db 537 CATGTGTGTTGGATTTTCTAATCTAATGTTGTCTCAAGTCAAGTAGATAGTGG 596
Qy 143 143
Db 597 ATCCAGATTGAT 656
Qy 143 143
Db 657 AAAGCTGAGTTGTTTAGACATTATTAATTAACATGATTAATGTAATTCAAAAA 716
Qy 143 143
Db 717 GTGATTAATGCTGCTGCTTCTCAAGCTATCATTTGCTTTATTTGCAAAATTCCTC 776
Qy 144 144
Db 777 TTCGTTTTTTTGTGACTCTCTACTGACTGAGCCAGGTTTTGTTTAAAGAACACAA 836
Qy 152 ValTyrGlyArgAspIleGluIleAspGlnIleValIleIleValIleAsnValSer 171
Db 837 GTTTATGAAAGACAAAGAAAGATGATGATGAAATCCGATTAACATTTGATG 896
Qy 172 AsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyIleGlyIleTyr 191
Db 897 GATGCCCAACACTTTTCAATGCTCTCCCAATCTTGTATGGGGGATTAAGAAACAGACA 956
Qy 192 LeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPheHisProIleTyr 211
Db 957 CTTGCCCAATGCTCTCAATGATCAGAGATTAATGACATTTCTCCCAAAATATGG 1016
Qy 212 lIleCysValSerGluAspPheAsnGlnIleArgGluIleIleGluIleValGluSerIle 231
Db 1017 ATTTGTCTCTCGAAGATTTTAAAGAAAGGTTGATTAAGAAATTTGATGAATCTAT 1076
Qy 232 GluGluIleSerLeuGlyIleMetAspLeuAlaProLeuGlnIleIleIleIleIleIle 251
Db 1077 GAAAGAAAGTCACTTGTGTGATGATCTGCTCCTCACTCAAAAGAACTTCAGACCTTG 1156
Qy 252 LeuAsnGlyIleIleIleIleValLeuValLeuAspAspValTTPAsnGluAspGlnAsp 271
Db 1137 CTGAATGAAAAAATATTTGCTTGTCTTAGATATATTTGGAATGAAGATCAAGATAG 1196
Qy 272 TTPAlaIleLeuAlaGlnValLeuIleValGlyAlaSerGlyAlaSerValLeuThrThr 291
Db 1197 TGGCTTAAGTTACAGAAAGTGTGAAGGTTTGACCAAGTGTGCTTCTTACTTAACACT 1256
Qy 292 ThrArgLeuGluIleValGlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAsn 311

QY 580 LeuHISGLYCYSHISSErLeuCYeSLeuProLYSGIuThrSeryLeuGLYSerLeu 599
 DB 1735 CTACAAATGTCACCAAGCTTTGTTGTTGCCAAAGAAACAAAGTAACTTGGTAGTCTC 1794
 QY 600 ArgAsnLeuLeuLeuAspGLYCYeTYrGLYLeuThrCYsMetProProArgILGLYSer 619
 DB 1795 CGAAATCTTTTACTGATGTTAGCCAGTCATCTTATGACCACCAAGATAGATCA 1854
 QY 620 LeuThrCYsLeuLYSThrLeuSerArgPheValValGLYILEGLINLYSLeuSeryGLN 639
 DB 1855 TTGACATGCCCTTAAGACTTACGTCAATTTGTGTGTGA---AGGAAGAAAGTTATCAA 1911
 QY 640 LeuGLYLeuLeuArgAsnLeuAsnLeuTYrGLYSerILEGLIILEThrHisLeuGLNArg 659
 DB 1912 CTGTGTGAACCTTAAGAAACCTTAATCTCTATGCTCAATTAATCTCGCATCTTGAGAGA 1971
 QY 660 ValLYSAsnAspMetAspAlaLYSGIuLAsnLeuSerAlaLYSGIuAsnLeuHISer 679
 DB 1972 GTGAAGAAATGATAGAGACGCAAAAGACCAATTTATCTGCAAAAGGAATCTGCATCT 2031
 QY 680 LeuSerMetLYSTrAspAspAspGLYArgProArgILETYrGLYSerGLYLYSValGLN 699
 DB 2032 TTAAACATGAGTTGG---AATACCTTGGACCACATATATATGATCAGAAAGTTTAA 2088
 QY 700 ValLeuGLIuAlaLeuLYSProHISerAsnLeuThrCYsLeuThrILEArgGLYpHeArg 719
 DB 2089 GTGCTTGGAAGCCCTCAAAACCACTCCCACTGACTCTTTAAATCTATGCTTCAGA 2148
 QY 720 GLYILEArgLeuProAspTrpMetAsnHISerValLeuLYSAsnValValSerILEGLI 739
 DB 2149 GGAATTCATCTCCAGAGTGAATGATCATCTGATATTGAATAATGTCTATTTCTA 2208
 QY 740 ILEISerCYsLYSAsnCYsSeryLeuProProPheGLYGLINLYSProCYsLeuLYS 759
 DB 2209 ATTAGCAACTTCAGAAACTGCTCATGCTTACCACTTGGTGAATCTGCTTGTAGAA 2268
 QY 760 SerLeuGLINLeuThrArgLYSerILEGLIuValGLIuTYrValAsp----- 774
 DB 2269 AGCTTAGAGTTTCACTGGGGGCTGCGAGTGGAGATATTGGAAGAAAGTGAATTTGAT 2328
 QY 775 -----SerGLYpHeProThrArgArgPheProSerLeuArgLYSLeuAsnILEArg 792
 DB 2329 GTTCATCTCGAATTCCTCCCAAGAAATAGATTTCATCTTGAGAAACTTGATATATG 2388
 QY 793 GluPheGLYAsnLeuLYSGIuLeuLYSGLYGLIuGLYGLINLYSProValLeu 812
 DB 2389 GACTTGTGATGCTGAAAGATTTGCTGAAAGAAAGAAAGAGCAATTCCTGTGCTT 2448
 QY 813 GluGLIuILEGLIuLYSCysProMetPheValILEProThrLeuSerSeryValLYS 832
 DB 2449 GAAGAGATGATTAATTACAGATGCCCTTTTCTG-----ACCTTTCT----- 2490
 QY 833 LysLeuValValSerGLYAspLYSAspAlaILEGLYpHeSerSeryILESerAsnLeu 852
 DB 2491 -----CTAATCTT 2499
 QY 853 MetAlaLeuThrSerLeuGLINILEArgLYrAsnLYSGIuAspAlaSerLeuProGLIu 872
 DB 2500 AGGGCTTCTACTTCCCTCAGAAATTTGCTTAATTAAGTAGCTTACTTCAATTCAGAA 2559
 QY 873 MetPheLYSserLeuLAsnLeuLYSTYrLeuAsnILESerPheTYrPheAsnLeuLYS 892
 DB 2560 ATCTTCAAAACCTTGCAAATCTCAATCTTGAATCTCTCGGTCGAATATCTCAAA 2619
 QY 893 GluLeuProThrSerLeuLAserLeuAsnAlaLeuLYSHISerLeuGLIuILEHISerCYs 912
 DB 2620 GACTGCTTACGAGCTTGGCTAGCTGAATGCTTGAAGTCTAAATTTCAATTTGTGT 2679
 QY 913 TYrAlaLeuGLINserLeuProGLIuGLIuValLYSGIuLeuILESerLeuThrGLIN 932
 DB 2680 TGGCAGACTAGAGAGTCTCCTTGAGAAAGGGCTGGAAGTTTATCTTCACTCAGAGTTA 2739

QY 933 SerILEThrTYrCYsGLINLeuLeuGLINLYSLeuProGLIuGLYLeuGLINHISerThra 952
 DB 2740 TTTGTTGAACACTGTAAACATTCCTAAATGTTTACGAGGGATTTGCAGACCTTAACACC 2799
 QY 953 LeuThrAsnLeuSerValGluPheCYsProThrLeuAlaLYSArgCYsGLIuLYSGLYILE 972
 DB 2800 CTCACAAGTTTAAATTTCCGGGATGTCCACAACATGATCAGGCGGTGTGAGAAAGGAAT 2859
 QY 973 GLYGLINAspTrpTYrLYSILEAlaHISILEProArgValPheILETYr 988
 DB 2860 GGAAGAGACTGGCACAAATTTCTCATCTTCTTAATGTGAATATATAT 2907
 RESULT 6
 US-10-360-522-51
 ; Sequence 51: Application US/10360522
 ; Publication No. US20030221215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allefs, Josephus J.H.M.
 ; APPLICANT: Vossen v.d., Edwin A.G.
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
 ; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
 ; FILE REFERENCE: U 014413-9
 ; CURRENT APPLICATION NUMBER: US/10/360,522
 ; PRIOR FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: EP 02075565.8
 ; PRIOR FILING DATE: 2003-02-07
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 51
 ; LENGTH: 3260
 ; TYPE: DNA
 ; ORGANISM: Solanum bulbocastanum
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(3260)
 ; OTHER INFORMATION: /note="RGCI-blb"
 US-10-360-522-51
 Alignment Scores:
 Pred. No.: 0 Length: 3260
 Score: 3648.00 Matches: 745
 Percent Similarity: 76.58% Conservative: 92
 Best Local Similarity: 68.16% Mismatches: 143
 Query Match: 71.15% Indels: 114
 DB: 17 Gaps: 9
 US-10-647-268-2 (1-988) x US-10-360-522-51 (1-3260)
 QY 1 MetaGLIuAlaPheLeuGLINValLeuLeuAspAsnLeuThrCYsPheILEGLINLYS 20
 DB 1 ATGGCTGAAGCTTTCCTTCAAGTTCTGTATATATCATCTTTTTCATTCAGAGGGA 60
 QY 21 LeuGLYLeuILEGLIuLYSPheLYSAspGLINPheGLIuLYSLeuGLINserThrPheThr 40
 DB 61 CTTCGATTGTTTGTGTTTCGAGAGAGATTAAAAAATTTCAAGATGTTTTCATG 120
 QY 41 ILEGLINAlaValLeuGLINAspAlaGLINLYSGLINLeuLYSAspLYSAlaILEGLIuAsn 60
 DB 121 ATCCAGAGCTGTGCTAGAGATGCTCAAGAAAGCACTGAAGTCAAGGCAATTAAGAAC 180
 QY 61 TrpLeuGLINLYSLeuAsnAlaAlaLYrGLIuAlaAspArgILEuAspGLUCYLYS 80
 DB 181 TGGTTACAGAAATCTCAATGTGCTGCATATGAAAGTTGATGACATCTTGGATGACTGTA 240
 QY 81 ThrGLIuAlaProILEArgGLINLYSAsnLYSTYrGLYCYSTYrHisProAsnValILE 100
 DB 241 ACTGAGGCA---GCAAGATTCAAGCAGGCTGATTTGGGCGGTATTCATCCAGACATC 297
 QY 101 ThrPheArgHISLYSILEGLYLYSArgMetLYSILeMetGLINLYSLeuAspValILE 120
 DB 298 ACTTCTGTTCACAGGTGGGAAAGAAAGAAATGAAGAAATGATGAAGAAATCTAGATGCAAT 357

121 AAlaGluArgIleLeuPheHISLeuAspGluArgThrIleGluArgGlnValAlaThr 140
141 ArgGlnThr----- 143
418 CGGCAAAC-AGGTGCTCATCTTAATTTTAAACAAATAGATTAACAATTGCG 476
413 ----- 143
477 AGAAACGAAGAAATTATATTCATTTTATTTGGCAATTATCAAAAGTCATTTGTGTT 536
143 ----- 143
537 TTAAGCTGGGGGAGTTTCAAAATATTTCTAGTCTTAATGTTTGTCTACCTCACTCA 596
143 ----- 143
597 GCATGATTTTCTCAATCCTTCACTTCAATCCCTCTACTGTGCAAAATATCTTCTATTT 656
144 -----GlyPheVal 146
657 TTCTGTGACTCTTAATAGCTTGAATGTAACACATTTCTGTTGAGCAGAGTTTGT 716
147 LeuAsnGluProGlnValIleValArgAspGluLeuValIleValIleLeu 166
717 TTAACGAGCCAAAGTTTATGGAAGGAAAGAGAGATGATAGTAAATCTTG 776
167 IleAsnAsnValSerAsnAlaGlnThrLeuProValIleuProIleuGlyMetGly 186
777 ATAAACAATGTTAGTTATCCGAAGAGTCCCAATCTCCCAATCTGTGATGGGGGA 836
187 LeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPhe 206
837 CTAGAAAGACGACTGAGCCCAATAGTCTTCAATGATCAAAAGATTAATCTGAGATTTTC 896
207 HisProIleIleThrIleCysValSerGluAspPheAsnGluValArgLeuIleGlyGlu 226
897 AATCAAAAGATATGGGTTGTGTCTCAGATGATTTTGTATGAAAGAGTTGATTAAGCA 956
227 IleValGluSerIleGluGluLeuSerLeuGlyMetAspLeuValProLeuGlnLeu 246
957 ATTGAGAAATCTAATTGAAGAAAGTCACTGGGTGATGATGAGTGGCTCCCTCAGAAA 1016
247 LysLeuArgAspLeuLeuAsnGlyLysLysThrLeuValIleuAspAspValIleTrpAsn 266
1017 AAGCTTCAGAGTGTGTAATGGAAGAAAGATCTTCTGTTTGGATGATGTTGGAT 1076
267 GluAspGlnAspLysThrAlaLysLeuArgGlnValIleLysValAlaSerGlyAla 286
1077 GAAGATCAAGAAAGTGGGATTAATTTAGACAGATTAAGATTTGAGCTAGTGTCT 1136
287 SerValLeuThrThrThrArgLeuGluLysValGlySerIleMetGlyThrLeuGlnPro 306
1137 TCAATTTCAATTACTACTCGTCTTGAAAAAATGGATCAATTATGGAACCTTTGCACTA 1196
307 TyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArgAlaPhe 326
1197 TATCAGTATCAAAATTTGTCTCAAGAAAGTGTGTGTGTCTCAACCAACGTGCATTT 1256
327 GlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLysLys 346
1257 TGCACCAACCAAGCAAGTCTTAATCTTAATGAAATCGAAGAGAAATGTGAGAAA 1316
347 CysGlyGlyValProLeuAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlu 366
1317 TGTGGGGGTGGCTCTAGACAGCCAAACTCTGAGGCTTTTACGCTTCAAGAGGGA 1376
367 GluArgGlnTrpGluHisValArgAspSerGluIleTrpLysLeuProGlnGluGluSer 386
1377 GAAAGTGAATGGGAACATGTGAGATGTGATGATTTGAAATTTTCACTCAAGATGAAAT 1436

387 SerIleLeuProAlaLeuArgLeuSerTyrrHisIleuProLeuAspLeuArgGlnCys 406
1437 TCTGTTTGCCTGCCTGAGCTGAGTATCATCTTCCACTGATTTGAGCAATGTT 1496
407 PheThrTyrrCysAlaValPheProLysAspThrGluMetGluValArgLysLeuIleSer 426
1497 TTGGATATTTCCGAGATATTTCCAAAGACACAAATAAGAAATATCTCATGCT 1556
427 LeuTrpMetAlaHisGlyPheIleuSerLysGlyAsnLeuGluLysValGly 446
1557 CTCTGATGCAACACAGTTTCTTTATCAAAAGAAACATGAGCTAGAGATGTGGGC 1616
447 AsnGluValIleProAsnGluLeuTyrrLeuArgSerPhePheGlnGluIleGluValLysSer 466
1617 AATGAAGTATGGAATGAAATTAATTAATCTGAGTCTTTTCCAAAGATTAAGATTAATCT 1676
467 GlyGlnThrTyrrPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSer 486
1677 GGTAAACTTATTTCAAGATCATGATCTCATGATGATTTGGCTACATCATGTTTCA 1736
487 AlaSerThrSerSerSerAsnIleArgGluIle----- 497
1737 GCAGGCGCATCAAGACAGAAAGTATACGCCCAATTAATGTAAGATGAAGATGATGAT 1796
498 ---IleValGluAsnTyrrIleHisMetMetSerIleGlyPheThrLysValIleSerSer 516
1797 TTCAATTTGAACAATTTAAGATATATGATGATGATGATGATGATGATGATGATGATGAT 1856
517 TyrrSerLeuSerHisLeuGlnLysPheValSerLeuArgValIleAsnLeuSerAspIle 536
1857 TACTCTCCTTCCTTTTAAAGAGTGTGTCTGTTAAGGGGCTTAACTGAATCA 1916
537 LysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrrLeuAsnLeu 556
1917 GAATTTGACAGTATACGCTCTTCCTGAGAGATCTAGTAACTTAATGATCTTGAAGCTG 1976
557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
1977 TCTGATAT---AAATTTGATGATCTTCCAAAGAGTGTGCAAGCTTCAAAATCTGCAG 2033
577 ThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGluThrSerLysLeu 596
2034 ACTCTTGAATCAATTAATTTGCACTGACTCTTCTGTTTGGCGAAACAAACAAAGTAT 2093
597 GlySerLeuArgAsnLeuLeuAspGlyCysTyrrGlyLeuThrCysMetProProArg 616
2094 TGTATCTCCGGAATCTTGATCTGATCAGT---CCATGACTTCTATGCCACCACTGA 2150
617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValAlaGlyIleGlnLysLys 636
2151 ATAGGATTTGATGATGCTTAAACATGACCTAGCTTAATCTTGTGTGAGC---GAGAGGAA 2207
637 SerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrrGlySerIleGluIleThrHis 656
2208 GGTATATCAACTGGTGAATCTAGAAATTTAACTCCGTGTGCAATTTCAATCACAT 2267
657 LeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsn 676
2268 CTTAAGAGAGTGAAGAAATGATATGAGGCAAAAGCAATTTATCTGCAAAAGCAAT 2327
677 LeuHisSerLeuSerMetLysTrpAspAspAspGluArgProArgIleTyrrGluSerGlu 696
2328 CTACACTCTTAAACATGATGATGGAT-----AGACCAACAGATATGATCCGAA 2378
697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
2379 GAAGTTAAAGTCTGGAAGCCCTCAAAACCATCCATCTGAATATTTTGAATCATTT 2438
717 GlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValIleLysAsnValVal 736
2439 GACTTCTGTGATTTCTGTCTCCCTGACTGATGATATCATCAGTTTGAAGAAATGTTGTC 2498
737 SerIleGluIleIleSerCysLysAsnCysSerCysLeuProPheGlyGluLeuPro 756

[illegible]

Db	1918	CCCAAGGATCCAAATGGAAGAAAGAAAGCTATCTCTCTCGATGGCGATGTTT	1977
Qy	433	eIleuSerIySgIyAsnIeuGIuIeuGIuAsnValGIyAsnGIuValTrpAsnGIuIe	453
Db	1978	TCCTTTATCAADAGGAACAATGAGAGCTTAGAGAGTGGGGGATGAAGATGGAAGAATT	2037
Qy	453	uTyIeuArGSeRhePheGInGIuIIeGIuValIySeRGIyGIInThyRheIySMe	473
Db	2038	ATACTTGAGGCTCTTTTCCAAAGAGATTGAAGTTAAAGATGGTAAACCTTAATTCAGAT	2097
Qy	473	ChIAspIeuIleHIsApIeuIaIThrSerIeuPheSerAlaSerThSerSerSae	493
Db	2098	GCAATGATTCATCCATGATTTGGCAACAATCTGTGTTTTCAGCAAAACATCAACACACAA	2157
Qy	493	nIleArGSIuIleIleValGIuEnTyIleHIsMeMetSerIleGIyPheThIySVal	513
Db	2158	TATCCGTGAATTAATAATAACACACTTACACACATATGATGTCATTGGTTTCGCCAGAT	2217
Qy	513	IValSerSerTySerIeuSerThIleuGIuIySPhenValSerIeuArGIuIeuAnIe	533
Db	2218	GGTGTGTTTTTACACTCTCCCGCTTGAAGAAAGTTATCTCGTTAAGATGGCTTAATCT	2277
Qy	533	uSerAspIleIySleuGIuIeuProSerSerIleGIyAspIeuValHIsIeuArGIy	553
Db	2278	AGGTGATTCGACATTTAATAATGATTCACATCTCCATTGGAGATCTAGATCAATTAAGATA	2337
Qy	553	rIeuAsnIeuSerGIyAsnThSerIleArGSeIeuProAsnGIuIeuCySlySleuGI	573
Db	2338	CTTGAACTGTAATGGC--ACTGGCATGGCATAGCTTCCAAAGCATTTATGCAAGCTTCA	2394
Qy	573	nAsnIeuGIInThIeuAspIeuHIsGIySValSereIeuCySleuProIySGIuTh	593
Db	2395	AAATCTGCAAACTCTGATCTTACAAATGTCACCAACCTTGTTGTGGCCAAAGAAAC	2454
Qy	593	rSerIySleuGIySerIeuArGAsnIeuIuIeuAspGIyCyStryGIyIeuThrCySMe	613
Db	2455	AAGTAACCTTGTAAGTCTCGAAATCTTTTATGTAAGTAGACCAATGATGACTGTAT	2514
Qy	613	tProProArGIleGIySerIeuThrCySleuIyThIeuSerArPheValGIyIle	633
Db	2515	GCCACCAAGATAGGATCATTTGACATGCTTAAAGACTCTAGGTCATTTGTTGTGGA--	2572
Qy	633	eGIuIySleuSerCySInIeuGIyGIuIeuArGAsnIeuAsnIeuTyGIySerIleGI	653
Db	2573	-AGGAGAAGAGCTTATCAACTGGTGAAGTAAGAAACCTTAATCTTATGGCTCAATTA	2631
Qy	653	uIleThnHIsleuGIuArGIyValIySAsnAspMetAspAlaIySGIuIleAsnIeuSerAl	673
Db	2632	AATCTCGATCTTGAGAGAGTAAGAAATGATAAGACGCAAAAGAACCAATTTATCTGC	2691
Qy	673	aIySGIuAsnIeuHIsSerIeuSerMetIySTrPAspAspGIuArGIProArGIleTy	693
Db	2692	AAAGAGGATCTGATCTTTAGACATGAAGTGG--AAATAACTTTGGACCACATATATA	2748
Qy	693	rGIuSerGIuIySValGIuValIeuGIuIleuIySProHIsSerAsnIeuThrCySle	713
Db	2749	TGATTCAGAGAAGATTAAAGTCTTGAAAGCCCTCAACACACATCCAAATCTGACTCTT	2808
Qy	713	uThrIleArGIyPheArGIyIleArGIeuProAspTrpMetAsnHIsSerValIeuIy	733
Db	2809	AAAATATCTATGGCTTCAGAGAAATCCATCTCCAGATGATAAATCACTACAGATTATGAA	2868
Qy	733	AsnValIValSerIleGIuIleIleSerCySlySAsnCySereCySleuProProPheGI	753
Db	2869	AAATATTGTCTATTTCTAATTTAGCAACTTCAGAAATCTCTCATGCTTACCACTTTGG	2928
Qy	753	yGIuIeuProCySleuIySerIeuGIuIeuTrpArGIySerAlaGIuValGIuTyAr	773
Db	2929	TGATCTGCTTGTCTTAAGAAAGTCAAGATTACACTGGAGGCTCTGCCGATGTGAAGATGT	2988
Qy	773	lAsp-----SerGIyPheProThrArGIArGIrPheProSerIe	786


```
Db      2889  TGAAGAAAGTGAATGATGTTTCATTTCCGATTCCTCCCAAGAAATAGATTTCATCTT 3048
Qy      786   uAArgLysLeuAniIleArgGluPheGlyAsnLeuLysGlyLeuLeuLysGluGlyGly
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3049  GAGGAAATCTGATATATGAGACTTTGGTAGCTGAAAGATTTGCTGAAAAAGAAAGAGAGA 3108
Qy      806   uGluGlnCysProValIleuGluGluIleGluIleLysCysCysProMetPheValIlePr 826
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3109  AGAGCAATTCCTCGTGTGAAGATGATATTCACGAGAGGCTCTTTCTG----- 3160
Qy      826   cThiLeuSerSerValLysLysLeuValValSerGlyAspLysSerAspAlaIleGlyPh 846
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3161  -ACCTTTCT----- 3169
Qy      846   eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgLysAsnLysGluAs 866
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3170  -----TCTATCTTAGGGCTCTTACTTCCTCCCTCAGAAATTCCTAATAAAGTAGC 3219
Qy      866   pAlaSerLeuProGluGluMetPheLysSerLeuAlaSerLeuLysLysLysLysLysLys 886
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3220  TACTTCATTCCTCCAGAGAGATGTTCAAAAACCTTGCAAAATCTGCAAAATCTGCAATCTC 3279
Qy      886   rPheThrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHi 906
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3280  TCGGTGCAATATATCTCAAGAGCTGCTACCAAGCTTGCTGAGTCTGAAATGCTTTGAAAAG 3339
Qy      906   sLeuGluIleHisSerCysTyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLe 926
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3340  TCTAAAAATTCATATGTTGTGTGGCACTAGAGAGTCTCCCTGAGAGAGGCTGGAAGGTTT 3399
Qy      926   uLleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCysLeuProGluGly 946
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3400  ATCTTCACCTCAGACGTTATTTGTTGAACACTGTAACATGCTAAATGTTTACCAAGAGGG 3459
Qy      946   YLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLys 966
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3460  ATTGAGACACCTTAACACCTCACAAGTTTAAATTTGGGGAGATTTTACCAACATGATCAA 3519
Qy      966   sArgCysGluLysGlyIleGlyLysAspTyrTyrLysIleAlaHisLysLeuProGlyValPh 986
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      3520  GGGGTGTGAGAGGAGATGAGAGAGACTGACCAAAATTTCTCATTCCTTAATGTGAA 3579
Qy      986   eLleTyr 988
          ::::::::::
Db      3580  TATATAT 3586
          ::::::::::

RESULT 8
US-10-360-522-50
; Sequence 50, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allels, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 5191
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence of
; OTHER INFORMATION: 5.2 kb Sca I genomic DNA fragment of S.
; OTHER INFORMATION: bulbocastanum BAC SPB 4 present in pRG2-b1b
; US-10-360-522-50
```

```
Alignment Scores:
Pred. No.: 0
Score: 3638.50
Percent Similarity: 68.03%
Best Local Similarity: 61.65%
Query Match: 70.97%
DB: 17
Gaps: 9

US-10-647-268-2 (1-988) x US-10-360-522-50 (1-5191)
Qy      1   MetAlaGluAlaPheLeuGlnValIleuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1191  ATGCTGAGAGCTTCATTCAGATCTGCTGAGACATCTCATCTTCTCCCAAGGGGAA 1250
Qy      21   LeuGlyLeuLeuLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1251  CTTGTAATTCCTTTTGGTGTTCAGATGAGTCCAAAGGCTTTCAAGCATGTTTCTACA 1310
Qy      41   ILeGlnAlaValIleuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsn 60
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1311  ATTCAAGCCGTCCTTGGAAGTGTCTCAGAGAGCACTCAACACAAAGCCCTGAAATAT 1370
Qy      61   TrpLeuGlnLysLeuAsnAlaAlaAlaTyrGluAlaAspAspIleLeuAspGluCysLys 80
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1371  TGGTTGCAAAAATCAATATGCTGTACATATGAAATGATGATCATCTTGATGAAATATATA 1430
Qy      81   ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1431  ACCAAGGCC--ACAAAGTTCTCCAGCTGAATATATGAGCGCTTATCATCCAAAGTTATC 1487
Qy      101  ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1488  CCTTTCCTCACAAGATCGGGAAGATGAGCAAGATGAAGAAATCTAAAGGCAATTT 1547
Qy      121  AlaAlaGluArgLysLysPheHisLeuAspGluArgThrIleGluLysGlnValAlaThr 140
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db      1548  GCTGAGAAAGAAAGAAATTTTTCATTGACAGAAAAAATTTGAGAGACAAAGCTGTAGA 1607
Qy      141  ArgGlnThrGly----- 144
          ::::::::::
Db      1608  CGGAAACAGGTACTCATCTTAATATGATTAACAACACTAAGTTTATTCATTTTTT 1667
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1668  TGGCAATTATCAATTCAGAAAAGGTTAAATATATCATGTCATGCTAATAATAGTGA 1727
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1728  TATATACCTCTCGTTGTACTTTGATCTGATCTGAATATATCTTGAATCTGGCAAGCTCAGAA 1787
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1788  TCAATTAATCAACCCCAACTTTTAATATCTGATATCTTTAGAAAATCCACCTGTACT 1847
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1848  CATCACTACCACTTCCTTTGCTTTGAATCTTTCTTACTATAAATCTGGAACT 1907
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1908  CGATCCGTTTGTCTTTCTTAACAAGAGCTCAGAGAAAAGAGTTTCTTATTTCTG 1967
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      1968  TTTCTGTGTGTGCTGACTTGAGTCTTAATCCCATTAATAAAGGAGATGTTATCCCA 2027
          ::::::::::
Qy      144  ----- 144
          ::::::::::
Db      2028  ACGAGGTAGCTTTCTGACAGCTGACTGTAATTTTGTCTAACAAAGAAAAAAGAGA 2087
          ::::::::::
Qy      144  ----- 144
          ::::::::::
```

Db 2088 TTAGACATGTTTTCTTGTGATTGATTAGCGATTCTTTGAGGTGAAACATAGCG 2147
Qy 144 ----- 144
Db 2148 GATATATTGGACCAAAAGTAGAATGGGTATATATTAAAGTATTTTGTGATGAAACAGAG 2207
Qy 144 ----- 144
Db 2208 TATATGTGGCAAAATATCTCTATTTTCTGTGTCTCTAATGAGTTTGAATGAAATA 2267
Qy 145 -----Phe-ValLeuBngluProGluValTyrGlu 154
Db 2268 TATTTCTCATGTGACATTTGCTTGACACGAGTTCTGTATTAAACCGACCGAGTTTATGG 2327
Qy 154 YARAspRlysgluysaspRlyuilevalysileuileasnasValiseraasVal 174
Db 2328 AAGAGACAAAGAAAGATGAGATAGTAATAATCTTAATAACAAATGTTAGATGCCCA 2387
Qy 174 nThrLeuProValleuProileuGlyMeGlyGlyLeuGlylysthrThrLeuVal 194
Db 2388 ACACCTTTCAGTCCCTCCCAATCTTGATGGGGGATTTAGGAAACAGACTCTTGCCCA 2447
Qy 194 nMetValPheasnasRglnatgValilegluHisPheHisProlysiLeTrrIleCyVa 214
Db 2448 AATGGTCTTCATGACACGAGAGATTACTGACATTTCCATTCCAAAATATGCAATTTGTGT 2507
Qy 214 lSerGluaspPheasngluysargleuileysgluilevalgluserillegluGlu 234
Db 2508 CTGCGAAATTTTATGAGAAAGGTATATAAAGCAATTTGATGATTTTGAAGAGAG 2567
Qy 234 sSer----LeuGlyGlyMeAspLeuValaProleuGlnlysiysLeuAspLeuVal 253
Db 2568 GCCACTACTTGSTGAGATGAGACTTGCTGCCACTCAAAAGAGCTTCAGAGTTGCTGAA 2627
Qy 253 nGlyLyyslysthrLeuValleuaspasPvalTrrpasngluaspRlyuileysTrrP 273
Db 2628 TGGAAAAAGATACCTTGCTGTCTTATGATGATGTTTGGATGAATGAACAGATCAACAG 2687
Qy 273 alyBleuBngluValleuysvalGlyValaserglyValaservalleuThrThrThr 293
Db 2888 TAAATTTAAGACAGCTTGAGAGGTGGAGCAAGTGTCTTCTGTCTTCAACACATCACTG 2747
Qy 293 glLeuGlyValaGlyserilleMeGlyThrLeuGlnProTrrGluLeuSerAsnLeu 313
Db 2748 TCTTGAAGAAAGTTGGATCAATTTATGGAAACATTCGAAACATTTGAACTGTCAATCTG 2807
Qy 313 rGlnGluaspCystrPLeuLeuPheMeGlnatgValaPhegluHisngluGluileas 333
Db 2808 TCAAGAAAGATTGGTGTGTTGTTCAACAGTGCATTTGAGACACCAAGAAAGAAATGAA 2867
Qy 333 nLeuBngluValaileglylyBngluilevallyBlyscysgluGlyValaProleuVal 353
Db 2868 TCCAAACCTTGTGCAATCGAAAGAGATTGTGAAAAAGTGTGTGTGCTCTTAGC 2927
Qy 353 aAlaIsthrLeuGlyGlyIleLeuArgPheLyysargGluGluatgGlnTrrPgluHisVa 373
Db 2928 AGCCAAACCTTGGAGGTATTTTGTCTTCAAGAGAAAGAAAGAGATGGAAACATGT 2987
Qy 373 lArgaspserGluileTrrPlyBleuProGlnGluGlnuserilleuProalaleuAr 393
Db 2988 GAGAGACAGTCCGATTGGATTGGCTTCAAGATGAAAGTTCTATTTGCGCTGCCCTGAG 3047
Qy 393 glLeuSerThrHisBleuProleuaspRlyuileGlyscPheThrTrrCyValaValPh 413
Db 3048 GCTTAGTACATCAACTTCACCTTGATTGAAACAAATGCTTGTGGTATTTGGCGTGT 3107
Qy 413 eProlyaspThrGluMeGlyuileGlyAsnleuileserleuTrrPMeAlaHisgluPh 433
Db 3108 CCCAAAGATGCCAAATGAGAAAGAAAGAAAGTAAATCTCTCTGATGGCGCATGTTT 3167
Qy 433 eIleuSerlysglyAsnleuGluLeuGluasValGlyasngluValTrrpasngluLe 453
Db 3168 TCTTTTATCAAAAGGAAACATGAGCTAGAGGATGTGGCGATGAAAGTATGAAAGAAAT 3227

Qy 453 uTrrLeuArgSerPhePheGlnGluileGluValyserglyGlnThrTrrPheLyMe 473
Db 3228 ATACTTAGAGCTTTTTTCCAAAGAGATTGAAGTTAAAGATGTAAGTATTTTCAACAT 3287
Qy 473 nHisaspRlyuileHisaspLeuAlaThrSerleuPheSerAlaSerThrSerSerSer 493
Db 3288 GCATGATCTCATGATGATTTGGCAACATCTCTGTTTTCACAAACACATACAGACGAA 3347
Qy 493 nIleargGluileilevalgluasentTrrIleHisMeMetSerillegluPheThrlyVa 513
Db 3348 TATCCGTGAATTAATAATTAACACAGTTACACACATATGATGTCATTTGTTGCGCGAGT 3407
Qy 513 lValSerSerTrrSerleuSerHisleuGlnlyPheValSerleuArgValleuAsnLe 533
Db 3408 GGTGTTTTTTTACACTCTTCCCTCGGAAAGATTTATCTCGTTAAGAGCTTAACT 3467
Qy 533 uSerAspRlyleuysleuysGlnleuProSerSerilleGlyaspLeuValHisleuArgTy 553
Db 3468 AGGTGATTCGACATTTAATAATGTTACCATCTTCATTTGAGATCATTAAGATA 3527
Qy 553 rLeuAsnleuSerGlyasnthrPserilleargSerleuProasngluLeuCyBlyBleuG 573
Db 3528 CTTGAACCTGTATGCG--AGTGGCATGCGTATGCTTCCAAAGCAATTATGCAAGCTTCA 3584
Qy 573 nAsnleuGlnThrLeuaspRlyuileGlyCyHisSerleuCyBlyeupProlysgluTh 593
Db 3585 AAATCTGCAACCTTTGATCTCAATATGCAACCAAGTTTGTGTTGCCAAAGAAAC 3644
Qy 593 rSerlyBleuGlySerleuArgAsnleuLeuLeuaspRlyCystrGlyLeuThrCyMe 613
Db 3645 AAGTAACTTGATGTCTCCGAAATCTTTTACTTGATGTGAGCCAGTCACTTGAT 3704
Qy 613 tProProarglleuysleuThrCyBlyeulysThrLeuSerArgPheValValGlyI 633
Db 3705 GCCACCAAGATGAGATCATTTGACATGCTTAAACCTTAGCTCAATTTGTGTGGA-- 3762
Qy 633 eGlnlyBlyserCyBngluGluGlyGluLeuArgAsnleuBngluTrrGlySerilleG 653
Db 3763 -AGGAAGAAAGTTATCAACTTGATGAACTTAGAAACCTTAATCTTATGCTCAATTA 3821
Qy 653 uIleThrHisleuGluArgValyAsnaspPheAspAlaLysgluAlaAsnleuSerAl 673
Db 3822 AATCTCGCATCTTGAGAGAGATGAAGATGATGAAGACGCAAAAGACCAATTTATCTGC 3881
Qy 673 alyGluBngluHisserleuSerMetlystrraspasPgluargProargilleTy 693
Db 3882 AAAAGGAAATCTGATCTTTTAAAGCATGAGTTGG--AATTAATTTGACACATATATA 3938
Qy 693 rGluSerGluysValGluValleuGluAlaLeuLyProHisserAsnleuThrCyBle 713
Db 3939 TGAATTCAGAAAGATTAAAGTGTGTAAGCTTGAAGCTTCAACACATCTCAATCTGACTT 3998
Qy 713 uThrIleargGlyPheargGlyIleargLeuProaspTrrPMeAsnHisserValleuLy 733
Db 3999 AAAATCATGAGCTTCAGAGAAATCCATCTCCAGAGATGATGATCACTCAGATTGAA 4058
Qy 733 asnValValserilleGluileIleSerCyBlyasncysSerCyBleuProProPheG 753
Db 4059 AAATATTGTCTCTATTCTTAATTACCACTTCAGAAACGCTCAAGCTTCAACACCTTTGG 4118
Qy 753 yGluLeuProCyBleuysSerleuGluLeuTrrPargGlyserAlaGluIleTrrVa 773
Db 4119 TGATCTGCTGTGTAGAAAGTCTTAGAGTTACACTGGGGAGTCTGGAGATGGAGTATGT 4178
Qy 773 lAsp-----SerGlyPheProThrArgArgPheProSerLe 786
Db 4179 TGAAGAGTGAATATGATGTTGATCTTGATTCGCCCAAGAAATAGTTTCCATCTT 4238
Qy 786 uArgLyysleuBngluileargGluPheGlyAsnleuLyGlyleuLeuyslysgluGly 806
Db 4239 GAGGAAACCTTGATATATGCGACTTGGTATGCTGAAGGATTTGCTGAAGAAAGAGAGA 4298

```

QY 806 uGluGlnCysProValLeuGluGluLeuGluLeuGluCysCysProMetPheValIlePr 826
Db 4299 AGACCAATCCCTGCTGTTGAAGAGATGATTAATTCACGAGGCGCTTTCTG----- 4350
QY 826 cThLeuSerSerValLysLysValValSerGlyAspLysSerAspAlaIleGlyPh 846
Db 4351 -ACCTTCTCT----- 4359
QY 846 eSerSerLysSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTyrAsnLysGluAs 866
Db 4360 -----TCTATCTTAGGGCTTACTTCCCTCAGAAATTCCTAATAATAAGTAGC 4409
QY 866 pAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSe 886
Db 4410 TACTTCATTTCCAGAGAGATGTTCAAAAACCTTGCAATCTCAAAATCTTGACAAATCTC 4469
QY 886 rPheTyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysH 906
Db 4470 TCGGTGCAATATCTCAAAAGAGCTCCCTACAGCTTGCTGATGCTGAATGCTTGAAG 4529
QY 906 sLeuGluLysSerCysTyrAlaLeuGluSerLeuProGluGluValLysGlyLe 926
Db 4530 TCTAAAATTCATATTGTTGTCGACCTAGAGAGTCTCCCTGAGAGGGCTGGAAAGGTTT 4589
QY 926 uLLeSerLeuThrGlnLeuSerLLeThrTyrCysGluMetLeuGlnCysLeuProGluG 946
Db 4590 ATCTTCACCTACAGAGTATTTGTTGAACACTGTAACATCTTAATGTTTACAGAGG 4649
QY 946 yLeuGlnIstLeuThrAlaLeuThrAsnLysSerValGluPheCysProThrLeuAlaL 966
Db 4650 ATTGACAGACCTTAACACCTCACAAGTTTAAAAATTCGGGGATGTCACAACTGATCA 4709
QY 966 sArgCysGluLysGlyIleGlyGluAspTyrTyrIstLeuAlaHsIleProArgValPh 986
Db 4710 GGGGTGTGAGAGGGAGATGAGAGACTGAGCAAAAATTTCTCATTTCTTAATGTGA 4769
QY 986 eLLeTyr 988
Db 4770 TATAAT 4776

```

```

RESULT 9
US-10-360-522-52
; Sequence 52, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Vossen V.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 3971
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3971)
; OTHER INFORMATION: /note="RG3-b1b"
US-10-360-522-52

```

```

Alignment Scores:
Pred. No.: 0
Score: 3606.50
Percent Similarity: 63.02%
Best Local Similarity: 57.24%

```

```

Length: 3971
Matches: 763
Conservatives: 77
Mismatch: 137

```

```

Query Match: 70.34% Indels: 357
DB: 17 Gaps: 9
US-10-647-268-2 (1-988) x US-10-360-522-52 (1-3971)
QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 1 ATGGCTGAAGCTTTCATTCAGATGTTGCTAGACAAATCTCATCTTCTCCCAAGGGAGAA 60
QY 21 LeuGlyLeuLysLeuGluGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThr 40
Db 61 CTGTGATGCTTTTCCGTTTTCAGATGTTTCCAAAGCTTTCAGAGCATGTTTCTTAC 120
QY 41 IleGlnAlaValLeuGluLysPalaIleAlaIstTyrGluAlaAspAspLysLeuAspGly 60
Db 121 ATCCAAAGCGTCTTGAAGATGCTCAAGAGAACCACTCAACAGACAGCGCTTAGAAGAT 180
QY 61 TrpLeuGlnLysLeuAsnAlaAlaAlaIstTyrGluAlaAspAspLysLeuAspGlyCys 80
Db 181 TGGTTGCAAAAACCTCAATGCTGCTACATAGAAAGTCATGATGATGATGATGATGAT 240
QY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHsProAsnValIle 100
Db 241 ACTAAGGCC--ACAAGATTCCTGCACTGCAATATGCGCGTTATCATCCAAAGTTATC 297
QY 101 ThrPheArgHsLysLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
Db 298 CTTTCCGTCACAAGGTTGGGAAAGAGATGACCAAGATGATGAAAGATGAAAGATGCAAT 357
QY 121 AlaAlaGluArgLysLysPheHsLysAspGluAspThrIleGluArgGlnValAlaThr 140
Db 358 GCTAGGAGAGCAAGAAATTTTCATTGTCAGAAAGATTTATAGAGACAAAGCTGCTACA 417
QY 141 ArgGlnThrGlyPhe----- 145
Db 418 CGGAAACAGGTAC-TGATCTTAATTAATTAACAATTAGTTATATTCATTTGTTT 476
QY 145 ----- 145
Db 477 GGGCAATGATCAATTAATTAAGTCAAAATATATCTGATCTACTGAAAAATAGTTAA 536
QY 145 ----- 145
Db 537 ATATACCTCTAGTATATCTTATTAAGAACATACCTCCCATATACCTTTGAAACAAT 596
QY 145 ----- 145
Db 597 ATTCCCTTAAGAAATAAGACAGCGTGAAGTTGAGATTCAAATTAATCAACCTCAATT 656
QY 145 ----- 145
Db 657 TAAGATCTGATTTCTTAGAAGAACCACTCATCTCCGTTTGAAGTTTACGAAGCA 716
QY 145 ----- 145
Db 717 GCTCAGAGAAAGAGTTTCTGTTCTGTTCTGTGATGATTTGTTGTTTAAATCAAT 776
QY 145 ----- 145
Db 777 AACAAACAATCAATTAATTAATTAATGTTACAGATGAGGTAGTCTTCTAGCTAGACATG 836
QY 145 ----- 145
Db 837 AACTGAGTAAATTTGTTTAAAGAAAGAAAGAAATGATTAGCTGATTTCTTTCA 896
QY 145 ----- 145
Db 897 GAGTGAATATAGGGGAGTAAGTTGAGACATAGAGTTCAATCGTTATTTCTTCTTA 956
QY 145 ----- 145
Db 957 AAGTAACAAGTTCACAAAAATGATATCAAGTACGTAATGAGAAATTAATTAAGACAGTC 1016

```

QY 145 ----- 145
 Db 1017 TAACTACAAAATGGAATAGAACTTAATATTCAGTGAATATCATCTTTAATAAA 1076
 QY 145 ----- 145
 Db 1077 GCTACCAAAATTTAAATCATGATACAGAGAAACCMAAAATTAAGGGGTAATTATT 1136
 QY 145 ----- 145
 Db 1137 GATTCTATGCTTATCATAGTCTTCCCATCAACATCAAGAAAAATTTGCGCAAGTAT 1196
 QY 145 ----- 145
 Db 1197 AAACGGTGGGTATATTGATTTGAATAAGTAAACAGAGATATCATTTGACTAAAGTA 1256
 QY 145 ----- 145
 Db 1257 TAACAATAGATATATTGATCATTTTATGATCAAAATTCATGCTGTTTGGGAGAAAG 1316
 QY 145 ----- 145
 Db 1317 GAAGTTCAATGTTTCAATCTGCTCCATCTCATCCATATCTCTTATTTGCAAAAC 1376
 QY 145 ----- 145
 Db 1377 CCTCTATTTAATTAATTTTCTGCGCACTCCTAATGAGCTTGATGATCAATATTCCTC 1436
 QY 146 -----ValleuabangluProgluValTyrGluArgAsp 156
 Db 1437 ATCTGGACATTCCTTGCACACAGGTTCTGTGTTTACCTGAACCAAGTTATGAGAGGAC 1496
 QY 157 LysGluLysAspGluIleValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeu 176
 Db 1497 AAGGAAAAGATGAGATAGTGAATAATCCATTAACCAATGATGAGCCCAAAACCTC 1556
 QY 177 ProValLeuProIleLeuGluYmetGluYleuGluYThrThrLeuAlaGlnMetVal 196
 Db 1557 TCAGTCCCTCCCAATCTTGATAGGGGGGACTAGGAAAGACAACCTTTCCCAATGGTTC 1616
 QY 197 PheAsnAspGlnArgValIleGluHisPheHisProLysIleTriePleCysValSerGlu 216
 Db 1617 TTCATATGATCAGAGAGTAACTGAGCGGTTCTATCCCAAAATATGATTTGCGTCCGAT 1676
 QY 217 AspPheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeu 236
 Db 1677 GATTTTGTAGAGAAAGGTTGATTAAGGCAATAGTAAATCTTATTAAGGAGGAAAGCCCTC 1736
 QY 237 GlyGluMetAspLeuAlaProLeuGluLysLysLeuArgAspLeuLeuAsnGluYlAsLys 256
 Db 1737 AGTGACATGAGACTTGCTCCACTTCATAAAGAACTTCAAGAGTTGCTGAATGGAAGAAAG 1796
 QY 257 TyrLeuLeuValIleAspAspValTriePangluAspGluAspLysTriePalaLysLeuArg 276
 Db 1797 TACTTCCTTGCTTGTATGATGATTTGGAATGAAATCAACATTAAGTGGCTTAATTAGA 1856
 QY 277 GlnValLeuLysValGluYlAsSerGluYlAsSerValLeuThrThrArgLeuGluLys 296
 Db 1857 GCAGCTTTGAAGGTGAGCAAGTGCTCATTTGTTTCACTACTACCTGCTTGAAG 1916
 QY 297 ValGluSerIleMetGluThrLeuGluProTyrGluLeuSerAsnLeuSerGluGluAsp 316
 Db 1917 GTTGATCATATTATGGAACATTTGCAACATTAATGATTTGCTTCTCCAGAGAT 1976
 QY 317 CysTriePleuLeuPheMetGluArgAlaPheGluYHisGluGluGluIleAsnLeuAsnLeu 336
 Db 1977 TGTGTGTTTGTGTCATGACAGGTCATTTGGACCAAGAAATAATCCAAACCTT 2036
 QY 337 ValAlaIleGluYlAsGluIleValLysLysCysGluYlValProLeuAlaAlaLysThr 356
 Db 2037 GTGGCAATCGGAAGAGATTTGTGAATAATGTGTGTGTGCTTGTGAGCCCAAGCT 2096
 QY 357 LeuGluYlIleLeuArgPheLysArgGluGluArgGlnTriePalaLysArgAspSer 376

Db 2097 CTGGAGGTATTTTGCCTTCAGAGAGAGAAAGAGATGGGAAACATGTCGAGACAGT 2156
 QY 377 GluIleTriePlyLysLeuProGluGluSerIleLeuProAlaLeuArgLeuSerYr 396
 Db 2157 CCGATTTGAAATTTGGCTCCAGAGTAAAGTTCTATTTGCTGCGCTCAGGCTTATGTTAC 2216
 QY 397 HisHisLeuProLeuAspLeuArgGluCysPheThrTyrCysAlaValPheProLysAsp 416
 Db 2217 CATCATCTTCCACTTGATTTGAGACAAATGCTTTGTGTATTTGTGCGGTATTTCCAAAGAC 2276
 QY 417 ThrGluMetGluYlAsnLeuIleSerLeuTriePalaHisGluPheIleLeuSer 436
 Db 2277 ACCAAATGCGAAAGAAATCTTATGCTTTTGGATGGACATAGGTTTCTTTATTCG 2336
 QY 437 LysGluYAsnLeuGluLeuGluLysAsnValGluYAsnGluValTriePangluLeuTrieLysArg 456
 Db 2337 AAAGGAAATTTGGAGCTAGAGAGATGATGATATGAATGAAATGAATTAATTAATCTTGAGG 2396
 QY 457 SerPhePheGluGluIleGluValLysSerGluYlAsnThrTyrPheLysMetHisAspLeu 476
 Db 2397 TCTTTCTTCAAGAGATTTGAAGTTGAATCTGTGTAATCTTATTTCCAGATCAGACCTC 2456
 QY 477 IleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlu 496
 Db 2457 ATCCATGATTTGGCTACATCTCTGTTTACAGCAACACATCAGACGCAATATTCGTGA 2516
 QY 497 IleIleValGluAsnTyrIleHisMetMetSerIleGluPheThrLysValLysSerSer 516
 Db 2517 ATTAATGCTAATTAATGATGATATATGATGATGCTGTTTGTGCTGAAGTGTATCTTCT 2576
 QY 517 TyrSerLeuSerHisLysGluLysPheValSerLeuArgValIleAsnLeuSerAspIle 536
 Db 2577 TACTTCTTCACTTTCGAAAGTTTGTCTCATTTAAGGAGCTTAATCTTAAGAAATCTCG 2636
 QY 537 LysLeuYsgluLeuProSerSerIleGluYAspLeuValHisLysArgTyrLeuAsnLeu 556
 Db 2637 AACCTAATCAATTAACATCTTCCATTCAGATGATGATCAATTAAGTATCTGAGACTTG 2696
 QY 557 SerGluYAsnThrSerIleArgSerLeuProAsnGluLeuCysLysLeuGluAsnLeuGlu 576
 Db 2697 TCTGCAATTTTGAATTCGTAATCTTCCAAAGATTAATCAGAGCTTCAAAATCTGAG 2756
 QY 577 ThrLeuAspLeuHisGluYlAsSerLeuYsgLysLeuProLysGluThrSerLysLeu 596
 Db 2757 ACTCTTAATCAATTAATGAGCTCTCTTCTGTTTGCACAAACAAACAGTAATTT 2816
 QY 597 GlySerLeuArgAsnLeuLeuLeuAspGluYlCysTyrGluLeuThrCysMetProProArg 616
 Db 2817 GGTAGTCTCCGAATCTTTTATCTTGATGCGTGT---TCATTGAGCTCAAGCCACCAAGG 2873
 QY 617 IleGluSerLeuThrCysLeuYsgThrLeuSerArgPheValValGluIleGluLysLys 636
 Db 2874 ATAGAGATTTGTAATGCTTAAGCTCTTAAGTTGCTTTGTTATGGC---AAGAGAAA 2930
 QY 637 SerCysGluLeuGluYlAsLysArgAsnLeuAsnLeuYrGluSerIleGluIleThrHis 656
 Db 2931 GGTATCAACTGTGTGAACCTTAACCAATTAATCTTAATGCTCAATTTCAATACAAA 2990
 QY 657 LeuGluLysArgValLysAsnAspMetAspAlaLysGluIleAsnLeuSerAlaLysGluAsn 676
 Db 2991 CTTACAGAGTGAAGAAAGATAGCGATGCCAAGAAAGCTAATTTATCTGCTAAAGCAAT 3050
 QY 677 LeuHisSerLeuSerMetLysTriePAspAspGluArgProArgIleTyrGluSerGlu 696
 Db 3051 CTGCACCTTATATCTGAGGTGGGACCTTGATGGAACATAGA---TATGATTA--- 3104
 QY 697 LysValGluValLeuGluAlaLeuLysProHisSerLeuLeuThrCysLeuThrIleArg 716
 Db 3105 -----GAAAGTCTTGAAGCCCTCAACACACATCCATCTGAATATTTAGAAATCAAT 3158
 QY 717 GlyPheArgGluIleArgLeuProAspTriePalaHisSerValLeuLysAsnValVal 736

Db 3159 GGCTTCGAGGAGATCCCTCCAGATTGATGATCATCATGTTTGAAAAATGTTGTC 3218
Qy SerileglnlleleSerCysleuAsnGlySerCysleuProProPhgGlyGluLeuPro 756
Db 3219 TCTATTAGATTAGAGGTTGTGAAAACTGCTCATCTTACACACCTTTGGGAGCTGCTC 3278
Qy CysleuSerSerleuGlnLeuThrArgGlySerIleGluValGluVal---AspSer 775
Db 3279 TGTCTAGAAAGTCTAGAGTTACACACCGGCTGACGAGATGTGGAGTATGTTGAGATAT 3338
Qy GlyPheProThrArgArgPheProSerleuArgIleAsnIleArgGluPheGly 795
Db 3339 GTTATCTCT-----GGAAGGTTTCATCTTGAAGAACTGTATATGGACTTACT 3392
Qy AsnleuGlyGlyLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 815
Db 3393 AATCTAAAAGATGCTGAAAAAGAGAGAGAAAGCAATTCCTGCTCTGAAAGAGATG 3452
Qy GluIleuGlyCysCysProMetPheValIleProThrIleSerSerValIleVal 835
Db 3453 ACATTTAAGTGTGCTGCTATGTTGTATTCGACCTTTCTTCTGTCAAGACATTGAAA 3512
Qy ValSerGlyAspIleSerAspAlaIleGlyPheSerSerIleSerAsnleuMetAlaLeu 855
Db 3513 GTTATTTGG-----ACAGATGCAACAGTTTGAAGTCCATCTATCTTAGGGCTCTT 3566
Qy ThrSerleuGlnIleArgGlyAsnIleGlyAspAlaSerleuProGluGluMetPheGly 875
Db 3567 ACTTCCTTGACATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAG 3626
Qy SerleuAlaAsnleuGlySerleuAsnIleSerPheThrPheAsnleuGlyLeuPro 895
Db 3627 AGCTTGCAATCTAATTAATCTAATTAATCTTCTTCTTGAAGAACTCAAGAGTGGCT 3686
Qy ThrSerleuAlaSerleuAsnAlaLeuGlyAsnIleGlyGlnIleSerCysTyAlaLeu 915
Db 3687 ACCACCTGGGCTAGCTCAATGCTTGAAGAGTCAATTAATTAATTAATTAATTAATTA 3746
Qy GluSerleuProGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 935
Db 3747 GAGAGTCTCCCGAG 3806
Qy TyrCysGluMetLeuGlnCysleuProGluGlyGlyGlyGlyGlyGlyGlyGlyGly 955
Db 3807 AACTGATGATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3866
Qy LeuSerValGluPheCysProThrleuAlaGlyArgCysGlyGlyGlyGlyGlyGly 975
Db 3867 TTAACAACTTACTCAATGTCATATGATTAATTAATTAATTAATTAATTAATTAATTAAT 3926
Qy TrpTyIleGlyIleAlaIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 988
Db 3927 TGGCACAAAATGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3965
RESULT 10
US-10-360-522-53
; Sequence 53, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53

LENGTH: 3899
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3899)
; OTHER INFORMATION: /note="RG4-b1b"
US-10-360-522-53
Alignment Scores:
Pred. No.: 7.23e-310 Length: 3899
Score: 3400.00 Matches: 717
Percent Similarity: 62.94% Conservative: 105
Best Local Similarity: 54.90% Mismatches: 159
Query Match: 66.32% Indels: 326
Gaps: 10
US-10-647-268-2 (1-988) x US-10-360-522-53 (1-3899)
Qy 1 MetAlaGluAlaPheLeuGlnValIleuLeuAspAsnleuThrCysPheIleGlnGlyGlu 20
Db 1 ATGGCGAAGCTTTCTTCAAGTCTGCTAGAAATCTCACTTCTTCATCGAGATATAA 60
Qy 21 LeuGlyLeuIleLeuGlyPheGlyAspGluPheGlyLeuGlnSerThrPheThr 40
Db 61 CTGTGATGATTTTCGGTTTCGAAAGAAATGTGAAAGAGTGTGAGTGTGTTCCACA 120
Qy 41 ILeuGlnAlaValIleuGluAspAlaGlnIleGlyGlnIleuGlyAspIleAlaIleGln 60
Db 121 ATTCAAGCTGTGCTCAAGATGCTCAGAGAGAAATTAAGAAAGCAATTAAGCAATTAAG 180
Qy 61 TrpLeuGlnIleuLeuAsnAlaAlaAlaTyrgIuAlaAspAlaIleuAspGluCysLys 80
Db 181 TGTGTTGCAAGAACTCAATTCGCTGCTATGAAGTGTATATATGGGGAATGATAA 240
Qy 81 ThrGluAlaProIleArgGlnIleGlyAsnIleGlyGlyCysTyIleProAsnValIle 100
Db 241 AATGAGGCA--ATTAAGATTGAGACAGTCTGATTAAGGTTTATCCACCGGATTAATC 297
Qy 101 ThrPheArgIleValIleGlyGlyArgMetLysIleMetGlyLysLeuAspValIle 120
Db 298 AATTTCGCTCAAAATTAAG 357
Qy 121 AlaIleGluArgIleGlyPheIleLeuAspGluArgThrIleGluArgGln----- 137
Db 358 TCTGAGGAAGAAGAGAGTTTCATTTCTGAAAAAATTAACAGAGACAGCTGCGCT 417
Qy 137 ----- 137
Db 418 GCTACGCGTGAAGACAGGTGTGAGTACGATTAATTAATTAATTAATTAATTAATTAAT 477
Qy 137 ----- 137
Db 478 TACACATCATGTGTTACCGCTGATCTTACATAGATGCAATGGGGCTGGGCGAGGT 537
Qy 137 ----- 137
Db 538 TGGAGGTGTGAGGTGTGTGGCGAACCCCAACTTGTGATCACTAGTAGTACTTAA 597
Qy 137 ----- 137
Db 598 ATTGTATAGATTGAACAGATGAACAAAGCGCTCTACTGTGTGCTTATGCGATTATG 657
Qy 137 ----- 137
Db 658 TCACTTAGATGATGTGTCTACTTGTCACTTATATAGATTAAAGTTCACTGTGC 717
Qy 137 ----- 137
Db 718 AACCCAAAGTTGAGCGCGTGAATGTCAATTGATACCAAGTTAAAGGATATTATG 777
Qy 137 ----- 137

Db 778 AATTATGCGCTTAAATATGATTCATTTTGTATGATCTGTCCAAAATANGTCTAGTG 837
 Qy 138 -----ValAlaThrArgIn 142
 Db 838 AAAGTTTAAACTAGTGTGATCTGCTATTGAAAGTGAATTTTGTGTGC-ACATAACAA 896
 Qy 142 ----- 142
 Db 897 TGCATAGGCTGTGATTCATTTTTCATTAACCTTTTGTAGACGATTTTCTTATCGAA 956
 Qy 142 ----- 142
 Db 957 TTTTACTGTAAATAATGCAAAAAGCAAAAGAAATTAAGAAATACAGAGGCTGACTTCTTC 1016
 Qy 142 ----- 142
 Db 1017 ATAGTATCTATCATATATAAAAAAACATTGATTAAGATATGAGGCTTTTAAATTAC 1076
 Qy 142 ----- 142
 Db 1077 AAATTTGTAGATTAAACAGTTCTGTGGAGAGATTAGATACAGCTGATAGTATCTA 1136
 Qy 142 ----- 142
 Db 1137 GAAGTTTAAATAAAAAATTAGCAAAATTATGCGGCTGCGGCGGTTGAAAAACAGCA 1196
 Qy 142 ----- 142
 Db 1197 ACTTTGCAAGGCTGGCGGGTCCGAATCTTTGCAAGTTGTGTGGGTTGCCCTGCACCA 1256
 Qy 142 ----- 142
 Db 1257 CCCAATCTGCATTCCTGTCTAATGTTTGTGTGTCTAATTCCTGCTGACTCATCT 1316
 Qy 143 -----ThrGlyPheValIeu 147
 Db 1317 AATGAGCTCAATTGTACAAATCTTTGTGTCTGTCACATTACTGTGAAAGGTTTGTGT 1376
 Qy 148 AenGluProGlnValTyrGlyArgAspLysGluLysAspGluIleValIleIleuIle 167
 Db 1377 ACTGAACCAAAAGTCTACGAAAGGACAAAGAGAGATGATGATGATAAATCTGTATA 1436
 Qy 168 AenAsnValSerAsnIleGlnThrIleuProValIleuProIleuGlyMetGlyIleu 187
 Db 1437 AACATGTTAATGTTGGCCGAAGAACTTCCAGTCTTCCCTATATATGATGGGGGACTA 1496
 Qy 188 GlyLysThrThrIleuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHis 207
 Db 1497 GGAAGAAGCAGACCTGGCCCAATGATCTTCAACGATGAGAGATTAACATAACATTTCAAT 1556
 Qy 208 ProLysIleThrIleCysValSerGlnAspPheAsnGluLysArgGluIleIleGluIle 227
 Db 1557 CCCAAATATGAGGTTGTGTCTCAGATGATTTTATGAGAAAGGTTATTAACAATTT 1616
 Qy 228 ValGlnSerIleGlnGluLysSerIleuGlyMetAspLysAlaProLysGlnLysLys 247
 Db 1617 ATAGAAATATATGAAAGAGTTCTCCCATCTGATGAGAGCTTGGCTTCAATTCAGAAAG 1676
 Qy 248 LeuArgAspLysLeuAsnGlyLysLysTyrIleuLysValIleuAspAspValTyrAsnGlu 267
 Db 1677 CTCACAGAGTATTTGAAATGCAAAACGATACCTGCTTGAAGATGATGTTGGAAATGAT 1726
 Qy 268 AspGlnAspLysTyrAlaLysLeuArgGlnValIleuLysValIleuAsnGlyLysSer 287
 Db 1737 GATCTAGAAAGTGGCTTAAGTTAAGACAGCTTAACTGTGAGACAGAGGCTCTCT 1796
 Qy 288 ValIleuThrThrArgLysGlnLysValGlySerIleMetGlyThrIleuGlnProTyr 307
 Db 1797 ATTCTAGCTACTACTCGCTTGAAGAGTTGATCAATATAGGAGACCTTGCAACCATAT 1856
 Qy 308 GlnLysSerAsnLysSerGlnLysAspCysThrLeuLysPheMetGlnArgValPheGly 327
 Db 1857 CATTTGTCNAATTTGTCTCCACATGATATGTTACTTTTGTATGCAACGGGCACTTGGG 1916

Qy 328 HisGlnGluIleLeuAsnLysLeuValAlaIleGlyLysGluIleValIleLysCys 347
 Db 1917 CAACAAAAGAGCAAAATCTTAATCTAGTGGCCATTGGAAAAGGATTTGTAAAGAAATGT 1976
 Qy 348 GlyGlyValProLeuAlaAlaLysThrLeuGlyLysIleLeuArgPheLysArgGlu 367
 Db 1977 GGTGTGTGCTTTTGAAGCCCAAGACTTGTGTGTCTTTTACCTTCAAGAGAAAGAG 2036
 Qy 368 ArgGlnThrPgiLysValArgAspSerGlnIleThrLysLeuProGlnGluSerSer 387
 Db 2037 AGTAATGGGAACATGTAGAGATTAATGAGATTGTGAGTCTGCTCAAGATGAAGATCT 2096
 Qy 388 IleuProAlaLeuArgLysSerTyrHisIleuProLeuAspLysArgGlnCysPhe 407
 Db 2097 ATTTGCTGTCTTAAGATGAGTTATCATCACTTCCACTTGATTTGAGCAATGCTTT 2156
 Qy 408 ThrTyrCysAlaValPheProLysAspThrGluMetGluLysGlyAsnLysIleSerIeu 427
 Db 2157 GCGTATTTGTGAGATTTCCCAAGACACCAAAATGATTAAGAAATCTCATTAATCTCTC 2216
 Qy 428 ThrMetAlaHisGlyPheIleLeuSerLysGlyAsnLysGluLysValGlyAsn 447
 Db 2217 TGGATGGCGAGTGTCTTTTATCAAGGGAACCTTGAGCTTGAAGATGTGGTAT 2276
 Qy 448 GlnValTyrAsnGluLysTyrLeuArgSerPheGlnGlnIleGlyValIleSerGly 467
 Db 2277 GAAGTATGAGATGATTAATTAATCTGAGTCTTCTTCCAAAGAAATGAAAGCTAAATCCGGT 2336
 Qy 468 GlnThrTyrPheLysMetHisAspLysIleHisAspLysAlaThrSerLysPheSerAla 487
 Db 2337 AATACTTATTTCAAGATACATGATCTAATCATGATTTGGCTACATCTGTTTCCGCA 2396
 Qy 488 SerThrSerSerSerAsnIleArgGluIleIleValGlnAsnTyrIleHisMetCysSer 507
 Db 2397 AGCGCATCAGCGCGCAATATCCGGAATATATGTCAAAGATTAATGACATACAGTCTCC 2456
 Qy 508 IleGlyPheThrLysValIleSerSerTyrSerIleuSerHisIleuGlnLysPheValSer 527
 Db 2457 ATTGCTTCCGTGACAGTGTGTCTTCTTACTCTCTTCCCTTGAAGAAAGTTGTCTCG 2516
 Qy 528 LeuArgValLeuAsnLysSerAspIleLysLeuLysGlnLysProSerSerIleGlyAsp 547
 Db 2517 TTAAGGCTGCTTAATCTAAGTTACTCAAACTTGAGCAATTAACGCTTCCATTGGAGAT 2576
 Qy 548 LeuValHisLeuArgTyrLeuAsnLysSerGlyAsnThrSerIleArgSerLysProAsn 567
 Db 2577 CTAATTACATTTAAGATACCTGAGACCTGTCTTGGCAAT--AACTTCCGTAGTCTTCCAGAG 2633
 Qy 568 GlnLysCysLysLeuGlnAsnLysGlnThrLeuAspLysHisGlyCysHisSerLeuCys 587
 Db 2634 AGGTTGCAAGCTTCAAAATCTTCACACTTGAATGTACATATGTCTACTCACTTAAT 2693
 Qy 588 CysLeuProLysGlnThrSerLysLeuGlySerIleuArgAsnLysLeuAspGlyCys 607
 Db 2694 TGTTTGCCAACAACAACATTAATTAAGTCAATCTCGAATCTTGTGTTGATGGCTGT 2753
 Qy 608 TyrGlyLeuThrCysMetProProArgIleGlySerLeuThrCysLysLysThrLeuSer 627
 Db 2754 ---CAATTGACTTCACTCCACCAAGGATGAGATTGTGTCAGAGCTTAAAGCTTACGT 2810
 Qy 628 ArgPheValValGlyIleGlnLysLysSerCysGlnLysGluLysLeuArgAsnLysAsn 647
 Db 2811 TTTCTTATTTGTGGGA--ACCAAGAAAGGTTATCACTTGTGTAACGAAAACCTTAAT 2867
 Qy 648 LeuTyrGlySerIleGlnIleThrHisLeuGlnArgValLysAsnAspMetAspAlaLys 667
 Db 2868 CTCTGGGGCTCATTTCAATCAACAACCTTGAGAGGTGAAGAACATACGATGCGA--- 2924
 Qy 668 GlnAlaAsnLysSerAlaLysGlnLysLysHisSerLeuSerMetLysTyrAspAspAsp 687
 Db 2925 GAAGCAATTTATCTCAAAAGCAAACTGCAATCTTTAAAGCATGAGTGGGATTAACGAT 2984

```
Qy 688 GUAARProarglleYrGluSerGluuylValGluValleuGluAlaLeuLysProHis 707
Db 2985 ---GGACCAAAACAGATATGAATCCAAAGAGTTAAAGCTTGAAGCACTCAAAACACAC 3041
Qy 708 SerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIleArgGluProAspTyrMet 727
Db 3042 CCCATCTCGAAATATTTTGAAGATCATCTTCCTCGAGAGATTCCTGTTTCCAAAGCTGGATA 3101
Qy 728 AsnHisSerValLeuLysAsnValValSerIleGluIleIleSerCysGlyAsnCysSer 747
Db 3102 AATCACTCAGTTTGGAGAGGTCACTCTCTGTGAATTTAAAGCTGCAAAACCTGCTTG 3161
Qy 748 CysLeuProProPheGluGluLeuProCysLeuLysSerLeuGluLeuTyrArgGlySer 767
Db 3162 TGCTTACCACTTGGAGAGCTTCTGTCTAGAAAATCTAGAGTTCAAAACGCACT 3221
Qy 768 AlaGluValGluTyrValAsp-----SerGlyPheProThrArgArgArg 782
Db 3222 GCGAGGTGGAGTATGTTGAAGAGAGATGATGCATCTTAGATTCCTCACAAGAAAGAGC 3281
Qy 783 PheProSerLeuArgGlyLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeuLeuLys 802
Db 3282 TTTCCATCCCTGCAAAAACCTTCGTATATGTTCTTTCGAGTTGAAAGGCTGATGAAA 3341
Qy 803 LysGluGluGluGluGluCysProValLeuGluGluIleGluIleLysCysCysProMet 822
Db 3342 GAGGAGAGAGAGAGAAATTCCTCCATGCTTGAAGAGATGGCACTTTTATTTGCCCTCTG 3401
Qy 823 PheValIleProThrLeuSerSerValIlyLysLeuValValSerGlyAspLysSerAsp 842
Db 3402 TTTGTTTTCCAACCTTCTTCTCTGCAAGAAATTAAGAAATTCACGCGAAC--ACAAC 3458
Qy 843 AlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgIyr 862
Db 3459 ACTAGAGTTTGAAGCTCATATCTATCTTAGCACTTACTTCTCCCTCGCATTCGTCT 3518
Qy 863 AsnLysGluAspAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysIyr 882
Db 3519 AACTACAGAGCACTTCACTCCCAAGAGAGATGTTCAAGCTTACAAATCTCGAATTC 3578
Qy 883 LeuAsnIleSerPheIyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsn 902
Db 3579 TTGAGTTCTTTCGACTTCMAAGATCTCAAAAGATCTGCTTACCAAGCTGCTGCTCAT 3638
Qy 903 AlaLeuLysLeuGluIleIleSerCysTyrAlaLeuGluSerLeuProGluGluGly 922
Db 3639 GCTTTGAAGCGTCTCCAAATTAAGAGTGTGACTCACTAGAGAGTTTCCCTGAACAAGG 3698
Qy 923 ValLysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCys 942
Db 3699 CTAGAAAGTTTAACCTTCACTCAACAGTTGTTTGAATATCTGAAGATGCTAAAGT 3758
Qy 943 LeuProGluGlyLeuGlnIleSerLeuThrAlaLeuThrAsnLeuSerValGluPheCysPro 962
Db 3759 TTACCGAGAGGATTTGAGACACCTTAACAGCCCTCACAAAATTTAGAGTTTCTGTTGTCCA 3818
Qy 963 ThrLeuAlaLysArgCysGluLysGlyIleGlyLysAspTyrTyrIleAlaHisIle 982
Db 3819 GAAGGAGAAACGCTGTGTATTAAGAAATTAAGAGAGAGAGCTGCACAAAATTTGCTCACT 3878
Qy 983 ProArgValPheIleTyr 988
Db 3879 CCAATCTGATATTTCTAT 3896

RESULT 11
US-10-647-268-7
; Sequence 7, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
```

```
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3222
; TYPE: DNA
; ORGANISM: Solanum Bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)..(528)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (529)..(690)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (691)..(3219)
; US-10-647-268-7

Alignment Scores:
Pred. No.: 1,66-304 Length: 3222
Score: 3342.00 Matches: 681
Percent Similarity: 74.98% Conservative: 116
Best Local Similarity: 64.06% Mismatches: 180
Query Match: 65.18% Indels: 86
DB: Gaps: 13

US-10-647-268-2 (1-988) x US-10-647-268-7 (1-3222)
Qy 1 MetaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyLys 20
Db 58 ATGCTGAAGCTTTCCTTCAAGTTCTGTCAGCAATATCTTCTTTCATCCAAAGGAAA 117
Qy 21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
Db 118 CTTGTATGCTTTCGTTGGTTTGAAGACGACTTCGAAAGCTTCAAGACATTTTCTACG 177
Qy 41 IleGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn 60
Db 178 ATCCACCTTGCTGTTGAAGATGCTTCAGAGAGCACTGAAGGACAAAGCAATGAGAAAT 237
Qy 61 TyrLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
Db 238 TGGTTGACGAATCACTAATTTGCTGCATATGATGATGATGATGATGATGATGATGATG 297
Qy 81 ThrGluAlaProIleArgGlnLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
Db 298 AATGAGCA--GCAAGATTCATCACTGCTTATTAAGGTATATTCATCCAAAGATCATC 354
Qy 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
Db 355 ATTTTTCCTTCAAGCTCGGAAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 414
Qy 121 AlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
Db 415 GCTGACGAAGAAAGAGAGTTTCATTTGCTGCAAGATGTGAGAGAAACAAGCTTCAAA 474
Qy 141 ArgGln----- 142
Db 475 CGTGAACAGGTGCTCATCTTAACGTGTGTTAGCCAAGTACTTAATAGCTTAGTTT 534
Qy 142 ----- 142
Db 535 TATATTCATCTTTTGTAGTTACAGATTTATACATGTGTTGCATGTCAGCCCTTCC 594
Qy 142 ----- 142
Db 595 TTGTGCTTTTGTGTTGCAAAATCTTATATTCCTGCTGACTCTTTTAGTGAAGCT 654
Qy 143 -----ThrGlyPheValLeuAsnGluPro 150
Db 655 TGAATTTAATAAATTTGTGTGCTGCTTGTGGAACAGGTTTGTGTTTGAAGAGCA 714
```



```

Db      2848  GAACCAACACACTCTCCAGAGAGATGTTCAAGCCCTTGAAATCTTGAGCTCTTAGCC 2907
Qy      885  ILeSerPheTyRPhaAsnLeuLeuGluLeuProThrSerLeuAlaSerLeuAsnAlaLeu 904
Db      2908  ATTATATCTTCAAAAACTCAGAGAGTTGCCAAGAGCCCTGGCTAGCTCAATGCTTTG 2967
Qy      905  LysHisLeuGluIleHisLeuSerCysTyRAlaLeuGluSerLeuProGluGluValLys 924
Db      2968  AAGGTCTAAAAATTCATTATGTTTACCGACTAGAGAGTCTCCCGAACAAGGATGGAA 3027
Qy      925  GlyLeuIleSerLeuThrGluLeuSerIleThrTyRArgGluMetLeuGluCysLeuPro 944
Db      3028  GGGTTAACTTCACTACCGACTTATATGTTCAAACTGTGAGTCTTAAATGTTTACT 3087
Qy      945  GluGlyLeuGluHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeu 964
Db      3088  GAGGATTTGCAGCACCTTAAGAGCCCTCACTAGTTTACAAATTTATGCTGTCCAGCATTG 3147
Qy      965  AlaIysArgCysGluLysGlyTlleglyGluAspTlPtyRlyIleAlaHisIleProArg 984
Db      3148  AAAAGCCGCTGTGCGAAGGGGATAGAGAGCATGGCAAAATTTGCTCACATTTCTTAAT 3207
Qy      985  ValPheIle 987
Db      3208  GTAGATATT 3216

RESULT 12
US-10-437-79971
Sequence 79971, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 79971
LENGTH: 3333
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1
US-10-437-963-79971

```

```

Db      130  TCTCAGTTACAGGCTTCTCTTGACGACGCTGAGAGACAGTGTGACATGCAATCTGTG 189
Qy      59  GluAsnTlPleuGluIleLysLeuAsnAlaAlaIleTyRAlaAspAspIleLeuAspGlu 78
Db      190  AGGGATGGCTTACAGAGCTCAAGATATGCGCTAGACCTTGATATCTGCTGGACAG 249
Qy      79  CysLeuThrGluAlaProIleArgGluLysAsnLysTyRlyCysTyRHisProAsn 98
Db      250  TATTACGCCAAAGT---ATGGCATGAAGCAGAGCAG-----GTGATATTTCCACCA 300
Qy      99  ValIleThrPhe-----ArgHisLysIleGly 107
Db      301  AAGGCAGATTTCTTTCTTCTCTCTTCTTGAAGAAATCTTACAGCATAGAGATTAAG 360
Qy      108  LysArgMetLysLysIleMetGluLysLeuAspValIleAlaIleArgIleLysPhe 127
Db      361  CATTAAGTTTAACATCATATTGGAGAGATTGATTAAGATTCCGCAABAAGCCGACACAT 420
Qy      128  HisLeuAspGluArgThrIleGluArgGluValAlaThrArg-----GlnThrGly 144
Db      421  GGGCTCCAGATGATATGTGAATGAGACGGTATGATPCTCAGAGCGCTCCGCAATCAAGT 480
Qy      145  PheValLeuAsnGluProGluValTyRglyArgAspLysGluLysAspGluIleValLys 164
Db      481  TCTCTTGATGATTTGCTGCTGATTTGTAGAGAGAGGACAGAGAGAAATGCTGAGG 540
Qy      165  ---IleLeuIleAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGly 183
Db      541  CTGGTGTCTCTGTATATATGACATTAATCTCGCACTTATGTGTATTCAGTTGTTGGC 600
Qy      184  MetGlyLysLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIle 203
Db      601  ATGGGTGGCTGGTGAATAACTTACTTATGACATGTGTGATGACATGATGACAGATGAGA 660
Qy      204  GluHisPheHisProLysIleTlPleCysValSerGluAspPheAsnGluLysArgLeu 223
Db      661  GAAACATTTGACTTGAGAGATCTGATCTTATGTATCTAAAGTTTGATGAGAGAAACCTA 720
Qy      224  IleLysGluIleValGluSerIleGlu---GluLysSerLeuGlyGlyMetAspLeuAla 242
Db      721  ACACAAAGAACTCTTGAGGCTTGCATGACATGACCAATCTGTGCTAGTAAACATGAAT 780
Qy      243  ProLeuGluLysLysLeuArgAspLeuLeuAsnGlyLysTyRtLeuLeuValLeuAsp 262
Db      781  ATGCTACAGAAACCTCTCCAGAGTATTTGGGGCAGAGAGTACTTGTCTTGTGGAT 840
Qy      263  AspValTlPleAsnGluAspGluAspLysTlPleAlaLysLeuArgGluValLeuLysValGly 282
Db      841  GATGCTGGAATGAGAGACTTGTATTAATGGCAGCAGCTRTAGAGCAGCTTATTTACGA 900
Qy      283  AlaSerGlyAlaSerValLeuThrThrArgLeuGluLysValGlySerIleMetGly 302
Db      901  GGGTTGGAACAGATATGTGTGATGACATCAGAAATGAGAAATGTTGGCAGAAATCATGGA 960
Qy      303  ThrLeuGluProTyRtGluLeuSerAsnLeuSerGlnGluAspCysTlPleLeuPheMet 322
Db      961  GGAATAGAGCCCTTCAAGTTTACAGAAATCTATCAATGATGATGACAGCTGTCTGTATTAAG 1020
Qy      323  GlnArgAlaPhe-----GlnHisGlnGluGluIleAsnLeuAsnLeu 336
Db      1021  AGCCATGAGATTTAGGAGTGTGACTGACAGCGGCACATCCGGAG-----TTG 1065
Qy      337  ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThr 356
Db      1066  GAGGGGATAGGAATGGAATTTGTGAAGAGCTGAAGGAGATTTGCCCTTGTGCAAAAGCA 1125
Qy      357  LeuGlyGlyIleLeuArgPheLysArgGluGluLysArgGlnTlPleGluHisLysArgAspSer 376
Db      1126  TTAGGAGAGCTCTCTTTTGGCAAAACAGATGAAGAGGTGAAGAGCATCTGCAAAAT 1165
Qy      377  GluIleTlPleLysLeuProGlnGluLysSerIleLeuProAlaLeuArgLeuSerTyR 396

```

Db 1186 GACATATGGAGTTACCGGAGATTAAGAAATACATCTCGACGCCCTCACTTAAGTTAC 1245
Oy HisHisLeuProLeuAspLeuArgGlnCysPheThrTrpCysAlaValPheProLysAsp 416
Db 1246 AACCATTTACCAACCATCTTAAGAGATGCTTGGATCTGTCTGTATATCTTAAGAT 1305
Oy 417 ThrGluMetGluValGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSer 436
Db 1306 TATATGTTCAAGAGAGAGAACTGGTTAAGATCTGGCTAGACCTTGTTTCATCAGACAG 1365
Oy 437 LysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTrpLeuArg 456
Db 1366 TCTAGAAAGAGAGAGATGAGATCTGAAATGATCACTTAAAGATTTAATTAAGCAGG 1425
Oy 457 SerPhePheGlnGluIleGluValLysSerGlyIleThrTrpPheLysMetHisAspLeu 476
Db 1426 TCTTTCTTCAGCCCATATGAG-----AATTAATATGATGATGATATGCA 1470
Oy 477 IleHisAspLeuAlaThrSerLeu----- 484
Db 1471 ATGCACGACCTTGCAAAATCTATCTCCATGGAAGACTGGACCACTTAAGATTAGGAGA 1530
Oy 484 ----- 484
Db 1531 AGACATGACAAATGCCATTAAAGACCCGTCATCTTTCCATTCATGACAGAGATGCCAAGTGC 1590
Oy 485 -----PheSerAlaSerThrSerSerSerSerAlaIleArgGluIleIleValGluAsnTrp 502
Db 1591 ATGCACCTTCAATCCACTGTATGGGTTTAGAAGCAAGCACTGACTACTT----- 1641
Oy 503 IleHisMetMetSerIleGlyPheThrTrpValLysSerTrpSerLeuSerHisLeu 522
Db 1642 ATCCAT-----GGATACAAAGTCAAAGAGATGCTCAATTGCCATGCTATTT 1689
Oy 523 GlnLysPheValSerLeuArgValIleAsnLeuSerAspIleLysLeuLysGlnLeuPro 542
Db 1690 ATGAAACTTGATATCTTAGAGTCTTGAATGATGATGATGCAAGAGCGCTTAAAGAGTTACCA 1749
Oy 543 SerSerIleGlyAspLeuValHisLeuArgTrpTrpLeuAsnLeuSerGlyAsnHisSerIle 562
Db 1750 GAATCTTAAGGAAATCTAATAACACTGCGCTTCCTAAGATCTCAGT---AGCACTGAATTC 1806
Oy 563 ArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGly 582
Db 1807 GAACATTACCAACGATCTCTTGTAAAGCTCTAATACTTGCAAAATCTAAAGCTGAGTGAC 1866
Oy 583 CysHisSerLeuCysValLeuProLysGluThrSerLysLeuGlySerLeuArgAsnLeu 602
Db 1867 TGCAATTTTCTAAGGAGAGTGCACAAAGCATCACTAGGCTCATTAATCTGCGCACATTA 1926
Oy 603 -----LeuLeuAspGlyCysTrpGlyLeuThrCysMetProProArgIle 617
Db 1927 GAAGCAATACAGACTACTGCTCCAGATACATGAG-----ATT 1965
Oy 618 GlySerLeuThrCysLeuLysThrLeuSerArgPheValIleGlyIleLysLysSer 637
Db 1966 GGAATTTGGTATGCTTACAGAACTAAGAAATTTGTAGTT-----CAGAAGGCTCA 2019
Oy 638 ---CysGlnLeuGlyGluLeuArgAsnLeuAsn---LeuTrpGlySerIleGluIleThr 655
Db 2020 GGGCAACAGCTCAGCAAGAACTAAATGAATGATGATGATGCAAGGCAACATTTCTATTGCT 2079
Oy 656 HisLeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGlu 675
Db 2080 GGCTTCATTAATGATCTTAATGGGCAAGATGCAAGTTTGCAAGATTAGAAACAAAG 2139
Oy 676 AsnLeuHisSerLeuSerMetLysTrpAspAspAsp-----GluArgProArgIleTrp 693
Db 2140 CATCTTGAACCTTACACTTATATGAGATGAGACTGAGCAAGCAATCTT----- 2190
Oy 694 GluSerGluLysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeu 713
Db 2191 ---TCAGAGCAGCAGAGAGTCTTAAGAGGTTCTTAACACCAATCTCGATCTCAAGGAATTA 2247

Oy 714 ThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValLeuLys 733
Db 2248 GTGATTTAAAGGGTTCCTGGGGGTAGAGTTCCCAAGCTGGCTGGGATTTCTTCCC 2307
Oy 734 AsnValValSerIleGluIleIleSerCysLysAsnCysSerCysLeuProProPheGly 753
Db 2308 AAGCTCAAAACCATATCATATATGCAACGTAGAACG---ACAAAGGCTTCCAGCTTTAGGC 2364
Oy 754 GluLeuProCysLeuLysSerLeuGluLeuThrArgIleSerAlaGluValGluTrpVal 773
Db 2365 CAGCTTCCCTTTTAAATATCTTGTCTATA---GCTGAGATTAAGTGAAGTACACAACTC 2421
Oy 774 AspSer-----GlyPheProThrArgArgPheProSerLeuArgLysLeuAsn 790
Db 2422 AGCAGTAGCTTACAGAGATTTGGACAAACAAAGGTTTCCAGCTTGAAGATCTTCTA 2481
Oy 791 IleArgLysPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGlnCysPro 810
Db 2482 TTGGAAATATGCAAAATCTGAGCGAGTGAATTTTGTGATGTTGCTGATCAATGTTTCCA 2541
Oy 811 ValLeuGluGluIleGluIleLysCysCysProMetPhe-----ValIleProThrLeu 828
Db 2542 CAATTAAGTAACTGTGCTCATCAAGTGCACACAGTTGAAGAACTTACTCTTAATGCCA 2601
Oy 829 SerSerValLysLysLeuValSerGlyAspLysSerAspAlaIleGlyPheSerSer 848
Db 2602 TCACACCTTAAGAACACTGTGATTTCTGAATCA-----GGCGTTGAGTCA 2646
Oy 849 IleSerAsnLeuMet----- 853
Db 2647 CTTCCAGAGCTTCAGAAATATCTTGTTCATCTTACCAACATCTCTATACATCAATGAT 2706
Oy 854 -----AlaLeuThr 856
Db 2707 TGCCCAATCTAATCTCTAAGTGAAGTTTACTTGTGATACAGACCAACAGCTTCAAA 2766
Oy 857 SerLeuGlnIleArgTrpAsnLysGluAspAlaSerLeuProGluGluMetPheLysSer 876
Db 2767 AGCTTAACAAATAGCCCATTTGMAAGGCTTGTTCACGCCAGAGAGATGTTCCGTCCA 2826
Oy 877 LeuAlaAsnLeuLysTrpLeuAsnIle-----Ser 886
Db 2827 TTAATATCACTCAAGAAAGCTGCACATCTAAGAGTGCCTTGTCTGTCCTTGCACAGCA 2886
Oy 887 PheTrpPheAsnLeuLysGluLeuProThrSer----- 897
Db 2887 CTGAGGAGAGGCTTG-----CTTCCCACTTCAATCGAAGATATCCGTAAACTCATGC 2940
Oy 898 -----LeuAlaSerLeuAsnAlaLeuLysHisLeu 907
Db 2941 ACTCATTAAGCAAGTGCCTTCTTAATGGCCTTAAGTACTTCCATCTTAAGCATTTT 3000
Oy 908 GluIleHisSerCysTrpAlaLeuGluSerLeuProGluGluValLysGlyLeuIle 927
Db 3001 GAAATGCTGATGTCCTGATATCAATTAATTTCCAGCAGAGGGGTTTACCTCAC----- 3054
Oy 928 SerLeuThrGlnLeuSerIleThrTrpCysGlyMetLeuGlnCysLeuProGluGlyLeu 947
Db 3055 ACACCTCAATTTTGGAGATATCATATGCTGATGATCTTCAATGCTTCACTCCGCTGCTG 3114
Oy 948 GlnHisLeuThrAla----- 952
Db 3115 CACAACATCTCTCACTTGAACACTAGCAATTAAGTACTGTCCGGGGGTTGAAGCTTG 3174
Oy 953 -----LeuThrAsnLeuSerValGluPheCysProThrLeu 964
Db 3175 CCAAAAGAGGCTGCGGATGGGGCTCAACGAGCTTTTACATCAAGAGGATGTCACAAAT 3234
Oy 965 AlaLysAspCysGlyLysGlyIleGlyGluAspTrpTrpLysIleAlaHisIle 982
Db 3235 AAGCAACATGTCCAAGAGGAT---GGGAGTATCATGCAAGAGATATGCTCAATC 3285

RESULT 13

US-10-437-963-51007

Sequence 51007, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Mu, Wei

APPLICANT: Bouharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 51007

LENGTH: 3669

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_53440C.1

US-10-437-963-51007

Alignment Scores:

Pred. No.: 5 44e-132 Length: 3669

Score: 1516.00 Matches: 408

Percent Similarity: 48.51% Conservative: 194

Best Local Similarity: 32.88% Mismatches: 355

Query Match: 29.57% Indels: 284

DB: 18 Gaps: 35

US-10-647-268-2 (1-988) x US-10-437-963-51007 (1-3669)

QY 1 MetAlaGlu-----AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIle 17

DB 1 ATGGGCGAGTCTACTATCGGCTCTTTGCTGCTGCTCCCTGAGAAAGACAGTGAATCTCTC 60

QY 18 GlnGlyGluLeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuLeuSerThr 37

DB 61 GGCACAGAGTTTATGTTTCTCGGGGTATGAAACAGCGCGCTTCGAGCTGATATACCTTG 120

QY 38 PheThrThrIleGlnAlaValLeuGluAspAlaGlnLeuLeuLeuLeuLeuLeuLeu 57

DB 121 CCGCTGCGCGTCAACCAAGTATCATGATGCCGAGATCAGGCATCCAAAGAGCTGCT 180

QY 58 IleGluAsnTrpLeuGlnLeuLeuAsnAlaAlaIleAlaIleGluAlaAspAspIleLeuAsp 77

DB 181 GGTAACTCTTGATCCCAAGCTGAAGCTGCTGCTGATGATGATGATGATGATGATGATGAT 240

QY 78 -----GluCysLeuThrGluAlaProIleArgGlnLeuLeuLeuLeuLeuLeuLeu 92

DB 241 GAGCTGCACTACGAGAGCTCCGCTCGGAGAGCTCCGCTCGGAGATTAATCATATACT 300

QY 93 Gly-----CysTrpHisProAsnValIleThrPheArgHisIleGly 107

DB 301 GGGGTAAAGGGCTTTCTCTCTCTCATTAATCCTTACTGTTCAAGTATGAGATGAGA 360

QY 108 LysArgMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 127

DB 361 AAGAGACTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 128 -----HisLeuAspGluArgThrIleGlnArgGlnValAlaThr 140

DB 421 GGGTTCCTTAATGCTCCATGCAAGTGAAGAGG----- 456

QY 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValIleGlyArgAspLeuGlyLeuLeuLeu 160

DB 457 ATGCAAACTATTCCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 516

QY 161 GluIleValLysIleLeuIleLeuAsnValSerAsnAlaGlnThrLeuProValLeuPro 180

DB 517 GAATTTGTCATATGCTTCTTAAT-----GCCGAGACGAGCAATTTGTAATATCTTCTT 570

QY 181 IleLeuGlyMetGlyLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200

DB 571 ATTGTTGGATGAG 630

QY 201 ArgValIleLeuHisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGlu 220

DB 631 AAGGTGAAGCAATTTTCAAAAGCATATGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 690

QY 221 LysArgLeuIleLeuGlnIleValGluSerIle-----GluLeuLysSerLeuGlyGly 238

DB 691 CCTGTTATTTGTCAGAGAGATTAATGACACCGCAATTTGGAATGATTTGTGAGTAAGATT 750

QY 239 MetAspLeuAlaProLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 258

DB 751 GATTAACCTGGAATTTGTCACAGCAACGCTTCGGGAGAACCTGGGCCCAAAAGAGTACTT 810

QY 259 LeuValLeuAspAspValIleTrpAsnGluAspGluAspLysTrpAlaLysLeuArgGlnVal 278

DB 811 TTGTACTAATGATGATGTTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 870

QY 279 LeuLysValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlyLysValGly 298

DB 871 CTGCTGCTTGTGGAATGAGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930

QY 299 SerIleMetGlyThrLeuGlnProTrpGluLeuSerAsnLeuSerGlnGluAspCysTrp 318

DB 931 TCAATCATGAGAGTCAATTAATGCTCATTTGCTGAGAGAACCTTAACCCAGAAAGATTCTTGG 990

QY 319 LeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGlnIleAsnLeuAsnLeuValAla 338

DB 991 ATTGTATTTACGACGAAGAAGCTTTGGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1050

QY 339 IleGlyLysGlnIleValLysLysCysGlyGlyValAlaProLeuAlaAlaLysTrpLeuGly 358

DB 1051 GTTGTAATAAGAAATTTGTAAGAAATGTTGGCGGCTCCGTTAGCCATTAAGAGATGATGGA 1110

QY 359 GlyIleLeuAspPheLysArgGlnGluArgGlnTrpGlnHisValAlaGAspSerGluIle 378

DB 1111 GCCTTGATGATCAAAACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1170

QY 379 TrpLysLeuProGlnGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTrpHisHis 398

DB 1171 TGG-----GATGAAGAAAGCCAGATATGCGACGGCTGCTTGGGCTACAAAAAT 1221

QY 399 LeuProLeuAspLeuArgGlnCysPheThrTrpCysAlaValIlePheProLysAspThrGlu 418

DB 1221 TTGCTCTCATATGAAACAAATGTTTGTGCTTTGTGTGCAATATCCGAAAGAGCTTACGAG 1281

QY 419 MetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGly 438

DB 1282 ATGTATAAGACGATCATATCATCTTTGGGTATCGAATGATTTATTCATCCAAAGAG 1341

QY 439 AsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTrpLeuArgSerPhe 458

DB 1342 ATGTACGATATGAAAGAAAGAGAGATCATGTTTTTGGAGCTGTGTTGAGAGTCAATTT 1401

QY 459 PheGlnGluIleGluVal-----Lys 465

DB 1402 TTCCAAATGTTAAGCAATTTGATCAATTTTCCAAAGCTAAAGTACAGGTATAGGAGCA 1461

QY 466 SerGlyGlnTrpTrpPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPhe 485

DB 1462 AGTAGTACATCAATTAATAATTCATATCTTATGATGATCTTGGCAGTTCATATAGC 1521

QY 486 ---SerAlaSerThrSerSerSerAsnIleArgGluIle-----IleValGluAsnTrp 502

DB 1522 GGTATGATGAGTGTATTGAGAAATCTGGCTAAATTAAGAAATATCCCAAAATATCTC 1581

QY 503 IleHisMet-----MetSerIleGlyPhe-----ThrLysVal 513

```

Db      1582 CATCATATGCGCTTTGAGGGTCACAAAGATGGTTCTTGATGACACATGTCAGATT 1641
Qy      514 ValSerSer---TyrSerLeuSer-----HisLeuGlnIlePheValSer--- 527
Db      1642 ATCCGACAGTATTTGCTTATAGATAGATGACATGATATTTGCCAGACATTAATTC 1701
Qy      528 -----LeuArgValIleuValSerAspIleValLeuLeuGlnLeuProSer 543
Db      1702 AATGAGTCTCTTATGAGTAGTGGCTTCATATTTCCGACATGAAAAATTTCTCTGT 1761
Qy      544 SerIleGlyAspLeuValHisLeuArgTyrIleuValSerGlyAsnThrSerIleArg 563
Db      1762 GAACGACGATTATGACACCTTATGATATCTTGATTGTCGTG---AGCTACATTAAT 1818
Qy      564 SerLeuProAsnGlnLeuCysValLeuGlnAsnLeuGlnThrIleuAspLeuHisGlyCys 583
Db      1819 ACATTACTTGAAGCAGCTAGCGCACTTATATTTACAAAGTGATGATACATGATGATGC 1878
Qy      584 HisSerLeuCysValLeuProLysGlnThrSerLysLeuGlySerIleuArgAsnLeu 603
Db      1879 AGAGGCTGACCCCACTTACAGATGCGCATGAATTTATGATTAGCTTCCGCAATGTGATC 1938
Qy      604 LeuAspGlyCysTyrGlyLeuThrCysMetProProAlaGlyIleGlySerLeuThrCysLeu 623
Db      1939 CTTATGACTGTGCTGCACTAACAGCAGCAGCTGTCTTACGACAGCTCATTAATTTA 1998
Qy      624 LysThrLeuSerArgPheValValGlyIleGlnIlyLysSerCysGlnLeuGlyGlnLeu 643
Db      1999 CGGACATGACAAAGTTGTAAGTCTGCTG---AATGATGCTGCTATAGGATTAACGAATGTG 2055
Qy      644 ArgAsnLeuAsnLeuTyrGlySerIleGlnIleThrHisLeuGlnArgValIleAsnAsp 663
Db      2056 AATGACTTAAACCTTGGGGGCAAGCTTCAGATATTATTTATTTGATTAAGTAAACAATCC 2115
Qy      664 MetAspAlaIlyGlnIleAsnLeuSerAlaLysGlnAsnLeuHisSerLeuSerMetLys 683
Db      2116 ATAAAGCAAAAGAAAGCAACCTTGAGTGAACAAATTTGACAGAGTTGACCTTTCG 2175
Qy      684 ThrAspAspAsp-----GluArgProArgIleTyrGlnSerGln 696
Db      2176 TGGGGCACATAAATCTCCGAGCTTACAGCTAAAGATTGCTATTTATATGCTCATGAA 2235
Qy      697 LysValGlnValLeuGlnAlaLeuLysProHisSerAsnLeuThrCysValThrIleArg 716
Db      2236 -----GAGTACTTGAAGCTCTTAAGCTCCCAAGCATTTGACCGTTCTAAAGCTGAG 2289
Qy      717 GlyPheArgGlyIleArgLeuProAspTyrPheAsnHisSerVal---LeuLysAsnVal 735
Db      2290 CAGTATATGGGCACTACGCTTCCCATATGATGAAATGGAATGACATCATTGCGCAACTT 2349
Qy      736 ValSerIleGlnIleIleSerCysLysAsnCysSerCysLeuProProPheGlyGlnLeu 755
Db      2350 GTTAAGCTCAAAAGTACGGAAGCTCCATTAATTTGTAAGAACTTCATCATGAGTGAAGCTT 2409
Qy      756 ProCysLeuLysSerLeuGlnLeuTyrArgGlySerAlaGlnValAlaGlyTyrValAspSer 775
Db      2410 CCGCTTCTCGAAGTCTCCGACTA---AAAGCATGAAGAAAGTTGAATCTTGTGTAAAC 2466
Qy      776 GlyPheProThrArgArgArg-----PheProSerLeuArgLys 788
Db      2467 GGGTTTGTGCTGTGTAATAAGAAATGATCATCATTAATGAGCATTTCCCAAAATTAAACTC 2526
Qy      789 LeuAsnIleArgGlnPheGlyAsnLeuLysGlyLeuLeuLysGlnGlyGlnGlu--- 807
Db      2527 TTGTCACTAGAACCAATGGAATCTTAGAAGAACTGCGAGAAATGATGTTGAAACAGATA 2586
Qy      808 -----GlnCysProValLeuGlnGlnIleGlnIleLysCysCysPro---MetPhe 823
Db      2587 ACACCGGCTATTTTCCGCTCTAGATGCATGAAATCATTTGATGTGCCAAATTTGACA 2646
Qy      824 ValIleProThrLeuSerSerValLysLysLeuValValSerGlyAspLysSerAspAla 843

```

```

Db      2647 GCTATGCCTAATGCTCCGGTTCTCAAGTCTGTAAGTGTATGAGAAACAATA---TTG 2703
Qy      844 IleGlyPhe---SerSerIleSerAsnLeuMet----- 853
Db      2704 ATTGGCTTATGCTCAAGTGTTAGTAAATCTGTGATCTATATCTTTGGTGCAGTCAAGG 2763
Qy      853 ----- 853
Db      2764 AGTTAGAGAGAAAAAACATATATCTATATCAATAAGAAAACTGGAAGAACACA 2823
Qy      854 ----- 854
Db      2824 GATTCAAGATCATGTTTGGCCCATCACTTTTCATCATGAGGGCTCATCACTAAATTA 2883
Qy      859 Gln----- 859
Db      2884 CACCTACAGGATTCAGTGTCTTAGACACAGAAATATACAAATATTAAGTGTACAGTGTG 2943
Qy      860 -----IleArgTyrAsnLysGln 865
Db      2944 ATGTCTGACAGACTTATGATCTAATTTCTGTGACTGTTCATTCATATGATATGATG 3003
Qy      866 AspAlaSerLeu----- 869
Db      3004 CAGTCACCACTGTGTTCTGGAATCATTTGCGCTGCGACAGCACTTAACAATGCAATGAC 3063
Qy      870 -----ProGlnGlyMetPheLysSerLeuAlaAsnLeuLysTyr 882
Db      3064 TGTAACAGCTCACCTTTTGGCCAGGGAGGAGTTCCAAAGCTTGACTTCTTAATAACGA 3123
Qy      883 LeuAsn----- 884
Db      3124 CTGCAATTAATGATATGCAACAACCTTCAAGGGTATGCAACTGCCCAAGTCTCAGTAAAG 3183
Qy      885 -----IleSerPheTyrPheAsn 890
Db      3184 TCCTTTGAAGATGAGGCACTGATATTTGGACGAGTAAAGAAATTCGTTGCTCAAC 3243
Qy      891 LeuLysGlnLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysValHisLeuGlnIleHis 910
Db      3244 TTAGTGGCTTCCCTTACAGCTTATGC-----TATCTGAGATATATGC 3285
Qy      911 SerCysTyrAlaLeuGlnIleSerLeuProGln----- 920
Db      3286 AGCTGCAATGATACTTGAAGCTTACGTGAAGAGATGAGGTTGCTGGGGGCTTAAGAAAGT 3345
Qy      920 ----- 920
Db      3346 CTGTCAATTGATTAATACCAAGACTGAAGTCCCTGCTCCACAGATTTCAACGTCTATCA 3405
Qy      921 -----GluGlyVal 923
Db      3406 AATTTGACAGAGCTTACCTGGGAATTAATGACAGCTTAACAACATTAACCGAAGGGATG 3465
Qy      924 LysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGlnMetLeuGlnCysLeu 943
Db      3466 CATATATGTGACAGCTCTCATATGATCTGTGCTATTTGGAATGTCCTTAATTAAGGCTTTA 3525
Qy      944 ProGlnGlyLeu---GlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysPro 962
Db      3526 CCGGAAAGTCTCCAGAGAGGCTGCACAGCTGGAAAGCTCTTTATTAAGCAATGCGCTT 3585
Qy      963 ThrIleuAlaLysArgCysGlnLysGlyIleGlyGlnAspTyrTyrLysIleAlaHisIle 982
Db      3586 ACGTGTGTGAGAGATCAAAACGTGA---GGAAGCTTACTGAGACAAAGTTAAAGATATT 3642
Qy      983 Pro 983
Db      3643 CCA 3645

```

RESULT 14
 US-10-437-963-33659
 / Sequence 33659, Application US/10437963

Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 33659
 LENGTH: 3852
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MKT4530_3774C.1
 US-10-437-963-33659

Alignment Scores:
 Pred. No.: 2,54e-128 Length: 3852
 Score: 1477.50 Matches: 397
 Percent Similarity: 50.79% Conservative: 179
 Best Local Similarity: 35.01% Mismatches: 348
 Query Match: 28.82% Indels: 212
 DB: Gaps: 36

US-10-647-268-2 (1-988) x US-10-437-963-33659 (1-3852)

QY 4 AAlpheuGlnValleuLeuAspAsnLeuThrCysPheIleGlnGlyLeuGlyLeu 23
 DB 380 GCGTTCATGACGAGCGCTTTTCAGAAAGCGGCGCTGCTTCAGAGAGCTGAATTC 439
 QY 24 ILeuGlyPheLeuAspGlyPheGlyLeuGlnSerThrPheThrIleGlnIle 43
 DB 440 CCTCAAAACATGAGCTGAGAGCTGCAAGATCTATCAGAGAGCTGTCGACATTTGGCT 499
 QY 44 ValIeuGluAspAlaGlnLeuLeuGlnLeuLeuAspAlaIleGlnAsnIlePheGln 63
 DB 500 CACGTTGAGATGCGAGAGCGGCGAGCTGAAGATCAGCGCGGCAAGAGCTGGCTTCC 559
 QY 64 LysLeuAsnAlaAlaIleGlyGlnIleAspAspIleLeuAspGlyCysLeuThrGlnIle 83
 DB 560 AGCGTGAAGAGCGTGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 619
 QY 84 ProIleArgGlnLeuLeuAsnLeuGlyCysIleGlnProAsnValIle----- 100
 DB 620 ---CTCCGATCCAACTTGCAGGCCCATCTCACTATCAGATCTGAAGTTGAATCTGC 676
 QY 101 -----ThrPheArgHisLeuIleGlyLeuAsnLeuLeu 111
 DB 677 TTCGTCGATTTGGTGAAGAAATGGGTATTTTAAACAGAGATTTGTAAACAAATATAG 736
 QY 112 LysIleMetGlnLysLeuAspValIleAlaIleGlnArg-----Ile 125
 DB 737 CGGATGAGAGGAGAGATGAGCTTATTAAGACAGACATATGTCTGCATCCGATCAG 796
 QY 126 LysPheHisLeuAspGlyLeuThrIleGlnArgGlnValAlaIleThrArgGlnThrGlyPhe 145
 DB 797 AGGTTTAAACAGGAAAG---ATTAAGAGAGAGGCC-----AAGACAGAGTTGC 841
 QY 146 ValLeuAsnGluProGlnValIleGlyArgAspLysGlnLysAspGlnIleValLysIle 165
 DB 842 TTAATGAGAGCTCGAGTGTGTATGCTAGAGAAAGATTAAGAGGTGATTTGAACATAG 901
 QY 166 LeuIle---AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
 DB 902 TTAAGTACACGAGATTAATCAAAACATGTCATCTTCTTATCTTCCATAGTGGGTATG 961

QY 185 GlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGln 204
 DB 962 GGAGAGTAGGAGAGACACTTTTAAACAGAGCTGTCTACATATGATGAGAGTAAAGAG 1021
 QY 205 HisPheHisProLysIleThrIleCysValSerGlnAspPheAsnGlnLysArgLeuIle 224
 DB 1022 CATTTCCAGTTAAGATAGT 1081
 QY 225 LysGlnIleValGlnSerIleGln-----GlnLysSerLeuGlyGlyMetAspLeu 241
 DB 1082 AAGGAAACGATTAAGATGAGTGGAGCGGATTAATCATCCGCCACACAAACATGAATCTTG 1141
 QY 242 AlaProLeuGlnLysLysAspLeuLeuAsnGlyLysLysTyThrLeuLeuValLeu 261
 DB 1142 -----CTTCAAGAGAGCTCTCAACAGCTGAAGAGCAAGAGTTCTTCTAGTATTTG 1195
 QY 262 AspAspValIleThrAsnGluAspGlnAspLysThrAlaLysLeuArgGlnValIleLysVal 281
 DB 1196 GATGATGATGAGATGAGATGCTGATGATGAGATGATGATGATGATGATGATGATGATGATG 1255
 QY 282 GlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlnLysValGlySerIleMet 301
 DB 1256 GTTCAAAAGAGATTAATTAATGAGTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1315
 QY 302 GlyThrLeuGlnProGlyGlnLeuSerAsnLeuSerGlnLysAspCysThrPheLeuPhe 321
 DB 1316 GCGCGGTGAGCTCTTATCTATCTTAAACAGTATCATATCAATGATGCTGGCATTTATTC 1375
 QY 322 MetGlnArgAlaPheGlyHis---GlnGlnGlnLysAsnLeuAsnValAlaIleGly 340
 DB 1376 AGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
 QY 341 LysGlnIleValLysLysCysGlyGlyValProLeuAlaIleAsnThrLeuGlyGlyIle 360
 DB 1436 AAGGAAATTTGCTTAAGTTGAAGGCTTACCTTACTCTCAAGAGCTTTAGTAGTCTTA 1495
 QY 361 LeuArgPheLysArgGlnGluArgGlnThrGlnHisValArgAspSerGlnIleThrLys 380
 DB 1496 TTATGTGCTAAGACCAACAGAGATGACGTGCAAAATATCTCAAGAAATGAAATTTGGAA 1555
 QY 381 LeuProGlnGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTyHisIleLeuPro 400
 DB 1556 TTGCATCAGACCAAAATTAATATCTTACAGCTCTGAGCTGAGTGAAGTTCATCATCTTCCA 1615
 QY 401 LeuAspLeuArgGlnCysPheThrTyrcysAlaValPheProLysAspThrGlnMetGln 420
 DB 1616 CCCATTTGAAGCGATGCTTTGCAATTCGTCGCGTCTTTCACAAAGACTATGTGTGGAG 1675
 QY 421 LysGlnAsnLeuIleSerLeuThrMetAlaHisGlyPheIleLeuSerLysGlyAsnLeu 440
 DB 1676 AAAGCATATATGTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1735
 QY 441 GlnLeuGlnAsnValGlnAsnGlnValIleThrAsnGlnLeuTyThrLeuAspSerPhePheGln 460
 DB 1736 AGGATGAGAGATGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1795
 QY 461 GlnIleGlnValLysSerGlyGlnThrTyrcPheLysMetHisAspLeuIleHisAspLeu 480
 DB 1796 -----AAACACAGAGATGGA-----TACGATGATGATGATGATGATGATGATGATG 1840
 QY 481 AlaThrSer-----LeuPheSerAlaSerThr 489
 DB 1841 GCGCAGTGTGTCTCCATTAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1900
 QY 490 SerSerSerAsnIleArgGlnIleIleVal-----GluAsnTyrcIle 503
 DB 1901 ACAGAAAGAAATGCCAGGCACT-ATCATTTCTCTTGACAAATAAATCAATCAATCAATTT 1959
 QY 504 HisMetMetSerIleGlyPheThrLysValLysSerTyrcSerLeuSerHisLeuGln 523
 DB 1960 TGAACCTTTTGT--GATTTTAATAGACACGAGCTTCTAAGCTGAATAGATATGATAA 2017

QY 524 Lys-----PheValSerLeuArgValLeuAsnLeuSer 534
 Db 2018 TCAGAAGACAGCTATCCCGAGTATGTCCTTCAATTTTAAGTACTCATCTCTT 2077
 QY 535 AspIle-----LysLeuLysGluLeuProSerSerIleGlyAspLeuValHisLeu 551
 Db 2078 GATTGGAAACGACAGAAATTACAGAAATTCGTCGTAATCTGTTGAAATTAAGATGCTC 2137
 QY 552 ArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGluLeuCysLys 571
 Db 2138 CGATTCCTGAACTTACAGGC---ACTGTTGTAAGAAAGCTGCTTCAATTCATTTGTAAG 2194
 QY 572 LeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCys---HisSerLeuCysSerLeuPro 590
 Db 2195 CTCTATTGCTTGGAAACCTTAAGTTAAGAACTCTGTCGATTAATCTGTAATCTC--- 2251
 QY 591 LysGluThrSerLysLeuGlySerLeuArgAsnLeuLeuAspGlyCysTyrGlyLeu 610
 Db 2252 -----CTATCCCTCGAAGCAAGAACTGAACCTG 2278
 QY 611 ThrCysMetProProArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheVal 630
 Db 2279 ATCACTGGCATAGCCAGAAATGGAATTAAGTCTTCAAAAGTGAAGAAATTTGTT 2338
 QY 631 ValGlyIleGlnLysLysSerCysGlnLeuGlyGluLeuArgAsnLeuAsn---LeuTyr 649
 Db 2339 GTCCAT---AAGCAAAAGATACAGGTAGTGAATTAAGAAAGCATTAAGATTCGA 2395
 QY 650 GlySerIleGluIleThrHisLeuGlnArgValLysAsnAspMetAspAlaLysGluAla 669
 Db 2396 GGACATATCTGCATTAATAATCTAAGAGAGCGTGTAGTGGCAAGAACAGATGAACGA 2455
 QY 670 AsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLysTrpAspAspArgLys 689
 Db 2456 TTGCTAAGTGAAGAGCAACACTGACATTTAGACCTTAATATGTTGTCAGTAGC----- 2509
 QY 690 ProArgIleTyrGluSerGluLys-----ValGluValLeuGluAlaLeuLys 705
 Db 2510 ---AGGATTTTACTTCAAGAAAGCAAAACGAGCATAGAAACATCATCTCCCTCGAA 2566
 QY 706 ProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIleArgLeuProAsp 725
 Db 2567 CCACATGATGAACCTCAAGAGCTGACATCAAGCATTTGCGAGATTCGAATTTCCACAT 2626
 QY 726 TrpMetAsnHisSerValLeuLysAsnValSerIleGluIleIleSerCysLysAsn 745
 Db 2627 TGG-----ATACTCTCACTTGCATAATCTCATCTGTCGATGATCAAT 2674
 QY 746 CysSerCysLeuProProPheGlyGluLeuProCysLeuLysSerLeuGluLeuTrpArg 765
 Db 2675 TGTTCATTTCTGCGACGACTTGACAGCTGCTCTACTCAAGGTATA----- 2722
 QY 766 GlySerAlaGluValGluTyrValAspSerGlyPheProThr----- 779
 Db 2723 -----ATCATTTGGGGTTTTTCTTACCATTAATAATTGAGAT 2761
 QY 780 -----ArgArgArgPheProSerLeuAspGlyLeuAsnIleArg 792
 Db 2762 GAGTTTTCAGTAGTAGTAAGATTAAGGGGTTTCGTCACAGAAAGAACTTGATTTGAA 2821
 QY 793 GluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGlnCysProValLeu 812
 Db 2822 GACACGCTTAATCTGAAAGGTGACCTTCACACAAAGATGAGTTCCTTCATCTCTT 2881
 QY 813 GluGluIleGluIleLysCysCysPheMetPheVal---IleProThrLeu---SerSer 830
 Db 2882 AGAGAACTTCAAGTCTGACGTGCTCCAAAGTAAGAAATTCCTCCCATCAACA 2941
 QY 831 ValLysLysLeuValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSer 850
 Db 2942 CTAGTGAACCTGAATAATTTCT-----GAGGACGAGCTTTTCTGTATCTTCT 2986
 QY 851 Asn-----LeuMetAlaLeuThrSerLeuGlnIleArgTyrAsnLys 864

Db 2987 GAAGTCACTGCTCCAGATTCTTCTACCATCATTTGACAGCCTTACAGATTCAAGAAATGCCCC 3046
 QY 865 GluAspAlaSerLeu----- 869
 Db 3047 AATTCATCTCTTCCAGCAAGAAATGCTTATGTCAGCAATTAATCAAGCCTCCAGCAACTA 3106
 QY 870 -----ProGluGluMetPheLysSerLeuAla 878
 Db 3107 ACCATCACTAATCTCCAGAACTAATTCACCCCACTGAAGATTAAGAACTTTAAT 3166
 QY 879 AsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuProThrSer--- 897
 Db 3167 GCTTCAGAGCTTTCACAT---TATGATTGTCAGAGCTGGCAACAGCAAGAA 3217
 QY 897 ----- 897
 Db 3218 CATGCTGCTTACTACTCGCATGATTAAGATTAAGCATCACTCACTGCTCAACATA 3277
 QY 898 -----LeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHis 910
 Db 3278 ATCAATCTCTTCTGATGAACCTTAATGAGCTCTTGTCTCAAGAAATCTTGTCAATGCG 3337
 QY 911 SerCysTyrAlaLeuGluSerLeuProGluGlu----- 921
 Db 3338 GATTGCGTTAGCTTAATTAATCTTTCCAGAAAGTTACCGGCTACCTCAAAAAATGGAG 3397
 QY 922 -----GlyValLysGlyLeuIleSer-----Leu 929
 Db 3398 ATCTTCATTCAGCAATTAATTCGCTCTGCTGCTGTTTCAAGAAAGCTCTTGTCTA 3457
 QY 930 ThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCysLeuPro---GluGlyLeuGln 948
 Db 3458 AAACTAGATCACTTAATATGTTGTTAGCATTAATAATCTTGGCCAGCATGAGCTTCCA 3517
 QY 949 HisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCys 968
 Db 3518 -----CTGCTCTTAAGAAATTAATTAATCAAGAGAGGCCCATTTCTGCGAGAGGTGT 3571
 QY 969 GluLysGlyIleGlyGluAspTyrTyrLysIleLeuHisIle 982
 Db 3572 CAGAAACAACTGAGAAAGATTGGCTTAATAATCTCATATA 3613

RESULT 15
 US-10-437-963-96697
 ; Sequence 96697, Application US/10437963
 ; Publication No. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yinhua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437, 963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ. ID NOS: 204966
 ; SEQ. ID NO 96697
 ; LENGTH: 4206
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9476C.1
 US-10-437-963-96697
 Alignment Scores: 5.89e-125 Length: 4206
 Pred. No.: 1442.50 Matches: 394

Percent Similarity: 46.83% Conservative: 189
 Best Local Similarity: 31.65% Mismatches: 375
 Query Match: 28.14% Indels: 287
 DB: 18 Gaps: 32
 US-10-647-268-2 (1-988) x US-10-437-963-96697 (1-4206)

OY 1 MetAlaGlu-----AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIle 17
 DB 1 ATGGGTGAGCTACTCTGACGCTTTCTACCTGCGCTTGGAAAGAAAGCTGGGAGCTCTC 60
 OY 18 GlnGluGluLeuGluLeuIleuGluPheLeuAspGluPheGluLeuGlnSerThr 37
 DB 61 TCCACAGAGTTTGAATTCATTTGGGGGATTTGAACCGCGCTTACAGACTGATATACCTTG 120
 OY 38 PheThrThrIleGlnAlaValLeuGluAspAlaGlnIleuGluLeuLeuAspIleuAsp 57
 DB 121 CTGCTTGGCATCAACCAAGTATCTATGTGCGCGAGAGCAGGCACTCCAAAGAGCTTCT 180
 OY 58 IleGluAsnThrPheGlnIleuLeuAsnAlaAlaAlaIleuGluIleuAspIleuAsp 77
 DB 181 GTGAAGTCTGTGATCCAAAGCTGAAGCTGCTGCTGTGATGCTGATGATGCTTCCAT 240
 OY 78 GluCysIleThrGluAlaProIleArgIleuGluLeuLeuAsnIleuGluLeuGly----- 93
 DB 241 GAGCTGCACACTGAGGCGC---CTTCCAGCGAGGAGCACTCCGTCGGGCAATAAATCAAC 297
 OY 94 -----CysTyrHisProAsnValIleThrPheArgHisIleValIle 106
 DB 258 AGTGGCGTAAGGCGTTTCTTCTCTCTCTATTAATCCCTTACTGTTCAAGATATGAGTA 357
 OY 107 GlnIleAspGluMetLeuLeuIleuGluLeuAspValIleAlaAlaGluArgIleLeu 126
 DB 358 GGAAGAAGAACTCCAGACAGTACGTGAACGATTGATCAGCTTGTTCGAAATGATCAA 417
 OY 127 PheHisLeu-----AspGluArgThrIleGluArgIleValAla 139
 DB 418 TTGGGGTCTTAATTTGCCCAATGCCAGACGATGAGAGS----- 456
 OY 140 ThrArgIleThrGlyPheValIleuAsnGluProGlnValIleGlyArgAspIleGluLeu 159
 DB 457 ---ATGCAGACCTATTCTTACGTCGACGAGGAGGATATTGGAAGGCAAGAAAGAGA 513
 OY 160 AspGluIleValIleLeuIleAsnValSerAsnAlaGluThrLeuProValLeu 179
 DB 514 GATGAATTCAACCATATGCTTCTTAAGT-----GCCAAGATGACAAATTTGTAATACT 567
 OY 180 ProIleLeuGlyMetGlyLeuGluGlyLeuGluLeuIleGlnMetValPheAsnAsp 199
 DB 568 CCTATTGTTGGGATAGAGGATTTGGGCAAGACAACTCTGACAGCTGCTTCAATGAC 627
 OY 200 GlnArgValIleGluHisPheHisProIleThrIleCysValSerGluPheAsn 219
 DB 628 GTGAAGTAAAGCAATTTTCMAAAGCATATGTGGTTGTGTCTTCAAGAACTTCAGT 687
 OY 220 GlnIleArgLeuIleLeuGluIleValGluSerIle-----GlnGluLeuSerLeuGly 237
 DB 688 GTTCTCGATATTTCAAGGGGATATTTGACACTGCAATTTGGGAATGATTTGGACGAG 747
 OY 238 GlnMetAspLeuAlaProLeuGluLeuLeuLeuAspIleuAsnGluLeuGlyLeuGly 257
 DB 748 AGTGAATACCTGGAATTGCTACAAACAGCTCTCGGGAAGAACTGACCAAAAGAGGTAC 807
 OY 258 LeuLeuValIleuAspAspValIlePheAsnGluAspGluAspIleThrAlaIleuArgIle 277
 DB 808 CTCTCTTGTACTATATATGTTTGAATGAGATGAACAAATATGGGAGGCTCTTAAGAAC 867
 OY 278 ValLeuLeuValGlyIleSerGlyAlaSerValLeuThrThrThrArgLeuGluLeuVal 297
 DB 868 TTCTCTTGTCTCTGTAATAAGGAGAGTGGCTGTGTGCACTACCCGAAATTCGATGTT 927
 OY 298 GlySerIleMetGlyThrLeuGlnProIleGluLeuSerAsnLeuSerGlnIleuAspCys 317

DB 928 GCGTACGTCAATGGGAGCAAGTTCCTCATTTGGCTCTTGAACCACTTACCAAGAAATTC 987
 OY 318 ThrLeuLeuPheMetGlnArgAlaPheGluHisGlnGluGluIleAsnLeuAsnValI 337
 DB 988 TGGACTATTTCTGTGAAGAGCGTTCCGTACAGGAGTGGCCAAAGTCTTGTGATTTGTC 1047
 OY 338 AlaIleGlyLeuGluIleValIleLeuGlyCysGlyGlyValProLeuAlaAlaIleu 357
 DB 1048 GAGATTGTCAAAAATTTGTTCAAAAATTTCTGAGGTCCCATTTAGCAATTAATAGTATG 1107
 OY 358 GlnGlyIleLeuLeuArgPheLeuArgGluGluArgGlnThrGlnHisValArgAspSerGlu 377
 DB 1108 GAGGCTGTCTGATGAAGAAACATGTGAAGGATTTGCTGCGCATCTTCAAAACAAT 1167
 OY 378 IleThrIleuProGlnGluGluSerIleLeuProAlaLeuArgLeuSerTyrHis 397
 DB 1168 ACTTGG-----GAGGAAATTAACATCTGACAGCTCATATGACTTACCTACAA 1215
 OY 398 HisLeuProLeuAspLeuArgIleCysPheThrTyrCysAlaValaPheProIleAspThr 417
 DB 1216 CATCTACCTTCTTTATGAACAGTGTGCTTTGTGTGCTGTATATCCAAAGAGACTAC 1275
 OY 418 GlnMetGluLeuGlyAsnLeuIleSerLeuThrMetAlaHisGlyPheIleLeuSerLeu 437
 DB 1276 GAGATTATTAAGATGATCTTAATACATCTGTGATATCAATGATTCATTCATCACTAA 1335
 OY 438 GlnAsnLeuGluLeuGluAsnValGlyAsnGluValIlePheAsnGluLeuTyrLeuAspSer 457
 DB 1336 GAGACCTCGCAATGAAGAACTGGGACAAAGTTTCTGAGAGCTTGTGGAGATCA 1395
 OY 458 PhePheGlnGluIleGluValIleSerGlyLeu----- 468
 DB 1396 TTTTTCMAAATGCGAAGCAAACTCGGTCCGCAAGAGAGTACATATATGGGTACAA 1455
 OY 469 -----ThrTyrPheLeuMetHisAspLeuIleHisAspLeuAlaThrSer----- 483
 DB 1456 GATGTAATCAATGCAAAATTCATGATCTTATGATGATCTTGCAAGTTCTATTAAGCGGG 1515
 OY 484 -----LeuPheSerAlaSerThrSerSerSerAsnIleArg 495
 DB 1516 GATGAGTCTATCTTTCMAAATCTTGTGAAATTAATTAATGCGAAGAAATTCAT 1575
 OY 496 GlnIleIleValGluAsnThrIleHisMetMetSerIleGlyPheThrIle 512
 DB 1576 CATCTAGTT-----TTCCACATCCACACAAAGATGTTCGTGATGACAGCTTGT 1626
 OY 513 -----ValIleSerSerTyrSerLeu-----SerHisLeuGlnIleuPheValSerLeu 528
 DB 1627 CCAATTATCCGAAGTCTATTAGTTTACATGAAGATCATATGAATTCATGAAGAGAGCTC 1686
 OY 529 -----ArgValIleuAsnLeuSerAspIleIleuLeuGlnLeu 541
 DB 1687 AGATTCAATGATGTCCTTGTGAAGCGGCTTGGCTTCATATCTGTGACAAATGAAGATTC 1746
 OY 542 ProSerSerIleGlyAspLeuValHisIleuArgTyrLeuAsnLeuSerGlyAsnThrSer 561
 DB 1747 TCAATTGAACCAAGCATATATGAAGACTTGGGATCTTGAATTTATTC---TCTACGAC 1803
 OY 562 IleArgSerLeuProAsnGlnLeuCysIleuAsnLeuGlnIleuAsnLeuIleHis 581
 DB 1804 ATAAAAACATCCCTGAAGCGGTGACAGTGCATGTAATTTACAAATCTAATCTCAAT 1863
 OY 582 GlnCysHisSerLeuCysCysLeuProIleGluThrSerIleuLeuGlySerLeuAsnAsn 601
 DB 1864 AGATGCAAGGCGCTGACCTCACCTGCTTACCGGCAAGAAATTAATGATCAGCTTTCGCAT 1923
 OY 602 LeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProArgIleGlySerLeuThr 621
 DB 1924 GTGATCTTGATGAGTGTCTTATGCTTACAAAGATGCGCGGCTGAGGCAAGCTGAC 1983
 OY 622 CysLeuIleuThrLeuSerArgPheValValGlyIleGlnIleuLeuSerCysGlnLeuGly 641
 DB 1984 AGTTTACGAACATTGACATGATATATGTTGGC---AATGAATCTGATTTGATCTTCAT 2040

QY 642 GluLeuArganLeuAsnLeuTyrGlySerIleGluIleThrIleLeuGluArgValys 661
 DB 2041 GAACTCAAGGACTTGAACCTTGGGGGCAAGCTACAAATACATTAATTTCTGAAGTACAA 2100
 QY 662 AsnAspMetAspAlaLeuGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSer 681
 DB 2101 AATCGGTACAGCAAAAGAGCCAACTTGAGAAATTAAGAAAATCTGCAGCAATACAA 2160
 QY 682 MetLysTrpAspAsp-----AspGluArgPro 690
 DB 2161 CTTCGTGGGACTCAGAAATTTCACTGTTCAATGTCATTTCTGCAGATGAATAATTTG 2220
 QY 691 ArgIleTyrGluSerGluLeuValGluValLeuGluAlaLeuLysProHisSerAsnLeu 710
 DB 2221 CAATTATCCGCTCCGAA-----GAACTGCTGAGTGTCTTTAGCCTCCCAACGATTA 2274
 QY 711 ThrCysLeuThrIleIleArgGlyPheArgGlyIleArgLysProAspTrpMetAsnHisSer 730
 DB 2275 AAAGTTTAAAGCTAAGGCAATATAGGCTCCAACTTCCAAATGTCAGATGGAAGATGCT 2334
 QY 731 Val---LeuLysAsnValSerIleGluIleIleSerCysLysAsnCysSerCysLeu 749
 DB 2335 GTGACACTGCAGAAATATGTTAACTCAGTTTGAGAGGCTCTGATGTGTCAAACTC 2394
 QY 750 ProProPheGlyGluLeuProCysLeuLysSerLeuGluLeuTrpArgGlySerAlaGlu 769
 DB 2395 CCACCACTGTGGCAGCTTCCCTTTTGAAGTTCCCTGCTCAACGA---ATGAGAGG 2451
 QY 770 ValGluTyrValAspSerGlyPheProThrArgArgArg----- 782
 DB 2452 TTGAATATCTGTGTATACAGGATACCCCACTGATGAAGATATGGCAACCAATTAGTGA 2511
 QY 783 PheProSerLeuArgLysLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeuLeuLys 802
 DB 2512 TTTCAAAATTTAAATTTATTTGCTACTAGATGAGATGATCTTGAAGAACTGCGCATGA 2571
 QY 803 LysGluGluGluGlu-----GlnCysProValLeuGluGluIleGluIleLys 818
 DB 2572 TATGACACTCAACAGTACATCACTTCTTTCCAAAGCTGAGCGCATGGAATTTATA 2631
 QY 819 CysCysPro---MetPheValIleProThrLeuSerSerValLysLysLeuValSer 837
 DB 2632 GACTGCCCAAACTGACAGCACTGCTTATGTTCGATTTCTTAAGTTTGACA 2691
 QY 838 GlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu----- 855
 DB 2692 GGAACAAAGTACTGCTGGGTTAGTGTCAAGTATTAGTAATCTATCATATCTGTATCTC 2751
 QY 856 -----ThrSerLeuGluIleArg-----TyrAsnLysGlu 865
 DB 2752 GGTGCACTCAAGGAGTTTCAAGGAGGAGAGAACATTAATCTATATATGAGAGA 2811
 QY 865 ----- 865
 DB 2812 CGTGAAGGAGAGCATGATACAAAGATGAGCATATTTTCCCGATCACTTGTGTGCATGG 2871
 QY 865 ----- 865
 DB 2872 GGTTCACCTCACTAACTACACCTACAGAGATTCAATACACGACAGAAAATGTGAAG 2931
 QY 866 -----AspAlaSerLeu----- 869
 DB 2932 AGTATAGTGTGCATATATGTCTGTGCAAGACTTAAGTCTGTCTTCTTGTGATGCTTC 2991
 QY 869 ----- 869
 DB 2992 ATCCAACATGAAGATTACAGTACACCATATGTTCTGTGATATCATTTGAGTCCCTACAA 3051
 QY 870 -----ProGluGluMetPheLysSer 876
 DB 3052 CAATTAGAATCTGGTACTGTGATAGCTTCACTTTTGGCCAGAGAGAGATTCCGAAGC 3111

QY 877 Leu----- 877
 DB 3112 TTGACTTTTAAAGAAAACCTTTCATTTGATGATGCAAAAACCTTCAACGGGTGACCACT 3171
 QY 878 -----AlaAsnLeuLysTyrLeuAsn 884
 DB 3172 GACCGACTGTGAGAGGCCCTTACAGATGAGAGGCCCATGTAAATTGGAAATACTTACAG 3231
 QY 885 IleSerPheTyrPheAsnLeu----- 891
 DB 3232 ATGATGCGCTGCCCACTTAAGTATTCCTTACAAACTTCATCTGCTACGATCCTT 3291
 QY 891 ----- 891
 DB 3292 GTGATTAACAGATTAATGACTTGAAGGGCTGCTGAGAGATTGTTGCCAGGGCACT 3351
 QY 892 -----LysGluLeuProThrSerLeuAla 899
 DB 3352 CTAAACACTCTGTAAATTTTGGGTGGCCCAAGTTTAACTCCCTGCGCCAGCATTTGG 3411
 QY 900 SerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeuGluSerLeuPro 919
 DB 3412 TGTCTTCAAAATCTGAAGAGCTTGAAGCTGACAAAGTAAATACAGCTTACCTTCTGCT 3471
 QY 920 GluGluGlyValysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMet 939
 DB 3472 ---GAGGAGATGCAAGATCTAAAGCTCTCAAAACACTACATTTTATTAATGTCTGCT 3528
 QY 940 LeuGlnCysLeuProGluGlyLeu---GlnHisLeuThrAlaLeuThrAsnLeuSerVal 958
 DB 3529 ATAAACCGCTTTACAGAGAGTCTCCAGCAAAAGACTGCGATGCGCTTCAACGTTCC 3588
 QY 959 GluPheCysProThrLeuAlaLysArgCysGluLysGlyIleGlyGluAspTrpTyrLys 978
 DB 3589 GAAGATGCGCTGCTGTGGCGAGAGATGACAGACTGG---GAGATTAATTTGGAGAAA 3645
 QY 979 IleAlaHisIlePro 983
 DB 3646 GTCAAGGACATTTCCCT 3660

Search completed: April 17, 2005, 07:25:47
 Job time : 1329 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 23:27:47 ; Search time 6346 Seconds
(without alignments)
5926.174 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAPLQVLNLTCTFIOGE.....EKIGEDWYKIAHPRVFY 988

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPFO_spool_p/US10647268/runat_15042005_154720_26496/app_query.fasta_1.1159
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10647268 @CGN 1.1 5180 @runat_15042005_154720_26496 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1:	gb_estc1:*
2:	gb_estc2:*
3:	gb_hc:*
4:	gb_estc3:*
5:	gb_estc4:*
6:	gb_estc5:*
7:	gb_estc6:*
8:	gb_gss1:*
9:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1515	29.5	3333	9	CL960744 OsIFRC037
2	1401	27.3	3408	9	CL976585 OsIFRC029
3	1335.5	26.0	3795	9	CL958853 OsIFRC036
4	1307.5	25.5	3318	9	CL975408 OsIFRC027
5	1293	25.2	3708	9	CL958564 OsIFRC001
6	1252	24.4	3354	9	CL975407 OsIFRC027
7	1241.5	24.2	3975	9	CL958562 OsIFRC001
8	1232.5	24.0	3003	9	CL966185 OsIFRC013
9	1212	23.6	3222	9	CL961820 OsIFRC037

10	1159.5	22.6	4236	9	CL962156 OsIFRC007
11	1145.5	22.3	3546	9	CL945091 OsIFRB001
12	1102.5	21.5	3273	9	CL962672 OsIFRC038
13	1101.5	21.5	3576	9	CL978496 OsIFRC031
14	1087.5	21.2	3996	9	CL957401 OsIFRC000
15	1062	20.7	670	7	CK861977 33106 1n
16	1061.5	20.7	4557	9	CL975789 OsIFRC028
17	1061	20.7	2409	9	CL979800 OsIFRC044
18	1058.5	20.6	4050	9	CL980521 OsIFRC034
19	1054.5	20.6	3264	9	CL964592 OsIFRC038
20	1052	20.5	2499	9	CL944015 OsIFRB001
21	1052	20.5	2499	9	CL965216 OsIFRC011
22	1051.5	20.5	3480	9	CL966533 OsIFRC039
23	1035	20.2	3459	9	CL947688 OsIFRB000
24	1025.5	20.0	1714	9	CL955053 OsIFRC036
25	1021	19.9	2628	9	CL976586 OsIFRC029
26	1009	19.7	3138	9	CL958931 OsIFRC036
27	987	19.3	1935	9	CL971348 OsIFRC041
28	983	19.2	4242	9	CL969777 OsIFRC018
29	981	19.1	3807	9	CL981299 OsIFRC036
30	978.5	19.1	3357	9	CL978519 OsIFRC032
31	977.5	19.1	3237	9	CL975780 OsIFRC028
32	977.5	19.1	3558	9	CL966532 OsIFRC039
33	977	19.1	1902	9	CL979799 OsIFRC016
34	964	18.8	4383	9	CL967922 OsIFRC043
35	963.5	18.8	3102	9	CL976854 OsIFRC043
36	962	18.8	2574	9	CL960528 OsIFRC004
37	961.5	18.8	4062	9	CL972598 OsIFRC023
38	957	18.7	3408	9	CL981346 OsIFRC036
39	955	18.6	2412	9	CL970995 OsIFRC020
40	949	18.5	3498	9	CL970551 OsIFRC020
41	943	18.4	3939	9	CL969775 OsIFRC018
42	942.5	18.4	2964	9	CL966199 OsIFRC013
43	934.5	18.2	2679	9	CL981493 OsIFRC045
44	927.5	18.1	3084	9	CL960027 OsIFRC003
45	926.5	18.1	3807	9	CL966328 OsIFRC013

ALIGNMENTS

RESULT 1
CL960744
LOCUS
DEFINITION OsIFRC037153 Oryza sativa Expressed library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL960744
VERSION CL960744.1 GI:52376202
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 3333)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen

JOURNAL COMMENT

Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1..3333

FEATURES
source
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"

ORIGIN /db_xref="taxon:39946"
/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences "

Alignment Scores:

Pred. No.:	1.3e-153	Length:	333
Score:	1515.00	Matches:	397
Percent Similarity:	51.05%	Conservative:	184
Best Local Similarity:	34.89%	Mismatches:	347
Query Match:	29.55%	Indels:	210
		Gaps:	34

US-10-647-268-2 (1-988) x CL960744 (1-3333)

```

Oy 4 AAlpheleugInValleuLeuaspAsnLeuThr-----CySphe1leGln 18
Db GCTTTCATGCAAAACCTCTCCAGAAATTGTCAGAAACACCTTGATCATTTCCATATCT 84
Oy 19 GlyIleuGlyLeuIleuGlyPheLeysAspGluPheGluIlyLeuGlnSerPhe 38
Db TGGAGA-----GGCATACATGGCAAGCTTAGAGAGCTCTTCCACACTG 129
Oy 39 ThrThrIleGlnAlaValleuGluAspAlaGlnIlySylsGlnLeuIlyAspAlaIle 58
Db TCTCAGATTACAGGCTTCTTCCAGATGCTGAGAGAAAGCACTTGACAGATGCATCTGTG 189
Oy 59 GluAsnTrpLeuGlnIlyLeuAsnAlaAlaIlyGluAlaAspAspIleLeuAspGlu 78
Db AGGGGATGGCTAGCGAAGCTCAGAGATATCGGTACGACCTTGATGATCTGTGAGAGGC 249
Oy 79 CysIlyStrGluAlaProIleArgGlnIlySylsAsnIlyTyGlyCySerThiAspAsn 98
Db TATTCAGCCAAAGT---ATGGCATGAGAGAGAGCAG-----GTGATTTCCCA 300
Oy 99 ValIleThrPhe-----ArgHisIlySylleGly 107
Db AAGGAAATTTTCTTCTTCCCTCCTCTTGAGTAGAATCTGTACACAGATAGATAAAG 360
Oy 108 LysArgMetIlySylleuMetGlnIlyLeuAspValIleAlaAlaGlnArgIleIlySph 127
Db CATAGATTACATCATATGAGAGATGAGATTAAGATTGCGCAAGAAAGGACACCAT 420
Oy 128 HisLeuAspGluArgThrIleGluArgGlnValAlaThrArg-----GlnThrGly 144
Db GGGCTCCAGATGATATGGAATGAGACGATATGATCTCAGAGCCGTCGCAATCAAGT 480
Oy 145 PheValIleuAsnGluProGlnValIlyArgIlyAspIlySylSylAspGlnIleValIly 164
Db TCTCTGTGATAGTATCGGCTGATATTGTTAGAGAGAGAGACAGAAAGAAATGTGAG 540
Oy 165 ---IleLeuIleAsnAsnValSerAsnAlaGlnTrpLeuProValLeuProIleuGly 183
Db CTGGGTCTCTGATTAATGACATATATTCCTGCAATTATGTGATCTCCAGTTTGGC 600
Oy 184 MetGlyIlyLeuGlyIlyLeuThrThrIleuAlaGlnMetValPheAsnAspGlnArgValIle 203
Db ATGGGTGGGCTGGTAAACCTACTCTTATGCAAGATGGTATCACCAGATGACAGAGTAA 660
Oy 204 GluHisPheHisPProIlyIleTrpIleCyValSerGluAspPheAsnGlnIlyArgIleu 223
Db GAACCTTTGACCTTAGAGATCTGATCTATGTCTGAAAGTTTGTGATGAGAAAGCTA 720
Oy 224 IleIlyGlnIleValGlnSerIleGlu---GluIlySerLeuGlyIlyMetAspLeuAla 242
Db ACACAAAGAACTCTTAGAGCTTCTGACATATGACATCTGTGCTAGTAACTAGAT 780
Oy 243 ProIleuGlnIlyIlyLeuArgAspLeuIlySylSylSylSylSylSylSylSylSyl 262
Db ATGCTTACAGAAACCTCTCCAGAGATATTCGGGGCAGAGGTTACTTGTCTGTGAT 840
Oy 263 AspValIlyPAsnGluAspGlnAspIlyStrAlaIlySylAspGlnValIleuIlyValIly 282

```

```

Db 841 GATGTCTGAATGAAGACCTTGATTAATGGCACAGTATAGAGACGCTTAATTTACGA 900
Oy 283 AAlaserGlyAlaSerValleuThrThrArgLeuGlnIlySylSylSerIleMetGly 302
Db GGGTTTGAAGCAAGATAGTGATGATCATCACAAATAGAAATGATGACAGATATAGGA 960
Oy 303 ThrLeuGlnProIlyGlyLeuSerAsnSerGlnIlyAspCyStrpLeuIlyPheMet 322
Db GGAATAGAGCCCTTCAAGATTACAGAACTATCAGATATAGACAGCTGTCTATTTCAAG 1020
Oy 323 GlnArgAlaPhe-----GlyHisGlnIlyGlnIleAsnLeuAsnLeu 336
Db AGCCATCATTTTAGAGATGGATGCTGACGCGCATCTCAGAG-----TTG 1065
Oy 337 ValAlaIleGlyIlySylSylIleValIlySylSylSylGlyValIProLeuAlaAlaIlyThr 356
Db GAGCGATAGAGATAGAAATGTGAAAGAGCTGAAAGGATTTGCTTGTGCATCAAGCA 1125
Oy 357 LeuGlyIlyIleLeuArgPheIlySylArgGlnIlyArgGlnTrpGlnHisValArgAspSer 376
Db TTAGAGAGCCTCCTGTTTGCAGAAACAGATGAGAGAGTGAGAGACATCTGCAAAAT 1185
Oy 377 GluIleTrpIlySylLeuProGlnIlyGlnIlySerIleLeuProAlaLeuArgLeuSerTy 396
Db GACATATGGAGATTACCGGAGATAGAAATACATCTGCGCAGCCCTAAGCTTAAGTTAC 1245
Oy 397 HisHisLeuProLeuAspLeuArgGlnCySpheThrTyCySylAlaValPheProIlyAsp 416
Db AACCATTTTACACACATCTTACAGAGTCTTGCATTTCTGTCTGTATATCTTAAGAT 1305
Oy 417 ThrIleuMetGlyIlySylAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSer 436
Db TATATGTTACAGAGAGAAACCTGTTAAAGATCTGGCAGACCTGGTTTCATCAGACAG 1365
Oy 437 LysGlyAsnLeuGlnIlyLeuGlnAsnValGlyAsnGlnValIlyPAsnGlnIlyLeuArg 456
Db TCTAGAAAGAGAGAAATGAGAAATCTGAAATGCATTAATTAAGATTATTAAGCAGG 1425
Oy 457 SerPhePheGlnIlyIleGlnValIlySerGlyGlnThrTyPheIlyMetHisAspLeu 476
Db TCTTCTTCCAGCCATATGAG-----AATACTATGTGATGATGATGCA 1470
Oy 477 IleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsn----- 493
Db ATGCACGACCTTGCAAAATCTATC-----TCCATGAAAGACTGCAACACTTAGAT 1521
Oy 493 ----- 493
Db 1522 TATGGAGAAACATGACAAATGCCATTAAAGCCGTCATCTTTCATTTCCATGCAAGAT 1581
Oy 494 -----IleArgGlnIleIleValGluAsnTy 502
Db GCCAAGTCATGACATTCATCCATCTGATGATGCTTTAGAGAGACGTAAGACATGATTT 1641
Oy 503 IleHisMetMetSerIleGlyPheThrIlyValIleValSerTyTySerLeuSerHisLeu 522
Db ATTCAT-----GATACAGTCAAGAGATGCTCAATGCGCTCATAGTCTATTT 1689
Oy 523 GlnIlySylPheValSerLeuArgValLeuAsnLeuSerAspIleIlySylIlySylLeuPro 542
Db ATGAAACTTGAATATCTTAAGTCTTGAATGATGACGACAAAGCCTTAAAGAGTTACA 1749
Oy 543 SerSerIleGlyAspLeuValHisLeuArgTyPheAsnLeuSerGlyAsnThrSerIle 562
Db GAACTTATAGGAATCTGAAACAACTGCGCTTCTCATATCTCAAT---AGACCTGAATC 1806
Oy 563 ArgSerLeuProAsnGlnLeuCySylSylGlnAsnLeuGlnIlyLeuAspLeuHisGly 582
Db GAAACATTACACAGATCTCTGTTAAGCTATATTAATCTTAAGCTTAAGCTGAGCAG 1866
Oy 583 CysHisSerLeuCySylLeuProIlySylIlyThrSerIlySylGlySerLeuArgAsnLeu 602
Db TGCAATTTTCTTAAGAGAGATGCAAGGACATCACTGAGCTCATTAATCTGCGCACTTA 1926

```

```

Oy 603 -----LeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIle 617
Db 1927 GAAGCAAGTACAAAGACTACTGCTCCAGATACATGA-----ATT 1965
Oy 618 GlySerLeuThrCysLeuLeuThrLeuSerArgPheValValGlyIleGlnIleLysSer 637
Db 1966 GGAATTTTGTGATGCTTACAGAACTGAGAAAGATTGTAGTT-----CAGAAAGCTCA 2019
Oy 638 ---CysGlnLeuGlyGlyLeuArgAsnLeuAsn---LeuTyrGlySerIleGlnIleThr 655
Db 2020 GGGCAACAGCTCACAGAACTTAATATACATGATGAGCTGCAGAGCAACATTTCTATTGCC 2079
Oy 656 HisLeuGluArgValIleAsnAspMetAspAlaLysGluIleAsnLeuSerAlaLysGlu 675
Db 2080 GAGCTCAATTAATGATCTTAATGGCAAGATGAGATTGTGCAGAACTTGAAGAAACAAAG 2139
Oy 676 AsnLeuHisSerLeuSerMetLysTyrAspAspAsp-----GluArgProArgIleTyr 693
Db 2140 CATCTTCAGACTCTACACCTTATATGATGATGAGCTGTGAAGCAATCCT----- 2190
Oy 694 GluSerGlyLysValGluValLeuGluIleLeuLysProHisSerAsnLeuThrCysLeu 713
Db 2191 ---TCAGAGCAAGAAAGTTCTAGAGAGTCTTCAACCAATCTCGATCTCAAGAAATTA 2247
Oy 714 ThrIleArgGlyPheArgGlyIleArgLeuProAspTyrMetAsnHisSerValLeuLys 733
Db 2248 GTGATTAAGAGGTTCCCTGGGGTGAAGTTCCTCCAGCTGGCTGGCTAGTTCTTTCTTCC 2307
Oy 734 AsnValValSerIleGlnIleIleSerCysLysAsnCysSerCysLeuProProPheGly 753
Db 2308 AAGCTGCAACCAATCATATATGACATGCTAGAACG---ACAAGGCTTCCAGCTTAGGC 2364
Oy 754 GluLeuProCysLeuLysSerLeuGluLeuThrPargGlySerAlaGluValGluTyrAl 773
Db 2365 CAGCTTCCCTTTTAAATATCTGTCTCA---GCTGAAGTACTGAGAGTACACCAACTGC 2421
Oy 774 AspSer-----GlyPheProThrArgArgPheProSerLeuArgLysLeuAsn 790
Db 2422 AGCAGTGAAGTTCACAGATTTTGAGAACCAAAAGTTTCCAGCTTGAAGATCTTCTTA 2481
Oy 791 IleArgGluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGlnCysPro 810
Db 2482 TTGGAAGATATGCCAAATCTGAGCAGAGGATTTTGTATGTTGCTGCAATGTGTTCCA 2541
Oy 811 ValLeuGluGluIleGluIleLysCysProMetPhe-----ValIleProThrLeu 828
Db 2542 CAATTAACTGAATCTGCTCATCAAGTCCACAGTGAAGAAATGCTCTTATTTCCA 2601
Oy 829 SerSerValLysLysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSer 848
Db 2602 TCACACACTGAAGAACCTGTGATTTCTGAATCA-----GGGCTTGAGTCA 2646
Oy 849 IleSerAsnLeuMet----- 853
Db 2647 CTTCCAGAGCTTCAAGATTAATTTCTTGCATCTTCCACCAACATCTCTATACATGAT 2706
Oy 854 -----AlaLeuThr 856
Db 2707 TGCCCAATCTAATCTCTACGTGAGTTTAACTTGATACAGACCAACAGCTCTCAA 2766
Oy 857 SerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLysSer 876
Db 2767 AGCTTAACAAATAGCCCATGTGAAGGCTTGTTCATGCGCAGAGAGTGTTCGCTCA 2826
Oy 877 LeuAlaAsnLeuLysTyrLeuAsnIle-----Ser 886
Db 2827 TTAATATACCTCAGAGAGCTGACATCTACAGAGTCCCTTGTCTGCTGCTTGACACGA 2886
Oy 887 PheTyrPheAsnLeuLysGluLeuProThrSer----- 897
Db 2887 CTGAGGAGAGGCTTG-----CTTCCCACTTCAATCGAAGATATCCGCTAACTCATGC 2940

```

```

Oy 898 -----LeuAlaSerLeuAsnAlaLeuLysHisLeu 907
Db 2941 ACTCCATTAGCAAGTGTCTTAAATGCGCTTAATGCTTCTCTCATAGTCATTTT 3000
Oy 908 GluIleHisSerCysTyrAlaLeuGluSerLeuProGluGluValIleGlyLeuIle 927
Db 3001 GAAATGTGTGATTTCTCTGATATCAATTAATCTTCCAGCAGAGGGGTTTACCTCAC- 3054
Oy 928 SerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCysLeuProGluGlyLeu 947
Db 3055 ACATTCAATCTTCTGAGATATCATGCTGTGATGATCTTCAATGCTTACCTCCGTGTG 3114
Oy 948 GlnHisLeuThrAla----- 952
Db 3115 CACAACATCTCTCACTTGAACACATACGATTAAGTCTCCGGGCTTGAAGCTTG 3174
Oy 953 -----LeuThrAsnLeuSerValGluPheCysProThrLeu 964
Db 3175 CCAAAAGAGGCTCCGAGTGGGCTCAACGAGCTTACATCAAGGAGTGTCCACAAATT 3234
Oy 965 AlaLysArgCysGlyLysGlyIleGlyGluAspTyrLysIleAlaHisIle 982
Db 3235 AAGCAACAAATCCAAAGAGT---GGGAGTATCATGCAAGATAGCTCACATC 3285

RESULT 2
LOCUS CL976585
DEFINITION Oryza sativa Expressed library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION CL976585
VERSION CL976585.1 GI:52407684
KEYWORDS GS.
SOURCE
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3408)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80486676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..3408
location/Qualifiers
1..3408
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_id="Oryza sativa Expressed library"
/notes="Oryza sativa exon trapped genomic sequences"

ORIGIN
Alignment Scores:
Pred. No.: 4.4e-141 length: 3408
Score: 1401.00 Matches: 372
Percent Similarity: 48.51% Conserved: 196
Best local Similarity: 31.77% Mismatches: 365
Query Match: 27.33% Indels: 239
DB: 9 Gaps: 33

US-10-647-268-2 (1-988) x CL976585 (1-3408)
Oy 1 MetLacIuAlaPheLeuGlnValIleLeuAspAsnLeuThr-----CysPhe 16

```



```

Qy 682 MetLysPASPASP-----GluArgProArgLysLeuSerGluLysVal 698
Db 2140 CTTGATGAGGATAGTAATGCGGTGTAGGAAACCAATTCGCATGAG----- 2187
Qy 699 GluValLeuGluValLeuLysProHisSerLeuLeuThrCysLeuThrLileArgLysPhe 718
Db 2188 AAGGTTCTGTAGTCTTAAACCTCATGCGCGCTGATGCTCACCCTAATTTCCAT 2247
Qy 719 ArgGlyLileArgLeuProAspTrpMetAsnHis-----SerValLeuLysAsnValValSer 737
Db 2248 AAAGACCTCATTTTCCAGCATGAGTGAAGATCTTAAATGCTGCAAACTTGCGTAG 2307
Qy 738 IleguLileSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuProCys 757
Db 2308 CTCGAATTGATGTTGTTACATGATGCGAAGAAATTTCCACGTTTATTCATGTAAGCT 2367
Qy 758 LeuLysSerLeuGluLeuTrpArg----- 765
Db 2368 CTTCAAGTCTCTATTTGATTAGACTTGAACAATTCGAACCCCTGTGTGAGGAGGA 2427
Qy 766 -----GlySerAlaGluVal----- 770
Db 2428 AGACAGGAAAGAAAGAACATTTCTACTTAAAGTTGTTATCGAGAGCTGTCCA 2487
Qy 771 -----GluTrpValAspSerGlyPheProThrArgArgArg--- 782
Db 2488 AAATTCGACATTAAGTTCATGACATGCGATCCACAAGCTTCCAGCAGAAAGAAATC 2547
Qy 782 ----- 782
Db 2548 AACTTACATGATGAGCTTAGACAGATGTTGTCGATTTGAGAGACAAAGAAATGACCA 2607
Qy 782 ----- 782
Db 2608 ACGTTCTCTGCTTGAAGAGATTGTAATGAGAAATGTCAAAACCTAACACTATGC 2667
Qy 783 -----PheProSerLeuArgLysLeuAsnLileArgGluPheGly 795
Db 2668 TATGAAATGGCTTCCACAGCATTTCCATCATTAAGAAATCAGTTATATGATTAGGC 2727
Qy 796 AsnLeuLysGlyLeuLysGlyGluGluGluGluGluGluGluGluGluGlu 815
Db 2728 GCGTTAGAGAGACTGTG-----GAAAACAATCACAATTATCTCTGTTGAAGTGT 2781
Qy 816 GluLileLysCysCysPro---MetPheValLileProThrLeuSerSerValLysLeu 834
Db 2782 GACATCAGAACTGTCCAAAACCTGAGAGTCTACCCGAAAGACCAAAAGCTCAGATTTC 2841
Qy 835 ValValSerGlyAspLysSerAspAlaLileGlyPhe-----Ser 847
Db 2842 ACGCTAAATGAAACAGAGCCAGCTGTCTGTTTTCATTCATTCAGATGCATGTC 2901
Qy 848 SerLileSerAsnLeuMetAlaLeuThrSerLeuGluLileArgTrpAsnLysGluAspAla 867
Db 2902 TCATTATCCAGACTATAT-----CTGACGCGGANTGACCAAAAAGAACACTG 2949
Qy 868 SerLeuProGluGluMetPheLysSerLeuAlaAsnLysTrpLysAsnLileSerPhe 887
Db 2950 CAGCTGTGTGATTCACGAATCATCTCTCAAAACCTGGAATTTAGCAGCTGCAACTTT 3009
Qy 888 TyrPheAsnLeuLysGluLeuProThrSerLeuLileSer----- 900
Db 3010 TTCTAC-----CCACAGAGCCCATCAACAACCAATTAATTTTGGAAA 3054
Qy 901 ---LeuAsnAlaLeuLysHisLeuGluLileHisSerCysTrpAlaLeuGluSerLeuPro 919
Db 3095 CGGCTTGACAACTTGCTGATTTGAGATGACGAATGATGAGCTCATCTACCTGCGCA 3114
Qy 920 GluGluGlyValLysGlyLeuLysSerLeuThrGluLeuSerLileThrTrpCysGluMet 939
Db 3115 GAGGAAGAGTTCCGATGCTTAGTATCTTGAAGACATGGAATTAATGCAATGATGATAG 3174

```

```

Qy 940 Leu-----GlnCys 942
Db 3175 CTAATAAGGCGTCCCATGCTGTGTAAGAGCAACTTCTGTGCAAGGATCAGCTC 3234
Qy 943 LeuPro-----GluGlyLeuGlnHisLeu----- 950
Db 3235 CTGCCACGCTTAACCTCACTTCAATTCGGCGGTGTATGACTGAGAGACTCTTGCTT 3294
Qy 951 -----ThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCys 968
Db 3295 CTTCCCATCTCTCCACAAATATGATATGATTAGTTGCTCTAATCTT----- 3342
Qy 969 GluLysGlyLileGlyGluAspTrpTrpLysLile 979
Db 3343 GAGTA-CATATGGGGGATGGGTGTATAGAGTTC 3374

RESULT 3
CL958853
LOCUS
DEFINITION
OsbIFC036417 Oryza sativa Express Library Oryza sativa (indica
cultiyar-group) genomic, genomic survey sequence.
ACCESSION
CL958853
VERSION
CL958853.1 GI:52372461
KEYWORDS
GSS.
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 3795)
Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.X.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
CONTACT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomic
Chinese Academy of Sciences, Beijing 10300, China
Tel.: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES
Source
1..3795
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "

ORIGIN
Alignment Scores:
Pred. No.: 8.3e-134 Length: 3795
Score: 1335.50 Matches: 379
Percent Similarity: 44.48% Conservative: 193
Best Local Similarity: 29.47% Mismatches: 359
Query Match: 26.05% Indels: 355
DB: 9 Gaps: 41

US-10-647-268-2 (1-988) x CL958853 (1-3795)
Qy 34 LeuGlnSerThrPheThrTrpLileGlnAlaValLeuGluAspAlaGlnLysLys----- 51
Db 1 ATGAGAGCCAGATTCGACCAATCCGCGCGCTGTCCGACGCGGAGCGCGCGCGC 60
Qy 52 GlnLeuLysAspLysAlaLileGluAsnTrpLeuGlnLysLeuAsnAlaLalaLysGlu 71
Db 61 GCCGCGCGGACCGCGCGCTGCGAGCTGCTCGAGCTCAGAGAGCGTCCGCGCAC 120
Qy 72 AlaAspAspLileLeuAspGluCysLysThrGluAlaProLileArgGlnLysLysAsnLys 91

```

```

Db      121  ATGACGAGCTTCCTGACGCTTGCACACCGAC-----CTCCGCGCGGCGAGGCGCG 174
Oy      92  TyrGlyCystrYhIsProAsnValIleThrPheArg---HisValIleGlyLysArgMet 110
Db      175  GGGAGCTGCTCGGTGTGGCGGCGCTCAAGCGCGCTGCTTCGCGATGCGGACAGGCTG 234
Oy      111  LysIlyslIleMetGluLysLeuAspValIleAlaIleGluArgIleLysPheHisIleu--- 129
Db      235  AGGTCCCTCAAGCGCGAGCTGGCGCGCTGCGCGCATGCCATGCCAAGACAGGTTCTCCCTGAGC 294
Oy      130  ---AspIlyArg---ThrIleGluArgIleValIleAlaIleThr-----ArgIleThr 143
Db      295  CCGAGCGCGCGCGCGCGCGCTGCGGAGAGCTCCCTCCGTCGCCACCCATGCGGAGACC 354
Oy      144  GlyPheValIleuAsnGluProGlnValIleArgIleAspIleGlyLysAspIleVal 163
Db      355  ATCTCCATGTCGACAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 414
Oy      164  LysIleIleuIleAsnAsnValSerAsnAlaGlnThr-----LeuProVal 178
Db      415  AGGCTGCTCTCGACGCGCGGCGGCGGACGACGACGACGACGACGACGCGCTCCGCTC 474
Oy      179  LeuProIleuGluMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsn 198
Db      475  ATCCCATGTCGCGGCGGCTCGGCGGCTCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 534
Oy      199  AspGlnArgVal---IleGluHisPheHisProLysIleTyrIleCysValSerIleuAsp 217
Db      535  GACCGGAGGCGGCGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 594
Oy      218  PheAsnGluLysArgLeuIleLysGluIle-----ValGluSer 230
Db      595  TTCACGCTCGCGCACGCTGCTCGAGGCGGCGGACCCCAATCGTCGCGCGCGCGCGGAG 654
Oy      231  IleGluIleuLysSerLeuGlyGlyMetAspIleuAlaProLeuGlnIleLysIleuArgAsp 250
Db      655  TGGCAGCTCGCGCACCAACCAACCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
Oy      251  LeuLeuAsnGlyLysLysIleLeuLeuValIleuAspAspValIleAsnGluAspIleuAsp 270
Db      715  GCGTTCAGCGGGAACAAGTACTGCTGCTGCTCGACGAGTGTGAGAGGAGGAGGAGGAG 774
Oy      271  LysTyrPalaLysLeuArgIleValIleuLysValIleGlyAlaSerGlyAlaSerValIleuThr 290
Db      775  GAGTGGAGCGGCTGAGGCTGCTCTCGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAG 834
Oy      291  ThrThrArgLeuGluLysValIleGlySerIleMetGlyThrLeuGlnProTyrGluLeuSer 310
Db      835  ACGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 894
Oy      311  AsnLeuSerGlnIleuAspCysTyrLeuLeuPheMetGlnArgAlaPheGlyHis---Gln 329
Db      895  AGCCTCTCTGAGAGAGATTGCTGGAGGCTTCAAGAGAGAGGAGGAGGAGGAGGAGGAG 954
Oy      330  GluGluIleAsnLeuAsnLeuValAlaIleGlyLysGluIleValIleLysIleGlyGly 349
Db      955  GAGGAGATTGTATCCCAAAATTTGTCAGAGATGAGAGAGAGAGAGATTGTCCTCCCAATGCGGCGGC 1014
Oy      350  ValIleProLeuAlaAlaLysThrIleuGlyLysIleLeuAsnArgPheLysArgGluIleuArgIle 369
Db      1015  GTGCGGCTGGCGGCGGAGAGGCGCTTGGAGAGAGCTGAGGAGGAGGAGGAGGAGGAGGAG 1074
Oy      370  TyrGluHisValIleArgAspSerGluIleTyrLysLeuProGlnGluIleuSerIleu 389
Db      1075  TGGATTGCTGTCAGAGAGAGTGAATTTGGCAGCTGAGATGAAGAGAGAG---ACCATTTTG 1131
Oy      390  ProAlaLeuArgLeuSerTyrHisIleuProLeuAspLeuArgIleCysPheThrTyr 409
Db      1132  CCATCTCTCAAACTCAGCTATGATCAAAATGCCGTTCTGAACCAATGCTTCGCGAT 1191
Oy      410  CysAlaValPheProLysAspThrGluMetGluLysGlyAsnLeuIleSerIleuTyrMet 429

Db      1192  TGTGCGGTGTTCTCTCAAAACATGATGATGACAGGAGTAACTTATTCAGCAATGGGTT 1251
Oy      430  AlaHisGlyPheIle-----LeuSerLysGlyAsnLeuGluLeuGluAsnValIleLysAsn 447
Db      1252  GCTCTGGCTTTGTTGAACCTCAAGATAGTGTGCCAGCGCGGTTTCTGATTAAGCGGAC 1311
Oy      448  GluValTyrPheAsnGluLeuTyrLeuArgSerPhePheGlnGluIleGluValLys----- 465
Db      1312  GACTGTTTGAAGACTTGTGTGTGATGTCATCTCTCAAGAGGTAGACCAATGATGATTTG 1371
Oy      466  -----SerGlyGlnThrTyrPheLysMetHisAspLeuIleHis 478
Db      1372  TCAAGAAAGAGATTAGAGTTAGATGAAAGATTAAAGTAAATTCACAGACTGTGTGAT 1431
Oy      479  AspLeuAlaThrSer-----LeuPheSerAla----- 487
Db      1432  GACCTTGCTGAGTGTGTGCGGGAGTAAAGTTCAGATCATTAACCGCTTAACCGAGTCAAT 1491
Oy      488  -----SerThrSerSerAsnIle 494
Db      1492  GGGAGACAGAGCTTGCCGCTATGATCATTTGATGATGATATATGGGGGTGACCGAGTGT 1551
Oy      495  -----ArgGluIleIleVal 499
Db      1552  CTTTGAGAGCATGCTTCGCAAAATCGGCGCTTTCATTCCTGGGCGCGTATGACATTT 1611
Oy      500  GluAsnTyrIleHisMet----- 505
Db      1612  AATTATTTCTTCCTCCAGGTTCTTGAGAGTACATAGATTGGCGGCGGCGCAAAATATAG 1671
Oy      506  -----MetSerIleGlyPheThrLysValIleSerSerTyrSerLeuSer----- 520
Db      1672  GAGCTCCCTCATGTGTTGTTGAATTTGAGACATTTGAGATCTTGAGACTTCTTCATCC 1731
Oy      521  -----HisIleu 522
Db      1732  CTTATCAGTACTCTGCCCAATTTGATGATGATGATCTCCACAAATTTGCAAACTCTTCATTTA 1791
Oy      523  GlnLysPheValSerLeuArgValIleu----- 531
Db      1792  TACAATTCATTAATTCATATGTGTGCTGCCATGTACAGTATGTGCCCTTGAGAACTAGAA 1851
Oy      531  ----- 531
Db      1852  ATCTTGAATCTTTGACGTTGCACTTCATAGCTTTCGCCAGATTCTATAGACATCTTCAA 1911
Oy      532  AsnLeuSerAspIleLysLeuLys-----GlnLeuProSerSerIle 545
Db      1912  AACCTTACAAAGATCTTAATCTTGTCCCTTGACATTTCTCTTGAGACATTAACCTTATAT 1971
Oy      546  GlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSerIleu 565
Db      1972  GGTACACTCCAAAGTTTGACTTGTCTGAACTTGAAGAGATGTGGCAACCTTGAATTTCTA 2031
Oy      566  ProAsnIleuCysLysLeuGln----- 573
Db      2032  CCTGACACTATATGACGCTGCAAAATTTTACATTTCTTGAACCTTTACAGATGTGTGT 2091
Oy      573  ----- 573
Db      2092  CTCCAAGACAGTCCCAAAATATTTGTAACCTTTCAAAATTTTGGACCTGAATTTATCA 2151
Oy      573  ----- 573
Db      2152  CAATGACTGATCTTGAATCAATCCCACTCAATATAGTGCATTAAGAGCTTGATATTT 2211
Oy      573  ----- 573
Db      2212  CTGATCTGTCTCACTGATAGTGTGTGACAGATTACAGAGATCATTTGTGTCTTCAT 2271
Oy      573  ----- 573
Db      2272  GAACCTTGATATTCATTTTATTCACACCATGCAAGAGAGTGGATTCGATTCATCACT 2331

```

QY 574 -----AsnLeuGlnThrLeuAspLeuHis----- 581
 Db 2332 AGTCATCTCCGAACCTTGACAGCTTATGATCTCTCATGAGAACTTAACTAGTAGAGAAATTG 2391
 QY 581 ----- 581
 Db 2392 CCTGATCAATATGGCAATCTTATGTTGAAGACCTGATCTTGTTCAGTGTGAGT 2451
 QY 581 ----- 581
 Db 2452 CTACGTAACTGCTGAGCTATTAACAACCTCATGATGTTAGAGAGTTGAACTTTGTT 2511
 QY 582 GTCYHISerLeuCyseLeuProLyseGluThrSerLyseGlySerLeuArgan 601
 Db 2512 GCGCTGAAAACCTAGCTAACTAGCTATGATGACAGATGACCAATCTGAAACAT 2571
 QY 602 LeuLeuLeuAspGlyCyseTyrglyLeuThrCyseMetProProArgLyseGlySerLeuThr 621
 Db 2572 TTAAGAAATGACCAATGTCGATCTTTAAACAACCTAATGATTTGGCGGATGACT 2631
 QY 622 CysLeuLyseThrLeuSerArgPheValValGlyLyseGlySerCyseGlnLeuGly 641
 Db 2632 AAACCTGAAACATGCTCTTACTCATGATAGGT-----GACAGCATAGACATATCAG 2685
 QY 642 GluLeuArganLeu-----AsnLeuTyrglySerLyseGlyThrHisLeuGlyVal 660
 Db 2686 GAGCTGAAAAGATCTTAACATCTTAAGCTGAGCTCAGATTT-----GAAATGTTGG 2736
 QY 661 LysAsnAspMetAsp-----AlaLyseGlyAlaAsnLeuSerAlaLyseGlyAsn 676
 Db 2737 TCACACAAGATGAGATCTGACAACCTGCTGCAAAAGACAACTGAGAAATTAAGAAAAA 2796
 QY 677 LeuHisSerLeuSerMetLyseTrp-----AspAspAspGluArgPro 690
 Db 2797 CTAGCAAGATGACCTTGTGTGTGACCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2856
 QY 691 ArgLyseGlySerGlyValValGlyValLeuGlyAlaLeuLyseProHisSerAsnLeu 710
 Db 2857 GAAACATTT-----CTTGAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2895
 QY 711 ThrCysLeuThrHisLeuArgLyseGlyPheArgLyseGlyLeuProAspTrpMetAsnHisSer 730
 Db 2896 GAGGCTCTTGAATATGATGCTTGAATATGCTTGAATATGCTTGAATATGCTTGAATATG 2955
 QY 731 Val-----LeuLysAsnValSerLyseGlyLeuLeuLeuLeuLeuLeuLeuLeuLeu 747
 Db 2956 ATGGAATCATGCTCCCAATCTTGTCTCATTAAGATTTAAGCAATTCCTTAAGCTGTAGC 3015
 QY 748 CysLeuProProPheGlyGluLeuProCysLeuLyseSerLeuGlyLeuTrpArgLyse 767
 Db 3016 TGCCCTACACCCCTCGACACATCTTATCTCCATGCTTCATCTC---CGATACATG 3072
 QY 768 AlaGluValGlyTyValAspSerGlyPheProThrArgArg-----Phe 783
 Db 3073 GCCGCTGCTCAGATGATGCTGAAATCTTGTGAAAAGACAAATATGCTGTCTGAC 3132
 QY 784 ProSerLeuArgLyseLeuAsnHisLeuArgGlyPheGlyLeuLeuLeuLeuLeuLeuLeu 798
 Db 3133 CAGTCACTGAAAGAACTCTTGAACATGCTTAACCTAGAGAACCTGCGCAACTTCA 3192
 QY 799 -----GlyLeuLeuLyseGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 813
 Db 3193 GCAGCGACAGATGACAGAGCTACTACGCAAGAGAA---TCGATGTTCTCTGTTCTTAAA 3249
 QY 814 GluLyseGlyLeuLyseCyseProMetPhe-----ValLyseProThrLeuSer 829
 Db 3250 ACTGTAACCGGAACAGATGCCAAAGCTCAGCGCAAAACATGCTTCCA-----GAT 3303
 QY 830 SerValLyseValLeuValValSerGlyAspLyseSerAspAlaIle----- 844
 Db 3304 GCTATTAACAGATTTGCTCAATCTCC---GACACAGCGGAGATATTTGCTCAGTCAGAGAAATG 3360

QY 845 ---GlyPheSerSerLyseSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTyran 863
 Db 3361 TTGGATCATCATCTTCCACATCCGACATCACTCTGAGAGAGATGTGTGATCAGA----- 3414
 QY 864 LysGluAspAlaSerLeuProGlu---GluMetPheLyseSerLeuAlaAsnLeuLyseTy 882
 Db 3415 AAGTCCAGATGATCATCCAGTGAAGTGAATTTGTGACGACAGCCCAAACTTGAGAAA 3474
 QY 883 LeuAsnHisSerPheTyPheAsnLeuLyseGlyLeuProThrSerLeuAlaSerLeuAsn 902
 Db 3475 CTAAACATCGAATCTGCGAAATGCTGCTGCTTGTGAGAAACCATAGTACTTACC 3534
 QY 903 AlaLeuLyseHisLeuGlyLeuHisSerCyseTyrglyAlaLeuGlySerLeuProGlyGly 922
 Db 3535 ACTCTGCGAAAGCTGGAAGATCAGCAATGCACTGAATTTGACGCGCTTCCA---GAATGG 3591
 QY 923 ValLyseGlyLeuLeuSerLeuThrGlnLeuSerLyseThrTyrglyGlyMetLeuGly 942
 Db 3592 ATTGATGATCTGTGACCTTGAATCTTCAATTAAGTGTGCTGCCAAAGTTGATCTCG 3651
 QY 943 LeuProGlyGlyLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysePro 962
 Db 3652 ATCCCAAAAGCTTGAACATCTTACCTGCTGAGAGAGTTAAGTCACTGCTGTAGC 3711
 QY 963 Thr---LeuAlaTyArgCyseGlyLeuGlyLyseGlyLeuGlyLeuMetTyrglyAlaHis 981
 Db 3712 TCTGATTTGAACGAAACTGCAAGAAAGATACAGCAAGAGATTTGTTCAATCTGTGAT 3771
 QY 982 IleProArgValPheIle 987
 Db 3772 ATCCCAAAACATCGTATATC 3789
 RESULT 4
 CL975408 3318 bp DNA linear GSS 21-SEP-2004
 LOCUS OeIFCC027481 Oryza sativa Expressed Library Oryza sativa (indica
 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL975408
 VERSION CL975408.1 GI:52405341
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.
 REFERENCE 1 (bases 1 to 3318)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 Unpublished (2004)
 JOURNAL COMMENT
 CONTACT Chen Chen
 Department of Bioinformatics
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.
 FEATURES
 source
 1..3318
 Location/Qualifiers
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_id="Oryza sativa Expressed Library"
 /note="Oryza sativa exon trapped genomic sequences"
 ORIGIN
 Alignment Scores: 7.65e-131 Length: 3318
 Pred. No.: 1307.50 Matches: 365
 Score:

Percent Similarity: 45.93% Conservative: 183
 Best Local Similarity: 30.60% Mismatches: 346
 Query Match: 25.50% Indels: 299
 DB: 9 Gaps: 35

US-10-647-268-2 (1-988) x CL975408 (1-3318)

OY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
 DB 1 ATGGGAGATCGCTGCTCTCCCGGTG-----GTGGCGGGGTG 39
 OY 21 LeuGly-----LeuIleLeuGlyPheLysAsp 29
 DB 40 CTCGGCAAGCGCGCGCGCTCTCCAGAGCTCCTCGCATGTGGCGGTGACGCG 99
 OY 30 GluPheGluLysLeuGlnSerThrPheThrThrIleGlnAlaValLeuGluAspAlaGln 49
 DB 100 GATCGCCACAAGCTGAGCGCGCAGCTTGGCCGTCAGTCAGTCAGACCTGTCCGACCGCCAG 159
 OY 50 LysLysGlnLeuLysAspLysAlaIleGluAsnThrPheGlnLysLeuAsnAlaAla 69
 DB 160 GCGAAGACGAGACCAAGCCCGCGCTGGAAGAGCTGATGAAGACCTCAAGCGCTCGCG 219
 OY 70 TyrGluAlaAspAspIleLeuAspGluCysLysThrGluAlaProIleArgGlnLysLys 89
 DB 220 TACGAGCGCGAGAGCTCTCGACACATTCACAGAGGACCTGCGCGGAGCGCCAG 279
 OY 90 -----AsnLysTyrGlyCysTyrHisPro--AsnValIleThr 101
 DB 280 ATCGCGACTCCACACCGACCAAGGTACTCGGCTCTCACCGCCGACACCGCCCTCTG 339
 OY 102 PheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIleAla 121
 DB 340 TTCCTGTGTCATAGACGAGAGCTGAACAGTGTCTTCAGAAAGATCAACAGCTGCT 399
 OY 122 AlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThrArg 141
 DB 400 GAAAGATGACAAACAAGTTTGCGCTTACGTGAGCGT-----GCATATGAC 441
 OY 142 GlnThrGlyPheValLeuAsnGluProGln----- 151
 DB 442 GCAACAGATCATGTGATTCAT--CCTCAGACGCACTCCGCGCTCGATGCTTGATGAG 498
 OY 152 ValTyrArgLysArgAspLysGluLysAspGluIleValLysIleLeuIleAsnValSer 171
 DB 499 ATCGTTGGAGAGACGACGACAGAGAGTGTGGTGAATTTGTACTTGACGAGGATCC 558
 OY 192 LeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPheHisProLysIleTyr 211
 DB 616 CTTCGGAAGATGTGTACAAACGACACCAAGGTTTCAACAGCTTGAAGTGGCCATGTGG 675
 OY 212 IleCysValSerGlnAspPheAsnGlnLysArgLeuIleLysGlnIleValGlnSerIle 231
 DB 676 CTCTGTGCTCAGATGATTTCAATGTTTCTCTAGTCAGATTCATTTAATTTGGGT 735
 OY 232 GluGlnLysSerLeuGlyLysMetAsp--LeuAlaProLeuGlnLysLysLeuArgAsp 250
 DB 736 ACCAGGGGAATTTGACCTTGGCAAGCAAGATCGAATCTATGGGAGCGCTTACATGAG 795
 OY 251 LeuLeuAsnGlyLysLysTyrLeuLeuValLeuAspAspValTTPAsnGluAspGlnAsp 270
 DB 796 GTGGTATAGCGCGCAAAAGGTATCTACTTGTCTTGATGATGTTTGATAGAGAGAACT 855
 OY 271 LysThrAlaLysLeuArgGlnValLeu--LysValGlyAlaSerGlyAlaSerValLeu 289
 DB 856 AATATGAGAGAGCTGAGCCATGTGCTGCTTCTGCTGAGCTCCAGAGAGTGAATGACTT 915
 OY 290 ThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLeu 309

DB 916 GTCAACAATCGAGACCGAGGTAGCATTCATATGAGGACAGTTCTCTGTCACAGCTA 975
 OY 310 SerAsnLeuSerGlnGluAspGlyTTPLeuLeuPheMetGlnArgAlaPheGlnIleGln 329
 DB 976 TCATATCTTAAACCATGTGATTCATGTGGAATTTATTCGGAAGAAAGCATTCAGTAAAGAA 1035
 OY 330 GluGlnIleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLysLysCysGlyGly 349
 DB 1036 GAGGAGGACGAGCCAGAGTTTGCAGAGATTTGGCAATGTATTGTCCAGAAAGTCGAAAGCG 1095
 OY 350 ValProLeuAlaAlaLysThrLeuGlyLysIleLeuArgPheLysArgGluGluArgGln 369
 DB 1096 TTACCTCTTGTCTGGAACATATGAGAGCGCTTATGTGCTTCAGAAAGCCGATCCAGAA 1155
 OY 370 TyrGlnHisValArgAspSerGluIleTTPLeuLeuProGlnGlnGlnSerIleLeu 389
 DB 1156 TGGAGAGCTATTGAGAGAGACAGAGAGTTGGAGATTTGGACTACAAATGAGATCTTA 1215
 OY 390 ProAlaLeuArgLeuSerTyrHisIleLeuProLeuAspLeuArgGlnCysPheThrTyr 409
 DB 1216 TCCATATCTTAAACTGAGCTATAGGCACTTACACTTGAAATGAAGCAATGTTTGCCTTT 1275
 OY 410 CysAlaValPheProLysAspThrGluMetGlnLysGlyAsnLeuIleSerLeuTTPMet 429
 DB 1276 TGCCCAATCTTCCAAAGACTACCATATGAGAGGACAAAGTTGGTCCAGCTTGAGATA 1335
 OY 430 AlaHisGlyPheIleLeuSerLysGlyAsnLeuGlnLeuGlnValGlyAsnGluVal 449
 DB 1336 GCGAATATTTTCATCCAGAGAGAGAGATGATGATTTGGAAAGAGAGACAGTTGTT 1395
 OY 450 TTPAsnGlnLeuTyrLeuArgSerPhePheGlnGlnIleGluValLysSer----- 466
 DB 1396 TTCATATGAGCTAGAGTGGAGGCTCTTCTTCAGATGTAAAGTGAAGATTTCATGTC 1455
 OY 467 -----GlyGlnThrTyrPheLys-----MetHisAspLeuIleHisAspLeu 480
 DB 1456 GGGATGTGACAGACTTTCAGACTCAGTTACATCTTACATGATTCATTAATGATGATCTA 1515
 OY 481 AlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlnIleIleValGln 500
 DB 1516 GCAAAATCTGACAGAGAGATGTGTGATGCGCAAGC----- 1554
 OY 501 AsnTyrIleHisMetMetSerIleGlyPheThrLysValValSerSerTyrSerLeuSer 520
 DB 1554 ----- 1554
 OY 521 HisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLysGln 540
 DB 1555 -----CTGAAACGAG 1563
 OY 541 LeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThr 560
 DB 1564 CAAAAGCTCTGAGAAAGAGTCCGCCATCTG-----ATGTCAAGTGGCCAAAG 1611
 OY 561 SerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeu 580
 DB 1612 TCTGCAAGA-----GAACTTGCAGAGCTTGAAGTTA 1644
 OY 581 HisGlyCysHisSerLeuCysCysLeuProLysGlnThrSerLysLeuGlySerLeuArg 600
 DB 1645 AATGGTGTCTGAAACTTCACACATTTACAGAGGATATGAGATTTATGACAACTCAGG 1704
 OY 601 AsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySerLeu 620
 DB 1705 CACCTTTATCTTATTTGTTGTTCATAGCTTGAAGAGCATGCGACCAAGAAATTTGTCACTA 1764
 OY 621 ThrCysLeuLysThrLeuSerArgPheValValGlyIleGlnLysLysSerCysGlnLeu 640
 DB 1765 AAGAAGCTCCGAGACTTACCAACATTTGTTGTGAT--ACCAAGATGAGCGTGGGCTT 1821
 OY 641 GlyGlnLeuAspAsnLeu--AsnLeuTyrGlySerIleGlnIleThrHisLeuGlnArg 659
 DB 1822 GAAGAACTGAAGAGCTTCATCATCTAGTGGCCGACTGAAGCTGTTAACTGAAGACT 1881

```

Qy 660 Vallyabamapmetapalalyglualabamleuseralalyglualabamleuser 679
Db 1882 ATACAAAGTGGGTCAATGACAGAGAGCCATCTCCATTCACAGAAATGTAAGTAC 1941
Qy 680 LeusermetlystPaspaspaspqluarPproarglyeryglu----- 694
Db 1942 TTGTGTGGCACTGTGTGCATGAT-----AATTCGAGTACAGTACAGAC 1989
Qy 695 -----SerglylyValglualValleuglualaleuylsProhiser 708
Db 1990 TTGTGATCGATGTTGTGTGACACAAAGAGATCGTAGATCTCTTTATCCCTTAGC 2049
Qy 709 Asnleuthrlyleuthrlylearglylearglylearglylearglylearglyle 727
Db 2050 AGACTTGAACATTGACAGATGAGGCTGTGTGTATGTAATGATCATCATGATGATAA 2109
Qy 728 AsnHiserValleyAsnValserleuglyleuglyleuglyleuglyleuglyle 747
Db 2110 AACCCCGCAATTTCTATGCTGCTAAAGACTCCACATGCTGATGCTGATGATGATG 2169
Qy 748 CysleupProphegylgluleupProCysleuylsSerleuglyleuglyleupArg 765
Db 2170 GATCTACCAACCGTATGCGAGTGTCTCTGTGAGTCCCTGTCTTATCCCGTTGGAT 2229
Qy 766 -----GlySerAla 768
Db 2230 AATTGACACATTATCTAGTGGCATGATGACATGCTGTTCCAGATGCAATGATCCCTG 2289
Qy 769 GluValgluValyAlaspserglyPheProthArgArgPheProSerleuArglys 788
Db 2290 GAAAT-----TTTCCAAACTGAGAGAG 2313
Qy 789 LeuAnilearglyleuglyleuglyleuglyleuglyleuglyleuglyleugly 807
Db 2314 ATGCAATTAATCTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 2373
Qy 808 GlncysPProvallleuglyleuglyleuglyleuglyleuglyleuglyleugly 824
Db 2374 ATGTTCCCTGAGCTCAAGAAATTAATAATTAATTAATTAATTAATTAATTAATTA 2433
Qy 824 ----- 824
Db 2434 AAAGCTCTATCTACAGAGAGCTGATATTTCCAGTGCAGAAATTCAGTCACTC 2493
Qy 824 ----- 824
Db 2494 AGCATCTTGACAGACTTTCCCACTCACTATGTTGTGATGAGAGTCTTAAAGAT 2553
Qy 824 ----- 824
Db 2554 TTGAGAGTAATACAAATAGCTCTGCGCATCTTGTGACATTAAGCCTGCTTTA 2613
Qy 825 ----- 825
Db 2614 GGGAACTGCTTCTCCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2673
Qy 833 LysleuValVal-----SerglyAspLysSer----- 841
Db 2674 AAGCTGACATTTGGTATTTAGTTGTTCTTCTCACTAATGCTCAACAGCCCTTT 2733
Qy 842 -----AapAlaileglyPheSerSer----- 848
Db 2734 GGTTCCTGGATTTGCTTGTGACAGAAATGATGATGATGATGATGATGATGATGATG 2793
Qy 849 -----IleSerAsnleuMetAlaLeuThrSerleuGln-----IleArgTyr----- 862
Db 2794 GTCCATTCGCTGTGAAGAGAGCTGTGTGCTTGAATTCCTTCTGTGTGAAGATTTAGT 2853
Qy 863 -----AsnlysglyAspAlaSerleuProgluGluMetPheLysSerleuAlaAsn 879
Db 2854 TATTGCAAGAAATCTGACCAAGTTCATCATCATCAAGAAATCTTATTCCTCT-----GCT 2907

```

```

Qy 880 LeuylsTyrleuAnileSerPheThrPheAnleuylsglu----- 893
Db 2908 CTGAGAAAGTTGTATCATAGATTTTGCATATTAATTAAGATTTCCCAAGCTCCCTGT 2967
Qy 894 -----LeuProthSerleu 898
Db 2968 TCACCTGAGACATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3027
Qy 899 AlaSerleuAnileuylsHleuGlyleuHleuHleuHleuHleuHleuHleuHleu 918
Db 3028 GCAAGACTTCCCAAGTTGAGAGATTCATTAATTTCTTCTCAAGCTGAGAAATTTG 3087
Qy 919 ProgluGlyVallysglyleuHleuHleuHleuHleuHleuHleuHleuHleuHleu 938
Db 3088 CCGATGTT-----ARGATGCTTCACTGCTTCAAGAGATGATGATGATGATGATGATG 3144
Qy 939 MetleuGlyleuProgluGly-----LeuGlnHleuThrAlaLeuThrAsnleuSer 957
Db 3145 GGGGTAGAGACACTGACAGAGCTTCTTCAAGAGCTCCCAACCTCAGAGAGCTATG 3204
Qy 958 ValgluHleuPheProthHleuAlaLeuArgCysgluylleuglyleuglyleupTyr 977
Db 3205 ACACCTAGAGACCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3261
Qy 978 LysleuAlaHleuHleuPro-----ArgValPheIle 987
Db 3262 TATGCTCTATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 3300

```

```

RESULT 5
CL958564 3708 bp DNA linear GSS 21-SEP-2004
LOCUS OeIFCC001687 Oryza sativa Expressed library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL958564
VERSION CL958564.1 GI:52371876
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

```

```

REFERENCE
1 (bases 1 to 3708)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL
Unpublished (2004)
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

```

FEATURES

```

source
1..3708
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences "
```

ORIGIN

```

Alignment Scores:
Pred. No.: 3,67e-129 Length: 3708
Score: 1293.00 Matches: 343
Percent Similarity: 50.23% Conservative: 194
Best Local Similarity: 32.09% Mismatches: 382
Query Match: 25.22% Indels: 150
DB: 9 Gaps: 31

```



```

Db 352 AAGAAAGCTGACCAATGCTCTCGAGAAAGATGAACAAGCTGTGACAAATGAACAGACTT 411
Qy 128 HisLeuAer---GluArgThrIleGluArgGlnValAla-----ThrArgGln 142
Db 412 GCGTGTGACGATGCGACAGAAATCACCAAGAAAGTAAACCTCTTATCTCCAGATG 471
Qy 143 ThrGluPheValLeuAsnGlu---ProGlnValTyrgIyArgAspLyGluTyAspGlu 161
Db 472 CATTCGTGCGACCTGGATGAATCAAGTACATTTGGCCAGAGACGACAGCAAGAGAGTGT 531
Qy 162 IleValIleGluIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIle 181
Db 532 GTGGTTAAGCTGTTGCTGTGATCAG---CGATATGACAGAGATTTGACAGTTCTCCCTGTC 588
Qy 182 LeuGluMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArg 201
Db 589 ATCGGGAATCGGGGGTTCCAGCAAGACGACGCTCGCAAGATGTGTGTACAAACGACGAGG 648
Qy 202 ValIleGluIlePheHisProLysIleThrIleCysValSerGluAspPheAsnGluLys 221
Db 649 GTACGTGACCAATTTTCACCTGAGATGTGGACCTGTGTTCAGAGAAATTTTGAAGCTGT 708
Qy 222 ArgLeuIleLysGluIleValIleGluSerIleGluGluLysSerLeuGlyGlyMetAsp--- 240
Db 709 CCCCTTCGAAATCCATCGTTGAATTTGGCTACAAATCGAAGATGTCAAAGTGCCTGACAAAG 768
Qy 241 -----LeuAlaProLeuGlnLysLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrlleu 258
Db 769 GACACCAATCGAGCTCTTGCGACGCGAGCTTGAGGAGCCATTTGTAGACAGAAAGTTTTTG 828
Qy 259 LeuValIleAspAspValTyrgAsnGluAspGlnAspLysTyrlPala---LysLeuArgGln 277
Db 829 TTAGTCTTGAAGATGATGAAACAGATGAAACAAATGCGACAGATGAATTAAGGCCA 888
Qy 278 ValLeu-----LysValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlu 295
Db 889 CTCTTGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
Qy 296 LysValIleGlySerIleMetGlyThrLeuGlnProTyrgIleLysSerAsnLeuSerGlnGlu 315
Db 949 CAAGTAGACATCTATGATGCGACCATGAGATCCCAATGAACTGATGCTGATGATGATAT 1008
Qy 316 AspCysTyrlPheLeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsn 335
Db 1009 GATTCAATGGGAATTTGTTCTCAAGAAAGCATTCAGTGAAGAAAGTACGAGACAGACAGAA 1068
Qy 336 LeuValAlaIleGlyLysGluIleValIleLysLysCysGlyGlyValProLeuAlaLys 355
Db 1069 TTGGTCACCATTGGAAGACTTATGTCAAGAAATGCAAGGGGGCTTCTCTTCTCTCAAT 1128
Qy 356 ThrLeuGlyGlyTyrlleuArgPheLysArgGluGluGlnThrProGlnHisValArgAsp 375
Db 1129 GCTATGGGGGTGGCTGATGAGCTCAAGCAAACTCCATGAAATGGAAGCCATCCGAGAC 1188
Qy 376 SerGluIleTyrlPheLeuProGlnGluSerSerIleLeuProAlaLeuArgLeuSer 395
Db 1189 ACT-----GCCAGACAAAGATGAATCTTTCATGCTTAATTTAAGC 1233
Qy 396 TyrlHisIleLeuProLeuAspLeuArgGlnCysPheThrTyrgAlaValPheProLys 415
Db 1234 TACAGACACTTACCAATCCGAATGAAGCAATGTTTGGCTTGCATATTTCCCAAGG 1293
Qy 416 AspThrGluMetGluLysGlyAsnLeuIleSerLeuThrMetAlaHisGlyPheIleLeu 435
Db 1294 AACCAATGATGAGCAAGAAAGTCTTGATCCAACTGTGATGCAAAATGGTTTCAATCCAA 1353
Qy 436 SerTyrgLysAsnLeuGluLeuGluAsnValGlyAsnGluValTyrgAsnGluLeuTyrlleu 455
Db 1354 GAAGATGAATATGATTTGGAACAAAGAAAGATACACCTTCAAAATTTGGTTGG 1413
Qy 456 ArgSerPhePheGlnGluIleGluValLysSerGlyGlnThrTyrlPhe----- 471

```

```

Db 1414 AGATCTTCTCTCCAAAGATGTCAAGCAAGAAAACTGTGACCATTTGGACAGACTCCAG 1473
Qy 471 ----- 471
Db 1474 CCGTGCACCATTTCTACAAAAGAAATTAATGACAGACCATTAACATATGATGCATTTGT 1533
Qy 472 ---LysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSer 490
Db 1534 TGCAAAATGACGATTTGATGATGACCTTAGCAAAAGACGTGCAGACGAATGTGTAAT 1593
Qy 491 SerSerAsnIleArgGluIleIleValGluAsnTyrlleHisMetMetSerIleGlyPhe 510
Db 1594 TCAGAACATGTA----- 1605
Qy 511 ThrTyrgValIleSerSerTyrlSerLeuSerHisIleGluIleLysPheValSerLeuArgVal 530
Db 1606 -----CTTCAGACGATGCATCTGTGCAGAAATGTCCGTAC 1641
Qy 531 LeuAsnLeuSerAsp-----IleLysLeuLysGlnLeuProSerSerIleGlyAsp 547
Db 1642 ATGAATATATCTGACACTTTGTGATCTTTCTAATAATATTTACCGGAAAGATAGGGA--- 1698
Qy 548 LeuValHisIleuArgTyrlleuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsn 567
Db 1698 ----- 1698
Qy 568 GlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCys 587
Db 1698 ----- 1698
Qy 588 CysLeuProLysGluThrSerTyrgLysLeuGlySerLeuArgAsnLeuLeuAspGlyCys 607
Db 1699 -----AAATGAGGAAGCTCTCCATCTTATCTTCTGGAGAT 1737
Qy 608 TyrgIleuThrCysMetProProArgIleGlySerLeuThrCysLeuLysThrLeuSer 627
Db 1738 GATAGTTTGGCGGATGCGACCAAACTTGTGTCTTTGGAACATCTTCGACCTTAACA 1797
Qy 628 ArgPheValValGlyIleGlnLysLysSerCysGlnLeuGlyGluLeuArgAsnLeu--- 646
Db 1798 ACATTTGTTTGGAC---ACATAAGCTGGTTGTGGAATGACGAGCTCAAGAACTTGCCT 1854
Qy 647 AsnLeuTyrgLysSerIleGluIleThrHisIleuGluArgValLysAsnAspMetAspAla 666
Db 1855 CACATTCGCCAACAGTTTGGAACTGTACAAATTTGGAATAATTAATTCAGAGAACAAATGGA 1914
Qy 667 LysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLysTyrlAspAsp 686
Db 1915 ATGAGAGCCAAATCTCCATCAGAAAGAAATTTAAGTGAACCTATGTCACATGGGGT--- 1971
Qy 687 AspGluArgProArgIleTyrgLysSerGlu-----LysValGluValLeu 701
Db 1972 -----CGTATTAATAATTATCACACCGGAAACAGTGCCTCAATGAGGAAGAAAGTTTG 2025
Qy 702 GluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIle 721
Db 2026 GAGTCACCTTACCACTCACTGATGAGCTCAAAATTTTGAAGCTGATGATATAGTGGCTG 2085
Qy 722 ArgLeuProAspTyrlMet---AsnHisSerValIleLysAsnValIleSerIleGluIle 740
Db 2086 AAGATCCCAATGATGATGAGACCCACAGATGTTTGACGTGCTTAACAACCTCCGATTT 2145
Qy 741 IleSerCysLysAsnCysSerCysLeuProPheGlyGluLeuProCysLeuLysSer 760
Db 2146 TCCAAGCTTTAGATGCAAGAGCTTACACACATGTGTTATGCGTTCCTGTGAGCAT 2205
Qy 761 LeuGluLeuTyrlPheGlySer-----AlaGluValGluTyrgValAsp 774
Db 2206 CTGCAGTATCCCGATGATGATATCTAACACATTTGTTGTAAGAAAGTTGGTGGAGACT 2265
Qy 775 SerGlyPheProThrArgArgArg---PheProSerLeuArgLysLeuAsnIle----- 791
Db 2266 GAAGATACCAATCCCTCAGCAAGTTTCCCAAGTTAAAGTCTCTGAACCTAGAGTTG 2325

```

```

Qy 792 -----ArgGluPheGlyAenLeuLysGlyLeuLeu--- 801
Db 2326 TTATTAGCTTGAGAAATGGGAGAAAATCTGAGGTGAGGCTAAGAAATTGGTTACA 2385
Qy 802 -----LysLysGlyGlyGluGluGln 808
Db 2386 TTTCAGAGCTCGAAATGCTACAGATCATCTGCTAGTAACTTGCAAGTGTCCAGAC 2445
Qy 809 CysProValLeuGluGluLeu-----LleLysCysCysPrometPheValIle 825
Db 2446 TGTCCGGTTCTAAAGAACTGAGACAGATTGGATCTTATATGCTTGCATAGACGAAC 2505
Qy 826 ProThrLeuSerSerValLysLysLeu---ValValSerGlyAAspLysSerAAlaIle 844
Db 2506 ACACATCTGACATCTATGCTCCAACTCAATTACGTTGCAAAACAGCTTTGTGATGTGTG 2565
Qy 845 Gly-----PheSerSerLysSerAsnLeuMetAlaLeu----- 855
Db 2566 AGCATGCTTTGGGCTCATGGCCATCTCTCGTAGAACTAGTTTATAGATCTTCAACACAC 2625
Qy 856 -----ThrSerLeuGlnIleArgTyrAsnLysGlyLysP 866
Db 2626 ATTCCAACTGCTGAGGTGAGGCAATCAAGGCCAGTAGAATACCTTGGAGTTTG 2685
Qy 866 ----- 866
Db 2686 AGTCTAGTAACTGCTTCAAGGCTGCATCCGCTCATCCGAAATGCCCTCTGGGCTCTGG 2745
Qy 866 ----- 866
Db 2746 AAATGCTTTGGCTTTGTGAGAGTATGTGCATATATGTGCTCAGTCTTGTGTGCTGG 2805
Qy 866 ----- 866
Db 2806 CCACTGAGAGTTCAGAGGCTTGATTCACCTTGACACCTATATATTAGACACTGTAT 2865
Qy 867 -----AlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLys 881
Db 2866 AGACTTGAGGAAAAGTTCTATCATCCAGGAAAATTCATGTCAGTCTCCATCTAGAG 2925
Qy 882 TyrLeuAsnLysSerPheTyrPheAsnLeuLysGlu----- 893
Db 2926 AGGTATACACATACAAACTGCTACATCTAGAGATCCCAATGCTGCTGCATCCCTG 2985
Qy 894 -----LeuProThrSerLeuAlaSer 900
Db 2986 CAGGATCTGCGGTTAGATCTTGCAGAAATGTTGTCGATTCCTTCGAACTTGGAAAT 3045
Qy 901 LeuAsnAlaLeuLysLysLeuGlnLysSerCysTyrAlaLeuGlnSerLeuProGlu 920
Db 3046 CTGGCCATGTTAAAGCATCTTTATTTATGATGATGCTATGCTCGAAGATCTTCTCT-- 3102
Qy 921 GluLysValLysGlyLeuLysSerLeuThrGlnLeuSerLysIleThrTyrCysGluMetLeu 940
Db 3103 GATGGAGATGATGAGCTCTGCTTCCCTTAAATTTTGAAGATTCAGGATGCGAGAGATA 3162
Qy 941 GlnCysLeuProGluGlyLysLeuGlnLysLeuThrAlaLeuThrAsnLeuSerValGlu 959
Db 3163 GAGGAATTCACAGAGGCTCTCTCAGGAGCTTCCAACTCAAGAAAGAACTGTCAATACAA 3222
Qy 960 PheCysProThrLeuAlaLysArgCysGlyLysGlyLysGlyLysGlyLysPThrTyrLysIle 979
Db 3223 GGGTGCCCTGATTTGAAAACAGGTCGAGAGAGGT---GGTGAATTTTGTGATCTTGTCT 3279
Qy 980 AlaHisIleProArgValPheIle 987
Db 3280 TCTTCGTTCAACGTATATGCAATT 3303

```

```

RESULT 7
LOCUS CL958562 3975 bp DNA linear GSS 21-SEP-2004
DEFINITION OrlFCC001685 Oryza sativa Express Library Oryza sativa (indica

```

```

ACCESSION CL958562
VERSION CL958562.1 GI:52371872
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE 1 to 3975
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Wang, Y., Sun, N., Zhang, X., Bao, D., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W., and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
location/Qualifiers
1..3975
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/notes="Oryza sativa exon trapped genomic sequences"
ORIGIN
Alignment Scores:
Pred. No.: 1,87e-123 Length: 3975
Score: 1241.50 Matches: 335
Percent Similarity: 49.17% Conservative: 196
Best Local Similarity: 31.02% Mismatches: 364
Query Match: 24.21% Indels: 185
DB: 9 Gaps: 29
US-10-647-268-2 (1-988) x CL958562 (1-3975)
Qy 26 GlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThrIleGlnAlaValLeu 45
Db 91 GGTATGAGAGAGCGCTCACAAATCTGAGCGCAAACTGCCGCAATTTGGATGTCATC 150
Qy 46 GluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsnTProLeuGlnLysLeu 65
Db 151 ATTGATCTGAGAGAGAGAGAACTCACCGCTCGGCTAAGTGTGCTGCTCAAGCACTC 210
Qy 66 AsnAlaAlaIleArgGlnAlaAspAspIleLeuAspGluCysLysThrGlnAlaProIle 85
Db 211 AAGCTGTGCTTAAAGCAAGCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 270
Qy 86 ArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIleThr----- 101
Db 271 CGTGAACTTAAAGAGAGGAGAAAT-----CATGGAATCTCAGCACTAGTATAGTCTT 324
Qy 102 -----PheArgHisLysIleGlyLysArgMetLysLysIleMetGlu 115
Db 325 GCTAACATCTCTAGTGTTCCTGTTACAGATGAGCAAGAAAGCTGCTAAATTTGTCACT 384
Qy 116 LysLeuAspValIleAlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGlu 135
Db 385 TCTATTGAGACCTGTGTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 438
Qy 136 ArgGlnValAlaThr-----ArgGlnThr---GlyPheValIleAsnGluPro 150
Db 439 ---CAATGCGCAACCTTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
Qy 151 GlnValTyrGlyArgAspLysGlyLysAspGluIleValLysIleLeuIleAsnAsnVal 170

```

```
Db 496 AATTGTGCACAGAGAGAGAGAGAGCATTTGTAAATTGTCTGTACGATCC 555
OY 171 SerAna1aGlnThrLeuProValLeuPro1leuGlyMetGlyLeuGlyLysThr 190
Db 556 AGCAAC---AGGAATCTCATGCTCTTCCAAATCATGTGAATGGGGTGGGCAAGACC 612
OY 191 ThrLeu1aGlnMetValPheAsnAspGlnArgVal1leGlnHisPheHisProLys1le 210
Db 613 ACTTGTGCTCAGATATATTACAGACGATCTTGAGATCCAAAGACATTTCTACGTCAGGAG 672
OY 211 Trp1leCysValSerGluAspPheAsnGlnLysArgLeu1leLysGlu1leValGluSer 230
Db 673 TGGGTGCTGCTCTTGATGATTTGATGTACAAACATTTGCAACAAGATCAGCATGCA 732
OY 231 IleGlnGluLysSerLeuGlyGlyMetAspLeu1aProLeuGlnLysLysLeuArgAsp 250
Db 733 ATTGAGAAAGAAATGCGAAATGCACTAGAG-----AAGCTCCAGCAG 774
OY 251 LeuLeuAsnGlyLysLeuThrLeuLeuValLeuAspAspValTrpAsnGluAspGlnAsp 270
Db 775 GAAGTCCGTGAAAGAGGACTCTCTTAATTGTGATGATGCCAT----- 819
OY 271 LysTrpAlaLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThr 290
Db 820 -----ATTATG 825
OY 291 ThrThrArgLeuGlnLysValGlySer1leMetGlyThrLeuGlnProTyrgLysLeuSer 310
Db 826 ACAACACGCTGATCAAGGGGTAGCTCAGCTAATGGGACAACTAAAGCCCATCAATTTGTA 885
OY 311 AsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlu 330
Db 886 AGAATGAGAAAGAGGATTTGCTTGCAATTTTGAAAAGAGCATTCGCTTTGATGAG 945
OY 331 Gln1leAsnLeuAsnLeuValAla1leGlyLysGln1leValLysCysGlyGlyVal 350
Db 946 CAGAAACCTGATGAGCTGTTCAATTTGGCTGGAGATTATGACAGATGTCACGGGCTC 1005
OY 351 ProLeu1aAlaLysThrLeuGlyGly1leLeuArgPheLysArgGlnGluArgGlnTrp 370
Db 1006 CCTTAGCTGCAAAAGCCTTGGGTTCAATGTTAAACACACGGAAGCTGTAGAGAAATGG 1065
OY 371 GlnHisValArgAspSerGln1leTrpLysLeuProGlnGlnLysSer1leLeuPro 390
Db 1066 AGGCGCGATTACCAAAAGT-----AGCATCTGTGATGACGAGAAATGCAATTTTACTT 1119
OY 391 AlaLeuArgLeuSerTyriHis1leuProLeuAspLeuArgGlnCysPheThrTyriCys 410
Db 1120 ATACTGAGCTCAGCTATGATGATCTGCCATCATCATGAAGCATGTTTGTCTTTGT 1179
OY 411 AlaValPheProLysAspTrpGlnMetGlnLysGlyAsnLeu1leSerLeuTrpMetAla 430
Db 1180 GCGATCTTTCCCAAAACATGATGTGATGTGAATGTGAATGCTGATTTCTCGATGTGCG 1239
OY 431 HisGlyPhe1leLeuSerLysGlyAsnLeuGlnLysGlnValAsnValGlyAsnGlnValTrp 450
Db 1240 AATGATTTTATTCATCTGAAGACAAATGCGCCCAAGAAACAAAGGCAAGCATTTTC 1299
OY 451 AsnGlnLeuTyriLysArgSerPhePheGlnGln1le---GluVal----- 464
Db 1300 AATGAGCTTCTGTCAGATCATTTCTTCAGATGTCAAGAGGTACCTTTACACAAGAT 1359
OY 465 LysSerGlyGlnThrTyri-----PheLysMetHisAspLeu1leHisAspLeu1a 481
Db 1360 GAAAGTGAACATAGTTACCGAATATATGATGATCATCATGATCATGATGATGCTT 1419
OY 482 ThrSer----- 483
Db 1420 GTTCTGTATTGAGAAAGATGTTTACTATAGCTGAGGGTCACAAATTAATTAAGTTT 1479
OY 484 -----LeuPheSerAlaSerThrSerSerSerAsn1leArgGlu 496
OY 1480 TTGCAAAATACCTGTTCGTCAATTTGTTCTGTGCTGTAGTGTCCAGAAACCTTCAAT 1539
OY 497 Ile1leValGlnAsnTyriLeHis---MetMetSer1leGlyPheThrLysValAlaSer 515
Db 1540 GTTTCACCTAAAGCAGAGATGTCAAGTATGCAAAACATTTTGTGCATTTATTAATACAGC 1599
OY 516 SerTyriSerLeuSerHis1leGlnLysPheValSerLeuArgValLeuAsnLeuSerAsp 535
Db 1600 AATTCCTGTATCAATTTATTAACAATAATGCCATTTCTCTGAGAGATTAACGCTCTATTA 1659
OY 536 IleLysLeuLysGlnLeuProSerSer1leGlyAspLeuValHisAspGlyTyriLeuAsn 555
Db 1660 CATTAATCTGGGTGACCTTCAGATTAAGTAGAGACCTTAAGACCTTCAGGTTCTTGAT 1719
OY 556 LeuSerGlyAsnThrSer1leArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeu 575
Db 1720 CTCTGTGCAATTTGTCAATATCAATCTCTCTTAAGAAATATGATTTTGTATTAATCTA 1779
OY 576 GlnThrLeuAspLeuHisGlyCysHisSerLeuCysLysLeuProLysGlnThrSerLys 595
Db 1780 CAACCATTAATCTTTGGGTTGATATCTCTGTGTCACCTTCTTAAGATATTAATAAAC 1839
OY 596 LeuGlySerLeuArgAsnLeuLeuAspGlyCysTyrgLysLeuThrCysMetProPro 615
Db 1840 ATGATTTGGCTTCGTCAATCTCTATACATGATGATGATGATGATGATGATGATGATGAT 1899
OY 616 Arg1leGlySerLeuThrCysLysLeuThrLeuSerArgPheValAlaGly1leGlnLys 635
Db 1900 AACCTTGGGACATTTACATCTCTTACAGACATTAATTTTGTGTGGGCAATTAATCT 1959
OY 636 LysSerCysGlnLeuGlyGlnLeuArgAsnLeuAsnLeuTyrgLys1leGln1leThr 655
Db 1960 GGTGTGATGACATTTGGAGAACTAAGCACCTCAACCTCCAGAGTCAACTCCACTATGT 2019
OY 656 HisLeuGlnArgValLysAsnAspMetAspAlaLysGlnAlaAsnLeuSerAlaLysGlu 675
Db 2020 CATCTACAAATGTA---ACAGAGCAGATGTATCCATGAGACACCATGGGGAAGGAA 2076
OY 676 AsnLeuHisSerLeuSerMetLysTrpAspAspGlnArgProArg1leTyrgLysLeu 695
Db 2077 GACCTTAACCCAGCTATCTTTTGGATGAGAGATATCATTAATGAAGTATGATTTACAT 2136
OY 696 GlnLysValGlnValLeuGlnAlaLeuLysProHisSerAsnLeuThrCysLeuThr1le 715
Db 2137 GAGAAAG-----GTACTAGATGCTTTTACTCAAAACAGACAGCTTAAATTTCTATCTGTG 2190
OY 716 ArgGlyPheArgGly1leArgLeuProAspTrpMet---AsnHisSerValLeuLysAsn 734
Db 2191 GATTCCTACAGAAAGTCCAAATTTTCCAACTTGGGTGACAAACCCACACATATGACAGAT 2250
OY 735 ValValSer1leGln1leHisSerCysLysAsnCysSerCysLeuProProPheGlyGlu 754
Db 2251 CTAAATCAAGCTCCAACTATGTTGATGCAATGTGCGAGAGCTTCCGCATTTGTGGCA 2310
OY 755 LeuProCysLeuLysSerLeuGlnLeuTrpArgLysGlySerAlaGlnValGlnTyriValAsp 774
Db 2311 TTGCCATCTGTGAATTTCTTCAATTTG---GAAAGGCTGCAAAAGTTGCAATTAACCTGTGC 2367
OY 775 SerGlyPhe-----ProThrArgArgArgPheProSerLeuArgLysLeuAsn1leArg 792
Db 2368 TCGGTTGTGTAACAATTCGACATCTTCAACGTTTCTTAATTAAGGAACTTAATTTAGTT 2427
OY 793 GlnPheGlyAsnLeuLysGlyLeuLeuLysLysGlnGly-----GlnGlnGln 808
Db 2428 GATCTAAAAAGTTGATGTTGTGTGGGAAATAAAGAGACCTGGGCAAAACCTAGTGTG 2487
OY 809 CysProValLeuGlnGln1leGln1leLysCysCysProMetPheVal1leProThrLeu 828
Db 2488 TTTCCTCTTAAGAGATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 2532
OY 829 SerSerValLysLysLeuValValSerGlyAspLysSerAspAla1leGly----- 845
Db 2533 GAAAACTTTCAGATGACGATATATTTGGTGAATCTTCTCAATTTCTTAATTAATTAAGG 2592
```

Oy	846	-----PheSerSeriSerAsnLeuMetAla-----LeuThrSerLeu-----	858
Db	2593	AACCTCCCATTTTCCAGCTTTAAAAAAACCCTCAAGTTGGCACAATCTGAAGAATTGAGGCCA	26522
Oy	859	-----GlnIleArgTyrAsn-----	863
Db	2653	TGGGGAACACAAAGAAAGATTCATCAACCAATATTTCTCAACTTGAGAAATGTATATATTATG	2712
Oy	864	-----LysGluAlaSerLeuProGlu-----MetPheLys	875
Db	2713	GAGTGCCCGGAGGTGGCAACTCTACCTGAAAACACCAAAGCTGAGAAATTATGATTTTCCC	2772
Oy	876	SerLeuAlaAsnLeuTyrlSerLeuAsnIleSerPheTyrPhe---AsnLeuLysGluLeu	894
Db	2773	GAAATTAATAATCATTCATGTGGTTATCTCCATAGCAAGATATATAGCAACACTGTCCGATGC	2832
Oy	895	ProThrSerLeuAlaSerLeuAsnAla-----	903
Db	2833	AGATTAAACAATTGCAGCTTTCTCTCAACAAGNACAAATGTGCATATACACAGGTCAATGCT	2892
Oy	903	-----	903
Db	2893	ACAGAGAATTAGTCATTAATACTTATATGCAACTATGAACTACGCGGATGTAATCTC	2952
Oy	904	-----LeuYshIleGluGlnIleHisSerCyetr	913
Db	2953	TTCTGATAGATTGGGAATGTTTTGTGAACCTGCACAGTTTAGTATACACTGCTGCAC	3012
Oy	914	AlaLeuGlnSerLeuProGluGlyValLysGlyLeuIleSerLeuThrGlnLeuSer	933
Db	3013	GAATCTCGTCATTTGGCCACATGAACAGCTCAATGCTTGATCTTGAAAAGATTAA	3072
Oy	934	IleThrTyrCys-----GluMetLeuGlnCysLeuProGluGly	946
Db	3073	GTTATATCTTGCAATATATCTGACTTAATCTGTATGTTCTAGAACGCCCATTAAGAAA	3132
Oy	947	LeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLys	966
Db	3133	AATCAGCTACTCCCATGCTTGAGATATATATAAATTAAGATTTGTCCAAATTTGTTGAG	3192
RESULT 8			
LOCUS	CL966185		
DEFINITION	OsIFPCO13486 Oryza sativa Expressed Sequence Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.		
ACCESSION	CU966185		
VERSION	CS966185.1		
KEYWORDS	GI:52387048 GSS.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group) Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euhatroidae; Oryzaceae; Oryza. 1 (bases 1 to 3003) Ma,L., Wang,C.J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis Unpublished (2004) Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 10300, China Tel.: 86-10-80481559 Fax: 86-10-80488676 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped.		
JOURNAL COMMENT			
TITLE			
FEATURES			
Source	location/Qualifiers		
	1..3003		
	/organism="Oryza sativa (indica cultivar-group)"		

Db	768	TCGATGAAATCGGAGTGTGACAGGTGGGAAACGTGTGACATGCCCTTAAAGCAAGTGG	827
Qy	283	aserglyalaserValleuthrThrThrArgleuglnlyrsValglyserile-----Me	301
Db	828	CAGGGGAGATGACATCTGACAAACATCTGTATGACAGAAAGTACGTCCAGATTATGACAT	887
Qy	301	rglyThrleuglnProtyrGlnleuserAsnleuserglnluuAspCystrpleuLeuph	321
Db	888	GGGTGTACCTGGAGCATATATACCTTGAAAATTTGGGTAAACAGTATATGAAGAAATAT	947
Qy	321	eMetGlnArgAlaPheGlyHisGlnGlnGlnLileasnlleuAsnleuValAlaIleGlyLy	341
Db	948	CCAGAGCAGAGCATTCAGAGTGCAGAAAGCCAAACAGTGCAGACTGATGATATTTGTA	1007
Qy	341	sglulleVallyLyCyseGlyGlyValAlaProleuAlaAlaLystrleuGlyGlyLele	361
Db	1008	CAAGATTGTGGACAGAGATGTGTGCTTCTGTGGCCAAAGCATTTGGCTCTATGTT	1067
Qy	361	uArgPheLyArgGlnGlnArgGlnTrpGlnHisValArgAspserGlnuIetrrplysle	381
Db	1068	GAGTACCAAGACTACATGACATGCAAGATGGAAGATATATTAATGCAAAAGC-----AACAT	1121
Qy	381	uProGlnGlnGlnSerSerleleuProAlaLeuArgleuSerTyrlHisleuProle	401
Db	1122	TTGGCAATGAGAGACAGAGATTTTACCTATACCTAAAGCTCAGCTCAGATGCCTACCC	1181
Qy	401	uAspLeuArgGlnCysePheThrTyrcysAlaValAPheProLyAspThrGlnleuGlyLy	421
Db	1182	ACAACATAAACAAATGCTTGATTTGTGTGTGTGTTCCAAAGATATCCAGTTAATGT	1241
Qy	421	sglyAsnleuIleSerleuTrpMetAlaHisGlyPheIleleuSerLysglyAsnleuGln	441
Db	1242	GGAGAGATTATCCACATTTGATGGCTATAGCTTATACCTGCACGGGAGAGATATA	1301
Qy	441	uLeuGlnAsnValGlyAsnGlnValTrpAsnGlnleuTyrlLeuArgserPhePheGlnGln	461
Db	1302	CCCTGACATGCTGAGGCAAAAGAAATTTTATATGATCTAGCTTGAGATCATCTTTCAAGA	1361
Qy	461	uIleGlnValLyserGlyGlnThr-----TyrPhe-----	471
Db	1362	TGTGGAAACAAGCCCTCCACCGACTGGTATATATGTAAGAAGACCAAAATCCGTTACAT	1421
Qy	472	-----LysMetHisAspLeuIleHisAspLeuAlaThrSerleuPheSerAlase	488
Db	1422	AATGTGTGCAAGATACATATCTTATGATGATGTGGCTCTATCTGTATGGGAAAGA	1481
Qy	488	rThrSerSer-----SerAsnIleArgGlnuIleIleValGlnAsnTyrlIleHis	504
Db	1482	ATGTGCAACATAGTCAATATGCCGACATGAGATCATTTATA-----AATCTACTCG	1535
Qy	504	SmetMetSerIleGlyPheThrIlyVal-----ValSerSerTy	517
Db	1536	CCACTTGTTCATATCAATCCGAGAAATTCACACTCATCTGGATGATCCCTACATTTATGT	1595
Qy	517	rSerleuSerHisleuGlnIlysrPheValSerleuArgValleuAsnleuSerAspIleLy	537
Db	1596	CTTCTCCACACGCGTTATCAAAAGCAATCTTTTACGGGCAATGCAATC-----TGTCG	1649
Qy	537	sleuLyGlnleuProSerSerIleGlyAspLeuValHisleuArgTyrlLeuAsnleuSe	557
Db	1650	ATTGAGAAATCTTCATATCCAGGCCAAGGCACTTGCAATACATTAGGATCTTAACTTTTC	1709
Qy	557	rglyAsnThrSerIleArgserleuProAsnGlnleuCylyleuGlnAsnleuGlnThr	577
Db	1710	CAACAATTTGTGTGATCAAAAACCTTCTCGAAGAAATTAAGTTTATATATATCTATGTC	1769
Qy	577	rLeuAspLeuHisGlyCyHisSerleuCyCySleuProLyGlnThrSerIlyleuGln	597
Db	1770	AATGAGCTTTCTATGTGTACCTCTATGTCCGCTTCCAAATGCTATGAAGATATGA	1829
Qy	597	ySerleuArgAsnleuLeuAspGlyCystrGlyleuThrCyMetProProArgGln	617

Db	1830	AAACCTTGCCATATCTACATGGTGGATGTGATCATTTGGAATGCAATGCCTCTGACCT	1888
Qy	617	eglyserleuthrCySleuLystrIleuserArgPheValValGlyIleGlnIlylysse	637
Db	1890	TGGACAACTGACTTCTCTACAGACATTAACCTTTTTGTGTGGTGTCTAGCTTGAATTG	1949
Qy	637	rcysGlnleuGlyGlnleuAsnleuAsnleuTyrlGlySerIleGlnIleThrHisle	657
Db	1950	CAGCAATGTTTCCGAACTCGAAACATTAATCTTGTGCGAGAAATTAAAGTTAGTGTGCT	2009
Qy	657	uGlnArgValIlysrAsnAspMetAspAlaLysglyAlaAsnleuSerAlaLysglyAsnle	677
Db	2010	AGAAATATGA---ACGAAAGCTCAAGAAAGCTCCAGATCTTGAGATGAAGAAAGAACT	2066
Qy	677	uHisSerleuSerMetLystrPAspAspAspGlnuArgProArgGlyIleTyrlGlnserGly	697
Db	2067	AACGCATTATCTCTTGAGTGAATAGTGGGGTCTCGAAGAACTAGTACAAAGATTGTCA	2126
Qy	697	sValGlnValleuGlnAlaLeuLyProHisSerAsnleuthrCystrleuthrIleArgGln	717
Db	2127	TGCGAAGGTGTAGATGCTTTAACTTCAGATGGGTGGAGATGCTTAAGATTTGTA	2186
Qy	717	yPheArgGlyIleArgleuProAspTrpMetAsnHisSerValleu-----LysAsnVal	735
Db	2187	CTTTAAAGCAGAGGTGCACCAACATGATGAAGAATTAGTTGTGTTGCAGAACATCT	2246
Qy	735	IvalSerIleGlnuIleIleSerCylysrAsnCyserCySleuProProPheGlyGlyLe	755
Db	2247	GACTGAGCTCCATCTGTGTGGCTGTACATTTGTATGCCATTCCTGAATTTTGCATTT	2306
Qy	755	uProCySleuLyserleuGlnleuTrpArgGlySer-----AlaGln	769
Db	2307	GAGGCTTCCTCAATTTCTACCTATATAAAGTATGAATTAACAGACATGTCACACA	2366
Qy	769	uValGlnTyrlValAspserGlyPheProThrArgArgPheProSerleuArgLySle	789
Db	2367	AATGCAATATGTGGAA-----TTTCACAGATTAAGAAGAACT	2402
Qy	789	uAsnIleArgGlnPheGlyAsnleuLyGlyleuLeuLylysglnGlyGlnGlnCy	809
Db	2403	CCAATTACATGATTAAGAGAGCTTGAGAGCTGGGTGCGAACACACGAAAGAAAGAGCT	2462
Qy	809	S-----ProValleuGlnGlnIleGlnuIleLyseCyseProMetPheValIleProth	827
Db	2463	GTCCTTCCAGTCTTGAGAGATTTGATTAAGAACTGTCCGAAG-----TGACAGAG	2516
Qy	827	rLeuSerSerValIlysrLeuValIalSerGlyAspLySerAspAlaIleGly-----	845
Db	2517	TCTACTGGAACACAAAGGGTGTCTTAAT-----TCAAGTGTATTGGGGGAGG	2567
Qy	846	-----PheSerSerIleSerAsnleuMetAla-----LeuthrSe	857
Db	2568	GGGACAGGTGATACAGATGCCGATTAAATTTACAGGTGAGCATGCAATGCACTCACGCC	2627
Qy	857	rLeuGlnIleArgTyrlAsnIlysglyAspAlaSerleuPro-----GlnuIleMetPhe-	874
Db	2628	CACAAAGTGTCTCAGAGAACCCAGAAATTAATATTACTTGTGCTTAGTACCCTATTTAT	2687
Qy	875	-----LysSerleuAlaAsnleuTyrlLeu-----AsnIleSe	886
Db			

QY 946 YleuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrIleuAlaIy 966
 Db 2916 TCTTGGAATTAAGTCTGCTCAGAGGGTTCTGCTCAAAATATCTCCAGCATTAAT 2975
 QY 966 sargCysGluLysGlyIleGlyGluAspTrpTyrIleAlaHisIlePro 983
 Db 2976 GAAG-----CCTCTTATTAAG-----CACCTACCA 3000
 RESULT 9
 LOCUS CL961820 3222 bp DNA linear GSS 21-SEP-2004
 DEFINITION OsJFCC037780 Oryza sativa Express Library Oryza sativa (Indica
 cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL961820
 VERSION CL961820.1 GI:52378383
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzoae; Oryza.
 REFERENCE 1 (bases 1 to 3222)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G. K. S., Deng, X. W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 TITLE Unpublished (2004)
 JOURNAL
 COMMENT Contact: Chen Chen
 Department of Bioinformatics
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.
 FEATURES
 source
 1..3222
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_lib="Oryza sativa Express Library"
 /note="Oryza sativa exon trapped genomic sequences"
 ORIGIN
 Alignment Scores:
 Pred. NO.: 2.19e-120 Length: 3222
 Score: 1212.00 Matches: 343
 Percent Similarity: 49.77% Conservative: 191
 Best Local Similarity: 31.97% Mismatches: 389
 Query Match: 23.64% Indels: 150
 Gaps: 34
 US-10-647-268-2 (1-988) x CL961820 (1-3222)
 QY 28 LysAspGluPheGluLysLeuGlnSerThrPheThrThrIleGlnAlaValLeuGluAsp 47
 Db 106 GAGGAGGAGCGCCGAGAACCTGCGCGCACCGAAGCCATCCGCGCCCTGCTCGAGGAC 165
 QY 48 AlaGlnLysLysGln--LeuLysAspLysAlaIleGluAsnTrpLeuGlnLysLeuAsn 66
 Db 166 GCCGAGGAGCGCGCTACATGACGACGAAATCCGTCAGCTCTGCTCTGAGGCTCAAG 225
 QY 67 AlaAlaLysLysGlnLysAspAspLysLeuAspGluCysLysThr----- 81
 Db 226 TCCGTCGCTACGACGCGAGCACTGCTCGACCGCTGACACCTTACCGCGCGTGGCC 285
 QY 82 -----GluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisPro 97
 Db 286 AGGCTGAAAGCGCGAGCCGCGGAAAGCGGAAAGCGCTCTCG----- 330

QY 98 AsnValIleThrPheArgHisLysIleGlyLysArgMetLys----- 111
 Db 331 -----CTCAATTTCAGCTCGTCCCGGACGGTGGGCTGACGCGAAG 378
 QY 112 -----LysIleMetGluLysLeuAspValIleAlaGluLysGlyLeuPheHisLeu 129
 Db 379 ATCACCGAGATCAACGAACGCGCTGACGAGATCCGTGGGGCCCAAGAGGTTCAAGTTC 438
 QY 130 AspGluArgThrIleGluArgGlnValAlaThrArgGln---ThrGlyPheValLeu--- 147
 Db 439 CAGCCCGGAGATGGCGGACGAGAGCGCCGACGACGAGCGCGCGGTTTCTTCAAGTT 498
 QY 148 -----AsnGluProGlnValTyrGlyArgAspLysGluLysAspGluIle 162
 Db 499 GCGGCTTCCATGATGAAGAGCTTCAGATTTTCCGTGCTGCGCAAGAGAGAGAGGTT 558
 QY 163 ValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeu 182
 Db 559 GTACAGACACTTTGTGTGGAT-----CACACATCCCGCGCGGTATCTCATTTAT 612
 QY 183 GlyMetGlyLysLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgVal 202
 Db 613 GCGCGGCGAGAAATGGAGACACACGTTGGCAGCGCTTGGTGTACACAAATCTGAGGTA 672
 QY 203 IleGlnHisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGluLysArg 222
 Db 673 CAGAGTTCTTTCCAACTAGAAATCTGGGTTTGTGTTCTGCAAAATGATGATGACAAAG 732
 QY 223 LeuIleLysGluIleValGluSerIleGluGluLysSerLeuGlyGlyMetAspLeuAla 242
 Db 733 GCTCAAAAGATGATCATGAGAACTATCACCAAAAGTAAATGTGATGATGATGAGCTTGAC 792
 QY 243 ProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysTyrTrpLeuValLeuAsp 262
 Db 793 ATATTGACGACGACGCTTCAGAGACCTGACCTGACCTACCAATTTTACTGTGTATAT 852
 QY 263 AspValTrpAsnGluAspGlnAspLysIleTrpAlaLysLeuArgGlnValLeuLysValGly 282
 Db 853 AATCTCTGGCTGAGATTAATTAACCTTCGGACATCGCTGGGTCCTGCTGCTGG 912
 QY 283 AlaSerGlyAlaSerValLeuThrThrThrArgLeuGluLysVal---GlySerIleMet 301
 Db 913 GAAAGGAGAACTAAGGTTTAAATAACTCGAATGAAGAAAGTTTGGAGAGGACGACGACG 972
 QY 302 GlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpTrpLeuPhe 321
 Db 973 TCTCAATCTCTCTGATACATTGAAGGTTTGAATGATGAAGATGCTGCTTCTCTTA 1032
 QY 322 MetGlnArgAlaPheGlyHis---GlnGluGluLysLeuAsnLeuValAlaIleGly 340
 Db 1033 AAAAAGTATGCGTTCTTGCAATGGGCAAGTAGGAGAAATGATGCTTGTCAAAAAGTGGG 1092
 QY 341 LysGlnIleValLysLysCysGlyGlyValProLeuAlaLysTrpLeuGlyGlyIle 360
 Db 1093 AGGATGATTGACGCGCACTGTGAGGTTCCCATTAAGCAGCAATCACTCGGAGTGGCTT 1152
 QY 361 LeuArg---PheLysArgGluGluArgGlnTrpGlnHisValArgAspSerGluIleTrp 379
 Db 1153 TTGTCGATACTAATGAGAGAGAAAGAAAGATGCTCATATA---TCAACCAAAATGGCG 1209
 QY 380 LysLeuProGlnGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrHisLeu 399
 Db 1210 ATTCTTATGAACACACACACAGATCTTGGCAAGTTTGGCAATGATATCATCACTTG 1269
 QY 400 ProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMet 419
 Db 1270 CCATATCATCTGAAGCAGTGTGTTACCTTGTGTGCTTGTCTGTTGGCATGAATTT 1329
 QY 420 GluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGlyAsn 439
 Db 1330 GAGAGAGATGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1389
 QY 440 LeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhePhe 459

Db 1390 AGCGCTTGGAGGAGAGAGAGATTTTGTATGAGCTTGTGAGATCAATCTT 1449
 Qy 460 GlnGluIleGluValysSerGlyGlnThrTyrPheIysMetHisAspLeuIleHisAsp 479
 Db 1450 GAACCTCTGGCAGTTTCACCAATTCAGATAC--AGGTCGCAAGCTCATGAATGAG 1506
 Qy 480 LeuAlaThrSerLeuPheSerAlaSer-----ThrSerSerSerAsnIleArg 495
 Db 1507 CTGCA--TCGCTGTTCAAAATCTGAATGTTGTGATGATGAGCCTGTGACTTACAG 1563
 Qy 496 GluIleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrIys----- 512
 Db 1564 GGTGCGATTAACCGTGAATGCTGGATATGATATCTGTCTGTCACAAAGATGAAC 1623
 Qy 513 -----ValIleSerSerTyr----- 517
 Db 1624 CCGAGCTGACATATGATCTGCAACTATGAAAACATAGATATTGAACTGTACTGAA 1683
 Qy 518 -----SerLeuSerHisIleGluIlePheValSer 527
 Db 1684 GTAAGGATTTCTCTAAATGTGTCTCCAGAGCTTTTCCAC-----AAGTTAAGTTGT 1737
 Qy 528 LeuAlaGluValIleuAsnLeuSerAspIleIysIleuIysGlnLeuProSerSerIleGlyAsp 547
 Db 1738 TTACGCAACACGTGAATAGTACAGTGAACAGTGAACAGTTCACAGACTCAGTTGATGC 1797
 Qy 548 LeuValHisIleuArgTyrIleuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsn 567
 Db 1798 TTGACACACCTTAAGATATACATGGCTTACGC--AAACACCTATTATTAAGGCTTCTTAC 1854
 Qy 568 GlnLeuCysIleuLeuGlnAsnLeuGlnThrIleuAsnLeuHisGlyCysHisSerLeuCys 587
 Db 1855 TCAGTTAGGACCTTGTCAACCTGCAGACTCTAGATCTCAGGAAAGCTACCGCTTACT 1914
 Qy 588 CysIleuProIysGlnThrSerIysLeuGlySerIleuArgAsnLeuLeu----- 604
 Db 1915 GAGTTACCTGAAAGAGTGAAGTGGTTAGTATTTACCTGACCTGACCTGCAACCTTGA 1974
 Qy 605 ---AspGlyCysTyrIleuThrCysMetProProArgIleGlySerLeuThrCysIleu 623
 Db 1975 TGGGATAGAAATGGATACCAATACCA--ATGCCAAGAGGATGACAAAGTTAATCTCCCT 2031
 Qy 624 LysThrLeuSerArgPheValValGlyIleGlnIlyIysSer---CysGlnLeuGlyIle 642
 Db 2032 CAACACCTTCCAGATTACTGTGACTGCTGATGCTGAGGGCTACTGCAACATGAAGAA 2091
 Qy 643 LeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHisIleuGlnArgValIysAsn 662
 Db 2092 TTCAAGACATCAATATAGTGTGAACTTGGCTGCTGAAATTTGGAATCTGCCACCAT 2151
 Qy 663 AspMetAspAlaIysGluAlaAsnLeuSerAlaIysGlnAsnLeuHisSerLeuSerMet 682
 Db 2152 GAG---AATGGCGGGGAGATCCAGTTGAGTGAGAACCAATATGTAAATCTGATGCTG 2208
 Qy 683 LysThrAspAspArgIleuArgProArgIleTyrGlnSerGlyIleValGlnValIleGln 702
 Db 2209 CAATGAGATTACATATATATCAAGACATGATGAAGC-----ATGGCGGTATAGAA 2262
 Qy 703 AlaLeuIysProHisSerAsnLeuThrCysIleuThrIleArgIlyPheArgIlyIleArg 722
 Db 2263 TCACCTCGCTCTATCTAGCTGAGAGAGCTATGGGTGATGATGACCTGGGAGAAAT 2322
 Qy 723 LeuProAspTyrPheAsnHisSerValIleuIysAsnValIleSerIleGluIleIleSer 742
 Db 2323 TTTCCTGATGAGATGGGGAAAGTTCTTTCACCTATCTTGAATAATCTGAGATTTGTAC 2382
 Qy 743 CysIleuAsnCysSerCysIleuProProPheGlyIleuLeuProCysIleuIysSerLeuGln 762
 Db 2383 TGCAGAAATTCGGGCTTCTTCCTCTTTTGGAGAACTGCCAAAGCTAAATAAATTCAT 2442
 Qy 763 LeuTyrArgIlySerAlaGluValGluTyrValIleAspSerGlyPheProThrArgArgArg 782

Db 2443 CTT---GAGAGCATGATAGCCTACAA-----AGATGGGACCTCTTTGGCT 2487
 Qy 783 PheProSerLeuArgIlyIleuAsnIleArgGluPheGlyAsnLeuIysGlyLeuLeuIys 802
 Db 2488 TTTCATCTCTTAAGGTTTGTGACTTGGAGACATCCCTATCTTCAACATGATGGCAG 2547
 Qy 803 LysGluGlyIleuGlnCysProValIleuGlnIleGlnIleIysCysCysPro--- 821
 Db 2548 TCGAG---GAGCAGAACTCTTAAGCTCAAGAGACTTATATTAAGCATTTGCCAGAA 2604
 Qy 821 ----- 821
 Db 2605 TTGCAAATATGCAAAATCTCTCGTGAAGCTTCTTAAGCTGAGATTAATTAATCTGGC 2664
 Qy 822 ---MetPheValIleProThrLeuSerSerValIlyIleuValIleSerGlyAspIys 840
 Db 2665 ATGTTGTGTTCTTCTCTGGGCTTCAACCTTCATGATTAATCTGTTAGAGCAAT 2724
 Qy 841 SerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIle 860
 Db 2725 GATCACTAATTCGATG---ATCAGCGAGCTGATGTCTGTGACTTCACTAACGCTG 2778
 Qy 861 ArgTyrAsnIlySerGluAspAlaSerLeuProGlnIleMetPheIysSerLeuAlaAsnLeu 880
 Db 2779 ATGCAATTCACAGAAACGATGATATA-----CAGCATTAACAACATTTGAGTGCCTG 2832
 Qy 881 LysTyrLeuAsnIleSerPheTyrPheAsnLeuIysGluLeuPro-----ThrSerLeu 898
 Db 2833 AAGGATTTAAAGTTGAGAGATTTAAACAGCTTCTCAGTGTCTGATTAATACCGGCAAT 2892
 Qy 899 AlaSerLeuAsnAlaLeuIyHisIleuGlnIleHisSerCysTyrAlaLeuGlnSerLeu 918
 Db 2893 GAGGACCTCTCTCCCTTGAAGTTCCTTGAATATCACTGCAAGAACTCCAGCATTT 2952
 Qy 919 ProGlnIleGlyValIysGlyIleuIleSerLeuThrGlnLeuSerIleThrTyrCysGln 938
 Db 2953 ---TGTGTGGGAGTTGATCACTCAAGAGATTTCAAGCTTCCCATTTGCAC 3003
 Qy 939 MetLeuGlnCysLeuProGlnIlyIleuGlnHisIleuThrAlaLeu----- 953
 Db 3004 AAGCTGAGAGCTGCCAAGGTTGGCAACTTGGATCTTATAGTGTGAAT 3063
 Qy 954 -----Thr 954
 Db 3064 CACGACATTCCTTAAGTGAATAGACAAATCTGCCACGGTATTCCTGATAGGCTTCC 3123
 Qy 955 AsnLeuSerValGluPheCysProThrLeuAlaIysArgCysGluIyIleGlyGln 974
 Db 3124 TATCTGACATTAAGTGAATGCCGATCTGAGAGTTGTGC---AGGAACACGGGCGCC 3180
 Qy 975 AspTyrTyrIleAlaHisIleProArgValPheIle 987
 Db 3181 CAG-----AGAGTAAAGAAATCCCTTAATGTAAAGATT 3213
 RESULT 10
 CL962156 4236 bp DNA linear GSS 21-SEP-2004
 LOCUS OSifCC007292 Oryza sativa Express Library Oryza sativa (indica
 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL962156
 VERSION CL962156.1 GI:52379048
 KEYWORDS GSS.
 ORGANISM Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiales; Oryzaceae; Oryza.
 1 (bases 1 to 4236)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G. K. S., Deng, X. W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis

JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

FEATURES
 Source Location/Qualifiers
 1..4236
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_lib="Oryza sativa Expressed Library"
 /note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Alignment Scores:

Pred. No.:	2,116-114	Length:	4236
Score:	1159.50	Matches:	336
Percent Similarity:	48.52%	Conservative:	172
Best Local Similarity:	32.09%	Mismatches:	398
Query Match:	22.62%	Indels:	141
DB:	9	Gaps:	32

US-10-647-268-2 (1-988) x CL62156 (1-4236)

OY 34 LeuGlnSerThrPheThrIleGlnAlaValLeuGluAspAlaGlnIleValLeuGlu 53
 DB 964 CTGCAGAGGAGCGATGCGGAGGATCCAGCGCGATCTGTACACCGATGAGGAGCATC 1023
 OY 54 LysAspIleValIleGlnAsnTrpLeuGlnIleValAsnAlaIleValIleValAsp 73
 DB 1024 AGAATGATGCTGAGAGGCTTCACTGAGGAGGAGCTTCAAGTTTCCCTACGATGCCAA 1083
 OY 74 AspIleValAspGluCysIleThrGlu----- 82
 DB 1084 GATGCAATCGATCTGTACAGTTTGAGCTTCTGCGGCGGAGGATGATCCAAACGT 1143
 OY 83 -----AlaProIleArgGlnIleValAsnIleValIleValIleValIleVal 98
 DB 1144 CATGAGATGCGGAGGAGGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1203
 OY 99 Val-----IleThrPheArgHisIleValIleValIleValIleValIleVal 114
 DB 1204 ACTGAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1263
 OY 115 GlnIleValAspValIleAlaIleValIleValIleValIleValIleValIleVal 131
 DB 1264 GAAAGATTGAAGAGATCAAAAGGATGATGATCTCCGCTGATGATGATGATGATGAT 1323
 OY 132 -----ArgThrIleGluArgGlnValIleValIleValIleValIleValIleVal 149
 DB 1324 ACATGCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1383
 OY 150 ProGlnValIleValIleValIleValIleValIleValIleValIleValIleVal 168
 DB 1384 CCCACTCTCTTGGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1443
 OY 169 AsnValSerAsnAlaGlnThrLeuProValLeuProIleGlnIleValIleValIleVal 188
 DB 1444 GGTGGTGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1503
 OY 189 LysThrThrLeuAlaGlnMetValPheAsnAspGlnIleValIleValIleValIleVal 208
 DB 1504 AAGACAGACCTTGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
 OY 209 LysIleTrpIleCysValSerGluAspPheAsnGlnIleValIleValIleValIleVal 228
 DB 1564 ATGGGCTGGTTCATGCTCAGAGAAATTTGATCTCAAAAGCATATATGCTAAATATTC 1623

OY 229 GluSerIleGlnIleValSerLeuGlnIleValMetAspLeuAlaProLeuGlnIleValSerLeu 248
 DB 1624 ATGCTCTTCAAGAAAACCATGTCAGATGACAAATGATGATGATGATGATGATGATGAT 1683
 OY 249 ArgAspLeuLeuAsnGlnIleValIleValIleValIleValIleValIleValIleVal 268
 DB 1684 ATGAAACAAGTTGTTGGCAAGAAAGTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1743
 OY 269 GlnAspIleTrpAlaIleValIleValIleValIleValIleValIleValIleValIleVal 288
 DB 1744 AAGGATATTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 OY 289 LeuThrThrThrArgLeuGlnIleValIleValIleValIleValIleValIleValIleVal 308
 DB 1801 TTGGTAATCTACCCGATATCAAGATGTCATCAATATGTCAGAGCAATGATGATGATGAT 1860
 OY 309 LeuSerAsnLeuSerGlnIleValIleValIleValIleValIleValIleValIleValIleVal 328
 DB 1861 GTGAGTGCCTTACCTTTTGAAGAAATCCCTGCACTATTCAGAGCATGATGATGATGAT 1920
 OY 329 GlnGlnGlu-----IleAsnLeuAsnLeuValIleGlnIleValIleValIleValIleVal 347
 DB 1921 CAAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
 OY 348 GlyGlyValProLeuAlaIleValIleValIleValIleValIleValIleValIleValIleVal 367
 DB 1981 GCTGGCTTGCCTTATGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
 OY 368 ArgGlnTrpGluHisValIleValIleValIleValIleValIleValIleValIleValIleVal 387
 DB 2041 GAGAAATGGAATGACATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
 OY 388 IleLeuProAlaIleValIleValIleValIleValIleValIleValIleValIleValIleVal 407
 DB 2101 GTGTATCCGCGGTTAAATTAAGCTATGATCAATGCAATTCACCTTAAGCGGAGCTTT 2160
 OY 408 ThrTyrcysAlaValPheProIleAspThrGlnMetGlnIleValIleValIleValIleVal 427
 DB 2161 GTTTCTTCGATATATTCCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
 OY 428 TrpMetAlaHisGlnPheIleLeuSerIleValIleValIleValIleValIleValIleVal 447
 DB 2221 TGATATCTTGGGCTTCTTAAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2277
 OY 448 GlnValIleProAsnGlnIleValIleValIleValIleValIleValIleValIleValIleVal 467
 DB 2278 AGTGCCCTTAATGACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2337
 OY 468 GlnThrTyrcysPheMetHisAspLeuIleHisAspLeuAlaIleValIleValIleValIleVal 485
 DB 2338 CATGATGCTTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2397
 OY 486 -----SerAlaSerThrSerSerSerSerSerSerSerSerSerSerSerSerSer 494
 DB 2398 GATATTTTGAATATGACACTCAACATGAAAGCTATGATGATGATGATGATGATGATGAT 2457
 OY 495 Arg-----GlnIleIleValIleValIleValIleValIleValIleValIleValIleVal 506
 DB 2458 AGGATATTATCTCGGTTGATGTTTCAAGACCATGAGAAATTTGATGATGATGATGAT 2517
 OY 507 -----SerIleGlnPheThrIleValIleValIleValIleValIleValIleValIleVal 518
 DB 2518 CCAATGTCAGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2577
 OY 519 -----LeuSerHis----- 521
 DB 2578 TATTTTCAATCTTCAAAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2637
 OY 522 -----LeuGlnIleValIleValIleValIleValIleValIleValIleValIleVal 532
 DB 2638 ATTAACCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2697
 OY 533 LeuSerAspIleValIleValIleValIleValIleValIleValIleValIleValIleVal 552

```

Db 2698 TTAAGCCGCACTCAATGATAGCATTTGCTTATTCATTTAGAGAACTGAACTTCTCAGS 2757
Qy 553 TyleuAsnleuSerGlyAsnThrSerileArgSerleuProAsnGlnleuCysleu 572
Db 2758 TATCTAAGTATTTTC---CAAAAGAAATCTCCAAAGCTCCAGATCAATATTGAGCTTC 2814
Qy 573 GlnAsnleuGlnThrleuAspLeuHsGlyCysHsSerleuCysCysleuProGlyGlu 592
Db 2815 CTTTAAATTGAAGATCTTAGATGCAAGA---ACAAACTTTTGAAGAGCTTCCCAAGGC 2871
Qy 593 ThrSerlyleuGlySerleuArg-----AsnleuLeuAspGlyCysTyrglyleu 610
Db 2872 ATTCAAGAGCTGTGCACAGCTCCAGATCTCAATTAGCTC-----TGGCTCCC 2922
Qy 611 ThrCysMetProProArgGlyGlySerleuThrCysleuTythrleuSerArgPheVal 630
Db 2923 CTGTGCATGCAAAAGAAATGGAATCTGACCAAACTCAAAACCTTGACAAAGGATATAGT 2982
Qy 631 ValGlyIleGlnlylySerCysGlnleuGlyGluLeuAsnleu---AsnleuTy 649
Db 2983 GTTGAAGTGGCAATTGGCACTGCAATATGCTGAACATTAATTACTTAGATATATCAT 3042
Qy 650 GlySerileGluIleThrHsileGlnlyArgVallyAsnAspMetAspAlalyGlyAla 669
Db 3043 GGTGAATGACCATTTACAGATTTAGAGTGAAGTGAACCAAGTTGATGATGCTCAAAAGCC 3102
Qy 670 AsnleuSerAlalyGlyAsnleuHsSerleuSerMetlySTTPAspAspGlyArg 689
Db 3103 AACCTGATTAATAAGAACTGCAATGCAACTCTAAGATTAAGATTGCTGATGCA----- 3156
Qy 690 ProArgIleTyrglySerGlu----- 696
Db 3157 -----TTCTACTTGAATGATGATCATATTTAGTCATATAGATTAAGCAACA 3210
Qy 697 -----LyValGluValleuGlnAlalylyProHsSerAsnleuThrCysleu 713
Db 3211 CCAGAAATTAGCAGAGAGATTTTGAAGCTTAAGCCAACTGACAACTTGAGAGAGTTA 3270
Qy 714 ThrIleArgGlyPheArgGlyIleArgleuProAspTrpMetAsnHsSerValleu 733
Db 3271 GAGGTAGCTGATTTTGGGTACAAATACCAAGCTTGGTGGAGTTTCCCTATTCA 3330
Qy 734 AsnValleuSerileGluIleleSerCyslyAsnCysSerCysleuProProPheGly 753
Db 3331 CAATTGGCCAAAGATTACTTATAGAG---CAAGCTGCAAGTCTCTTCCAACTTGGC 3387
Qy 754 GlnleuProCysleuLySerleuIleuTrpArglySerAlalyValGlyIleVal 773
Db 3388 CAGTTACTCAGTTCGTAATCTTGAATTATACG---ATGAGAGAAAGTAGAGAAATC 3444
Qy 774 AspSerGlyPhe-----ProThrArgGlyPheProSerleuArglyleuAsn 790
Db 3445 GGGCAGAGATTTCATGCGAGAAATTCACAAATTCATTCCTCCAGTATGAGGAATGG--- 3501
Qy 791 IleArgGlnPheGlyAsnleuLyGlyleuLeuLylyGlyGlyIle-----GlnGluGln 808
Db 3502 -----GAGTTTGAAGAACGTCGCAAAATGGGTGAGTGAAGTCTGAGTTTGTGAC 3555
Qy 809 CysProValleuGlnIleGluIlelyly---CysCysPrometPheValIlePro--- 826
Db 3556 TTCCTTACCTTCGAGAGCTGAATAATCAAGAGAGGATGAGAACTTCCACAT 3615
Qy 827 ---ThrleuSerSerVallylyleuValIleSerGlyAspLySerAspAlale--- 844
Db 3616 CAATTATCATCTCTTGAATAAATGGTCATCAAG-----AAATGTGAAAAGCTGACA 3669
Qy 845 GlyPheSerSerileSerAsnleuMetAlaleuThrSerleuGlnIleArgTyranlys 864
Db 3670 AGACTGCCAACATATTCACCACTTAACATCTTATTATG----- 3711
Qy 865 GlnAspAlaserleuProGlnIleuMetPheLysserleu-----AlaAsnleuTy 882

```

```

Db 3712 -----GGCAATCTTTAGCGAAGAAATACACAAATAGTCTGANTTTCCATGCTCCAAATA 3765
Qy 883 LeuAsnIleSerPheTyrrPheAsnleuLyGluLeuProThrSerleuAlaserleuAsn 902
Db 3766 TTAAGAGTGTTTTCACGCAAAACCTTGTGCTTGAATTTGACATATAGAACCTTACA 3825
Qy 903 AlaIleuLyHsIleuGlnIleHsSerCysTyrrAlaIleuGlnSerleuProGlnGly 922
Db 3826 ATCTGGAGGCACTAGCTATAGTGATGATCGCGGAGCTATTTCTGTG-----GTAGGA 3879
Qy 923 VallyGlyleuIleSerleuThrGlnleuSerileThrTyrrCysGluMetleuGlnCys 942
Db 3880 TTGTCAGCTTGAATCTTCAGCTTCTTAATAAATAAGATTGCCAACTGCACTGC 3939
Qy 943 LeuProGlnGlyleuGlnHsIleuThrAlaIleuThrAsnleuSerValGluPheCysPro 962
Db 3940 CCTTACACCACTTCAACAG-----CACTTCAGCAATGATTAATACAGAACTGCTCT 3993
Qy 963 ThrleuAlalyArgCysGlu 969
Db 3994 CAATTACAGGAATGATGAG 4014

RESULT 11
CL945091 3546 bp DNA linear GSS 21-SEP-2004
LOCUS OaIFSB001967 Oryza sativa Expressed library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL945091.1 GI:52357100
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 3546)
AUTHORS Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..3546
Location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:3946"
/clone_id="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Alignment Scores:
Pred. No.: 5,21e-113 Length: 3546
Score: 1145.50 Matches: 330
Percent Similarity: 47.76% Conservative: 181
Best Local Similarity: 30.84% Mismatches: 398
Query Match: 22.34% Indels: 161
DB: 9 Gaps: 34

US-10-647-268-2 (1-988) x CL945091 (1-3546)
Qy 4 AlapheleuGlnValleuLeuAspAsnleuThrCysPheIleGlnGlyGluLeuGlyleu 23
Db 22 GCTTTTTCGAAGTGCTTTTTCAGAAATCCATGAGCTGTGGAAGAAAGAACTGAGATT 81

```


Oy 128 HisleuAargluAargThrllegluAarglnVala1aThrAarglnThrclyPheValleu 147
 Db 484 CCAGAGAAAGCCAGGACACAGCAGATATACAGATCAAGATCAAGACGTCAGTGGCC----- 534
 Oy 148 AengluProGlnValIyrgIyAargAarglyuAarggluIleValIyglleuIle 167
 Db 535 ---CATGGGAAATCTTCGGGGGAGATATCAAGAAATCCAAACAGTTGGTAAGTACTTTTA 591
 Oy 168 AenAen---ValSerAenAlaglnThrlleuProValleuProIleleuglyMetglly 186
 Db 592 AGCTCTCAGGTGATGATGATATATCCAGATCTCGGTGGTTCCTCAATGTTGGAGTTGGTGGC 651
 Oy 187 LeuglyuSerThrlleuAlaglnMetValPheAenAarglnAargValIlegluHisPhe 206
 Db 652 GTGGGCAAGACTGCTTCAGCAGATGATGTACAAACACTAGAGTACAGCATTAATTT 711
 Oy 207 HisProllysIleTrpIleCyValSergluAargPheAenglnIyAargleuIleuysglu 226
 Db 712 GACATGAAATATGTGATCTGTGTATCTGATGCTTTATGATGATCCAGATATCAAGAG 771
 Oy 227 IleValIgluSerIlegluIgluIySerleuglyMetAargPheVala1-----Pro 243
 Db 772 ATGCTAGAGTCAAGTTCCAGCAGTCGATTTAGGSCATGACAGCATTAACAAATTTCAACAG 831
 Oy 244 LeuglnlyuIyAargAargPheleuAenAlaglnlyuIyStryrleuIleValleuAargP 263
 Db 832 CTTCAGGTGGCAGCTCGCAGCAAGGCTCGTATCCAAAGGTTTCTGCTGTCTTATGATGAT 891
 Oy 264 ValITrapAengluAargGln-----AspIyStryrAlaIyAargleuAarg 276
 Db 892 GTCTGGACCAATGACAAATATACCTGGCGATAGACAGCAAGAACTGGCAGAAAGCTTCT 951
 Oy 277 GlnValleuIyValGlyAlaSerGlyAlaSerValleuThrThrlThrxleuglnlyu 296
 Db 952 TCTCCCTCCAAAGGCTGCAGCAAAATGGGAGCAAAATCTTCGACCAAGCCGATTCACATGAT 1011
 Oy 297 ValIgluSerIleMetGlyThrlleuIlnProIyrgIleuSerAenIleuSerGlnIyAarg 316
 Db 1012 GTGGCGGAGATGCTTACAGTCAAGCCCATTAACATACTCGAAGTGGTTCGATATGAGAT 1071
 Oy 317 CysITrpleuIleuPheMetGlnAargAlaPhegluHisgluIglu---IleAsnIleuAen 335
 Db 1072 TGTGTGTCTCCGATTAATAATGATGTTGTGTATGATATACAAACATCTTATTAATTCACAG 1131
 Oy 336 LeuValAlaIleGlyIyAarggluIleValIyIyStryrGlyValProleuAlaIyA 355
 Db 1132 TTGGCGAATATTTGGAGGAGATATGCTTAAGACACTTAATGTGCTTAACCTCTTGGCGAAG 1191
 Oy 356 ThrleuIgluIyIleleuAargPheIyAargIgluIgluAargIlnTrpGlnHisVala1---Arg 374
 Db 1192 GTGTGCTGTAACAGCTGAATATGTAAACACACACACAGATAGGTGAACAAAGTCTTACAG 1251
 Oy 375 AspSerGluIleTrpIyAargProGlnIgluIleuSerIleleuProAlaIleuAargIleu 394
 Db 1252 AGAATATGACATATG-----GATGAATATCAGGCCAAATTTTCAAGAT 1293
 Oy 395 SerIyTrpHisIleuProleuAargIleuAargIlnCysPheThrIyrgValaValaPhePro 414
 Db 1294 AGCATATGAAATCTCCACAGTCAACCTTCAACAAATGCCCTTGACATTTGACAGTATCTTCCC 1353
 Oy 415 LysAargThrxIleMetGluIyGlyAenIleuIleSerIleuTrpMetAlaHisGlyPheIle 434
 Db 1354 AAGACATGGGAATTTGAAGCTGAGCAGATTTATCTCATGTGATGAGGACAAAGTATATGA 1413
 Oy 435 LeuSerIyStryrAenIleuIgluAenValGlyAengluValITrapAengluIleuIy 454
 Db 1414 TACCACAGATGTTGCAGAGAAATGGAACAATTTGGGAAGCAAAATGTGTTGAAGATATGT 1473
 Oy 455 LeuAargSerPhePheGlnIgluIleIgluValIySerGlyIlnTrpIyPheIyMetHis 474
 Db 1474 AGTCGCTAATTTT---GCCATTCAGAAACAAATTTGTCAGCTAATATGTATGTATGCTT 1530

QY	475	AspLeuIleHisAspLeuIleAlaThrSerLeuPheSerAlaSer-----	488
DB	1531	CCCGTATTTCACAACTTGGCCAAATCGATTGATTCACGACAGAAATGTTCCGAAATAGAGGT	1590
QY	489	-----ThrSerSerAsnIleArgGluIleIleValGlu-----	500
DB	1531	GATGAACAGAGAAAGATCCCATCTCTGTACGCCATCTATCATTCATCTAGATAGCTT	1650
QY	501	-----AsnTyrIleHisMetSerIleGlyPhe-----Thr	511
DB	1651	TCAATGCTTGACGAGACAAATACCATATCATGACCTGGCAGCTCTCATTTCTTTAGACAGC	1710
QY	512	LySValValSerSerTyrSerLeuSer-----HisLeuGlnLysPheValSer	527
DB	1711	AGATTGGGTGGCTCCAAATCAATTCATTCATCCACMACTAGTTCTGTATTAACCTTCAAGC	1770
QY	528	LeuArgValLeuAsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAsp	547
DB	1771	CTTGCTGTCTTGAGATTATACCTTGCAAGATTAACAGACTCTCTGACAGTATACGACAG	1830
QY	548	LeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnHisSerIleArgSerLeuProAsn	567
DB	1831	TGTGTGCATCTCCGATACCTTAATATCTCA---TCACTGCATCAACATGTTATACAGAA	1887
QY	568	GlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCys	587
DB	1888	TACTTGGGTAAACTTTACCACTTGCAAGTCTTAACATTACAGGCTGCAGG---CTTGAA	1944
QY	588	CysLeuProLysGluThrSerLysLeuGlySerLeuArgAsnLeuLeuAspGlyCys	607
DB	1945	AAGTATACCTTCAGACATTAACAACTGCTGCTGATTAGGCAT-----CTGACAGCAGCT	1998
QY	608	TyrGlyLeuThrCysMetProProArgIleGlySerLeuThrCysLeuLysThrLeuSer	627
DB	1999	AACCAAGATCTTCCACTATTAACAGACATAGAGAACTTAAGATATCCTCAGAGATTGCC	2058
QY	628	ArgPheValValGlyIleGlnLysLysSer-----CysGlnLeuGlyLysLeuArgAsn	645
DB	2059	ATTTTCAAGGTCCACCAGTGAAGAAACAACAGCATTAATTCAGCTTGTTATCTTCAACAG	2118
QY	646	LeuAsnLeuTyrGlySerIleGlnIleThrHisLysGlnLysArgValLysAsnAspMetAsp	665
DB	2119	CTTGTGT-----GGATCCCTCCACATTAGAGAACTTGAAGACATTGATGCTCTGATGAG	2172
QY	666	AlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLysTyrAsp	685
DB	2173	GCAAGAGAAAGCATGTTGTGTGAAGAAAGTAACCTGCAATGCTGCAGCTGATGTGG---	2229
QY	686	AspAspGluArgProArgIleTyrGlnSerGlnLysValGluValLeuGlnAlaLeuLys	705
DB	2230	GCACCTGCTCGAGATTGTGTAACTCAGATTAAGAACAGAGGGTGTATAGATATCTCCAG	2289
QY	706	ProHisSerAsnLeuThrCysLysLeuThrIleArgGlyPheArgGlyIleArgLeuProAsp	725
DB	2290	CCACAACCCAAATCTGAAGAGGCTGAGACATATCGGTGTGAGGGAGTCAAGCCCCAGT	2349
QY	726	TyrPheAsnHisSerValLeuLysAsnValValSerIleGluIleLysSerCysLysAsn	745
DB	2350	TGGCTTGAAAGCAATGGCTAATATCTTGAAGCTATCTTCTCTCACTGGTTGCATGCT	2409
QY	746	CysSerCysLeuProProPheGlyGluLeuProCysLeuLysSerLeuGlnLeuTyrArg	765
DB	2410	TGGAGGACAGCTTCACACACTTGGTCACTTCCATCTGTGACGACTAATTTGGTGG-----	2463
QY	766	GlySerAlaGluValGluTyrValAspSerGlyPheProThrArgArgAlaGlyPheProSer	785
DB	2464	-----CAGCTTTGAAACA	2478
QY	786	LeuArgLysLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeuLeuLysLysGlnGly	805
DB	2479	GTGAGGCAAAATGGCTTAAGAGTATATGAGCAATTAAGAGTTCAATGTGGCTTCCAGTCA	2538
QY	806	GluIuGlnLysCysProVal-----	811

```

Db      2539 TTAAAGAGAGTAGTCTTATGATGACATGACAGAACTAAATGATGTCATGACAGCGCAG 2558
      |||:::
      |||:::
Qy      812 -----LeuGluGluIleGluIleLysCysCys----- 820
      |||:::
      |||:::
Db      2599 GAAATGATGAATCTCCGCAATATTTGATTAAGACATCCAAAGCTCAAGAGCTGCTT 2658
      |||:::
      |||:::
Qy      821 Promet-----PheValIlePro--- 826
      |||:::
      |||:::
Db      2659 CCACACTACTCCAAAGCTTACAGAGCTGACAAATGCAAAAAAGGGTCTCGGTTCCATAC 2718
      |||:::
      |||:::
Qy      827 -----ThiLeuSerSerValLysLysValVal 836
      |||:::
      |||:::
Db      2719 CATCATGATGTGAAGATGACACAAATTTGACCACTGTCACACTGTCATCTCTTCATCA 2778
      |||:::
      |||:::
Qy      837 SerGlyAspLysSerAspAlaIleGlyPheSerSer-----IleSer 850
      |||:::
      |||:::
Db      2779 TTCAATTGCCCCAGCTACTTGTCCGATTTTCTCTCCGACGATGACCAATGAGTTGTAGA 2838
      |||:::
      |||:::
Qy      851 AsnLeuMetAlaLeuThrSerLeuGluIleArgTyrAsnLys----- 864
      |||:::
      |||:::
Db      2839 AGCTTTCAGTACTTAGAAGCTTATCGTTGATCATATGAGATATCTCACATGCCCCCTT 2898
      |||:::
      |||:::
Qy      865 -----GluAspAlaSerLeu----- 869
      |||:::
      |||:::
Db      2899 TTAAAGGAAAGGCTTGACGACATTTAGAACTTACATCCAGATTCCTCAGATCACC 2958
      |||:::
      |||:::
Qy      870 -----ProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLeuAsn 884
      |||:::
      |||:::
Db      2959 ACCTTCATCGCAGACATAGAGATGTCTTCTTCAATCTTAAGATCACTCAAAAGCTCTTGC 3018
      |||:::
      |||:::
Qy      885 IleSerPheTyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeu 904
      |||:::
      |||:::
Db      3019 ATAACTGGCTGCAACATCTTACATCGCTCCCTTCTCAATGTCCAGCTGAGTCCCTG 3078
      |||:::
      |||:::
Qy      905 LysHisLeuGluIleHisSerCysTyrAlaLeuGluSerLeuProGluGluValLys 924
      |||:::
      |||:::
Db      3079 GATTAATTAATCTTGGGATTTGCCCTGAGTTGGATTTACTCCACAGACAGAGCTGCCA 3138
      |||:::
      |||:::
Qy      925 GlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCysLeuPro 944
      |||:::
      |||:::
Db      3139 -----CTGCTCTTATGAAGAGCTTGAAGTCGCACTGTAAAC----- 3174
      |||:::
      |||:::
Qy      945 GluGlyLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeu 964
      |||:::
      |||:::
Db      3175 -----COAGTCTC 3183
      |||:::
      |||:::
Qy      965 AlaLysArgCysGluLysGlyIleGlyLysAspTyrTyrLysIleAlaHisIleProArg 984
      |||:::
      |||:::
Db      3184 AAGGATAGACTCAGAAAAGAAATGTGCGATTGACTGCGCAAAAGTTGCGCATATCCCTTGG 3243
      |||:::
      |||:::
Qy      985 ValPheIle 987
      |||:::
      |||:::
Db      3244 GTTGAGATA 3252
      |||:::
      |||:::

```

```

RESULT 13
CL978496 3576 bp DNA linear GSS 21-SEP-2004
LOCUS CL978496
DEFINITION Oryza sativa (indica cultivar-group)
ACCESSION CL978496
VERSION CL978496.1 GI:52411494
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriophytaceae; Oryzaceae; Oryza.
1 (bases 1 to 3576)
Ma,L., Wang,C., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and

```

```

JOURNAL
COMMENT
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
source
1..3576
/location/Qualifiers
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"

```

```

ORIGIN
Alignment Scores:
Pred. No.: 3.57e-108 Length: 3576
Score: 1101.50 Matches: 332
Percent Similarity: 45.57% Conservative: 203
Best Local Similarity: 28.28% Mismatches: 380
Query Match: 21.48% Indels: 259
DB: 9 Gaps: 35

```

```

US-10-647-268-2 (1-988) x CL978496 (1-3576)
Qy      38 PheThrThrIleGlnAlaValLeuGluAspAlaGluLysGluLeuLysAspLysAla 57
      |||:::
      |||:::
Db      151 TATAGTCTCTTATGAGGTGTATACGAAAGATCTCCAGAGCTTCAAGATTTAGTTGAGAG 210
      |||:::
      |||:::
Qy      58 IleGluAsnThrLeuGluGlnLysLeuAsnAlaAlaLysTyrGluAlaAspAlaIleLeuAsp 77
      |||:::
      |||:::
Db      211 ATCAAAAGCGGCTTACG-----TCTGAGAAACATGACACAGTATATGATCGTGAC 261
      |||:::
      |||:::
Qy      78 GluCysLysThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisPro 97
      |||:::
      |||:::
Db      262 AAGATATGCTGTGCTCAATATCAATCGGCACAAA-----CCA 297
      |||:::
      |||:::
Qy      98 AsnValIleThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeu 117
      |||:::
      |||:::
Db      298 AAACATGACCATGTTCACCAATATGCGCCAAACAGATTAAGACAAATCAAAACAGATT 357
      |||:::
      |||:::
Qy      118 AspValIleAlaIleGluArg-----IleYspHisLeuAspGluArgThrIleGlu 135
      |||:::
      |||:::
Db      358 GCTGCAATTTGCGACCAAGGCGGATGCTCAATATGATGCTATATCCATCGAT 417
      |||:::
      |||:::
Qy      136 ArgGlnValAlaThrArgGlnThrGlyPheValLeuAsnGluProGlnValTyrGly--- 154
      |||:::
      |||:::
Db      418 CATATGTTTCAATAAAACAAG-----ATTATCATGAGCATCTTATTTGGGCAT 468
      |||:::
      |||:::
Qy      155 -----ArgAspLysGluLysAspGluIleValLysIleLeu 166
      |||:::
      |||:::
Db      469 GTTGATGACTCAAAATATCATGTGAGATGAGAGGACCAAGATCATATCGTAAGTTA 528
      |||:::
      |||:::
Qy      167 IleAsnValLeuSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyGly 186
      |||:::
      |||:::
Db      529 ATAGAT-----GACCAACAGAAATCTCATATGTTCAATTTGTTGACTGTGGAGA 579
      |||:::
      |||:::
Qy      187 LeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGluHisPhe 206
      |||:::
      |||:::
Db      580 ACCGTTAAATATCATATGAGCCACACATCTGTATGACCAAAATTAAGACATTTT 639
      |||:::
      |||:::
Qy      207 HisProLysIle---TrpIleCysValSerGluAspPheAsnGluLysArgLeuIleLys 225
      |||:::
      |||:::
Db      640 GAAGGCTCAATATTTTGGGTTCACTGTCAAGATTTGATTAATACAAACTCGTCGC 699
      |||:::
      |||:::
Qy      226 GluIleValGluSerIleGluGluLysSerLeuGlyMetAspLeuAlaProLeuGln 245
      |||:::
      |||:::
Db      700 AAGCTGTATGAAGCATTTTAAAGAAACATCATATCTTCGACGACCAACAGATGCTT 759
      |||:::
      |||:::

```



```

Db      2866 ATCATCCGAGACCTCCTCCCTCCAGATCTTTGATCTCGGGTGGCCAGTTCTTCC 2925
Oy      844 Tle-----GlyPheSerSerIleSerAnleu----- 852
Db      2926 ATGCTGCAGAGTGCGTGGGGGATTCGCGTCTCTGCAACTGATGTTCTGAAAGAAATC 2985
Oy      853 -----MetAlaLeuThrSerLeuGlnIleArgTyr 862
Db      2986 CCACTATTGCTAGCCTCCCAAGTCGATCAATGCTCTTACATCCCTGAGAGAGTTGGCT 3045
Oy      863 AsnLysGluAspAlaSerLeuProGlu-----GluMetPheLysSerLeuAlaAnleu 880
Db      3046 ATGTGTGAATGCGACAAATCTAAGAGATGGCTGTGAGTGAATCATCTCACTCCCTC 3105
Oy      881 LysTyrLeuAnlIleSerPheTyrPheAnleuLysGluLeuProThrSerLeuAlaSer 900
Db      3106 AAGGAATTGATATTCTTAGTTGCAGAAATCTGAGCCAGTTGCCCTGAGGGAATTCAGCAT 3165
Oy      901 LeuAnlAlaLeuLysHisLeuGlnIleHisSerCysTyrAlaLeuGluSerLeuProGlu 920
Db      3166 CTTACCAACTTGAAGACCTAGTATACAGACATGTCTTGGCCCTCCACAGCTGCCAGAA 3225
Oy      920 ----- 920
Db      3226 GGACTGGGAGATGTTAGTCTCTAGAGACCTTATGATCAATCTTGCTGTCTTACG 3285
Oy      921 -----GluGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCys 937
Db      3286 ACCCTTCTGAGTGCAGAGGGGCTCACTCATCTCCGCAATCATCACTTGAATGAGTGC 3345
Oy      938 GluMetLeuGlnCysLeuProGluGlyLeu----- 947
Db      3346 CCTATGCTCACCGTCTGCCAGATCATCTCAGACAACTCTCGCGCTCCGATCGTTAT 3405
Oy      948 ----- 948
Db      3406 ATGCAAGCTGCATCGGCTTCGATCTTGCCAGCTCCATACACACTTACTCTCTT 3465
Oy      954 ThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIleGly 973
Db      3466 CAGCATTTGGTGAATTAATTAACAACCTTCACTTGAATGAGCATTAACAAATAGGGTGG 3525
Oy      974 GluAspTyrPyrLysIleAlaHisIleProArgValPheIle 987
Db      3526 AAGGACTGGACATCATCTCCATATCTCTGTGTGGAGATA 3567

RESULT 14
CL957401 3996 bp DNA linear GSS 21-SBP-2004
LOCUS CL957401
DEFINITION OstrCC000538 Oryza sativa Express Library Oryza sativa (indica
ACCESSION CL957401
VERSION CL957401.1 GI:52369776
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 3996)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676

```

```

FEATURES
    source
        1..3996
            /organism="Oryza sativa (indica cultivar-group)"
            /mol_type="genomic DNA"
            /db_xref="taxon:39946"
            /clone_lib="Oryza sativa Express Library"
            /note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Alignment Scores:
Pred. No.: 1,51e-106 Length: 3996
Score: 1087.50 Matches: 355
Percent Similarity: 41.60% Conservative: 187
Best Local Similarity: 27.24% Mismatches: 370
Query Match: 21.21% Indels: 391
DB: 9 Gaps: 44

US-10-647-268-2 (1-988) x CL957401 (1-3996)
Oy      5 PheLeuGlnValLeuLeuAspAnleuThrCysPheIleGlnGlyLeu----- 21
Db      37 TTTCAATGCAAGTAATCTTCGACAAAG-----TACCTAAGCTCCAAAGTTAGAGCACTGG 87
Oy      22 -----GlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThr 39
Db      88 GCAATAGTGCAAACTTACGA-----GTTGAATTTCAAAACCTGTGCGACCTGAT 141
Oy      40 ThrIleGlnAlaValLeuGluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGlu 59
Db      142 ATGCTAAGGCAATATATTATGACCCCTGAAAGGCACTGCTGTGATGAGAGAGGAGCATCTGG 201
Oy      60 AsnThrPheGlnLysLeuAnlAlaAlaTyrGlnLysAspAlaLeuAspAlaLeuAspGlyCys 79
Db      202 CAACTATTGGTGGATTTGAAAGCTTCACTTATATATGACAGAGATGTGCTTGAATGATTA 261
Oy      80 Lys-----ThrGluAlaProIleArgGlnLysAsnLys----- 91
Db      262 GACTACATTTGCCCTTATAGAAATAGTGAGACAAAGAGGCAAAACAAGCTTGCTGATGC 321
Oy      92 TyrGlyCysTyrHisProAnValIle----- 100
Db      322 ATTGGATTATCAATCTTAAAGCTTTCGGAACCTTTTGACCAAGGATTCCTCCTT 381
Oy      101 -----ThrPheArgHis-----Lys 105
Db      382 TTCCCTCCATTCAAAAAAGCCAGACCAACTTTTATATATGTATGTGATGACTGGGATTTCA 441
Oy      106 IleGlyLysArgMetLysLysIleMetGlnLysLeuAspValIleAlaIle-----Glu 123
Db      442 GTCTCTTGCAAGATGAATTCATTCGATGCTCTCAAAAGAGCTACCGCCCATATTGAG 501
Oy      124 ArgIle-----LysPheHisLeuAspGluArgThrIleGluArgGlnValAla 139
Db      502 CGTGTGTGCTCAGTTCAAGAAAGTTGTGACTGATATATGACCAACCAAAATTTCCAAAC 561
Oy      140 ThrArgGlnThrGlyPheValLeuAnlGluProGlnValTyrGlyLysArgAspLysGlyLys 159
Db      562 TCAGACCAACCAAGCTCATCTTATCTGAACCAAGAGGTGTCGCGCAGAGATGAGAGAGAG 621
Oy      160 AspGluIleValLysIleLeuIle-----AsnAnValSerAnAlaIle-----Gln 174
Db      622 AAACACATTTGAATGATATCTCTGAAACAAAGTTTCAATATTTCAAAATAGGTACAAAG 681
Oy      175 ThrLeuProValLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaGln 194
Db      682 AGCTTCTTGCTGCTCCCGATGTGAGGCAATGTGTGTGGAGAAAGACAAACCTTGTGAG 741
Oy      195 MetValPheAnlAspGlnArgValIleGluHisPheHisProLysIleThrIleCysVal 214
Db      742 TATGTATATATGATCTAGTCAATCACTCTGTTTGTGAGTAAAGGCATGGGCAATGTGTG 801

```

Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.


```

Db      |||      :|||      |||      :|||
2890 CCTAGCCTGATCAATTCCTCCACTTCACATTTCTTCAAGCTTGCAAGATAGTTTG 2949
QY      832      -----LysLeuValValSerGly 838
                :|||      :|||      :|||
Db      2950 AAAAATGACAGGATATCTCTCTCATGAGTTGATGATGAGAGATTTGATTTCTGCG 3009
QY      839      Asp----- 839
Db      3010 ATATCTGATTTGTGCTGGAAGACATATTATTTCTGCATTTCAATCTGAGAGCCTC 3069
QY      840      LysSerAspAlaLeu----- 844
                :|||      :|||      :|||
Db      3070 AAGAGTTTCAGCAATCCAGGTTGTGATATTTCACTGACTACCTGAAAGCCAGGGA 3129
QY      845      -----GlyPheSerSerIleSerAsn 851
                :|||      :|||      :|||
Db      3130 AAGCATGATTTTCTGAGTATCCAGCACTATGATGATTTCTGATCTCTCACTGCTAAC 3189
QY      852      LeuMetAlaLeu----- 855
                :|||      :|||      :|||
Db      3190 ATCATGTAACCTCAAGATATGCGGTTCTGGGATATCTGAGATGTACTACATGAAATTTTA 3249
QY      856      -----ThrSerLeu 858
                :|||      :|||      :|||
Db      3250 TCMAATGTTGGATCTTGTACTGCTTGTCAATAAAGACCTCCAGGTTACTTCCCTT 3309
QY      859      GluIle----- 860
                :|||      :|||      :|||
Db      3310 GAGCTGAACCCAAATGTAAGACTGATTAACGATTATAGAAATTTGCTAGAGCTCAG 3369
QY      860      ----- 860
Db      3370 ACATTGAAATGTATGAAAACTCTCATCTACATTAACAGAACTGACTGTGTAAGAACTCT 3429
QY      860      ----- 860
Db      3430 AAGTTCAAGAGGAGATGAAAAATCTGCTGTAGAGGACAGAGGATCACATCTCAGAAAT 3489
QY      861      -----ArgTyrAsnLysGluAspAlaSerLeu----- 869
                :|||      :|||      :|||
Db      3490 ACTGCCTCACTGAAAAAGACTGCATATTTGATGATTTATCTCTTACATGCCAATTGTT 3549
QY      869      ----- 869
Db      3550 AGGACACTTGGGATCTTCATATTTGATGATTGACACGGAATCAGCAACATATGCTTA 3609
QY      870      -----ProGluIleMetPheLysSerLeuAlaAsnLysTyrLeuAsnIleSer 886
                :|||      :|||      :|||
Db      3610 ACTCCAGACGACAGACAGACATTTGTATACATGACTTCAATGAAAAACACTCGTGTCACT 3669
QY      887      PheTyrPheAsnLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHis 906
                :|||      :|||      :|||
Db      3670 GAATGCTCATATCTCGCTCATCTGCAACGCTGCAACAGATTTCTCCCTGGAAGAC 3729
QY      907      LeuGluIleHisSerCysTyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLeu 926
                :|||      :|||      :|||
Db      3730 CTGCATTTATCTCGGTGAGAGCATGACCTCCATCCACACACTGGAGTTGCCAGGA--- 3786
QY      927      IleSerLeuThrGluLeuSerIleThrTyrCysGluMetLeu-----GlnCysLeuPro 944
                :|||      :|||      :|||
Db      3787 ---TCACTGGAAGAGTTGTTCACTGCTGATGATGACCTGTGAGACAAAGTCCGTAGAA 3843
QY      945      GluGlyLeu 947
                :|||      :|||
Db      3844 GAAACAGTA 3852

```

```

RESULT 15
LOCUS      CK861977      670 bp      mRNA      linear      EST 09-MAR-2004
DEFINITION 33106 In vitro Root Solanum tuberosum cDNA, mRNA sequence.
ACCESSION  CK861977
VERSION     CK861977.1 GI:45291634

```

```

KEYWORDS   EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; Lamiales; Solanales; Solanaceae; Solanum.
REFERENCE   1 (bases 1 to 670)
AUTHORS     Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Laque,M., De
            Keyser,D., Andy,P., Goyer,C., Li,X.-O., Wang-Pruski,G. and Regan,S.
            Generation of ESTs from in vitro root tissues of potato
            Unpublished (2004)
TITLE       The Canadian Potato Genome Project - BioAtlantech
JOURNAL     Contact: Barry Flinn
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflinn@bioatlantech.nb.ca
            Seq primer: T3.
FEATURES
  source
    1..670
        Location/Qualifiers
            /organism="Solanum tuberosum"
            /mol_type="mRNA"
            /cuiovar="Shepody"
            /db_xref="taxon:4113"
            /tissue_type="Root"
            /lab_host="XLI0-Gold"
            /clone_1db="In Vitro Root"
            /note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
            Site 2: XhoI; supplier: Developmental series. Sterile stem
            sections from pathogen-free Solanum tuberosum var.
            Shepody, clone 1756; nuclear stock were cultured in
            Magenta boxes containing 1/10 strength MS medium,
            solidified with 0.8% (w/v) Phytagar. Roots of all sizes,
            originating from the stem bottoms were collected from
            these cultures, washed to remove residual Phytagar, and
            used in RNA isolations and library construction."

```

ORIGIN

Alignment Scores:

```

Pred. No.:      3,43e-105      Length:      670
Score:           1062.00      Matches:      203
Percent Similarity: 95.50%      Conservative: 9
Best Local Similarity: 91.44%      Mismatches: 10
Query Match:      20..71%      Indels:      0
DB:                7      Gaps:      0

```

US-10-647-268-2 (1-988) x CK861977 (1-670)

```

QY      297      ValGlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnLysAsp 316
Db      1      GTTGATCAATTTATGGGAACTTTCACACCATATGAAATTTGCTCAAGAGAT 60
QY      317      CysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeu 336
Db      61      TGTGATGTTGTTGTTCAATTCACAGTGCAATTTGGGACCAAGAAATTAATCATTAATCTT 120
QY      337      ValAlaIleGlyLeuGluIleValLysLysCysGlyGlyValLProLeuAlaAlaLysThr 356
Db      121      ATGGCTATCGAAGAGAGATTTGTGAAAAATGTGTGTGTGCTCTAGCAGCTTAACCT 180
QY      357      LeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnTyrGluHisValArgAspSer 376
Db      181      CTGGAGGATATTTTGGCTTCAAGAGAGAAAGACAGTGGGAACATGTAGAGATAGT 240
QY      377      GluIleTTrpLysLeuProGlnGluLysSerIleLeuProAlaLeuArgLeuSerTyr 396
Db      241      GAGATTTGGAAGTTACCTCAAGAGAAAGTTCTATCTGCTTGCCTGAGACTTAGTTAC 300
QY      397      HisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAsp 416
Db      301      CATCATCTTCCACTTGATTTGAGCAATGCTTGACATTTTGAGAGATATTCCTCAAGGAT 360
QY      417      ThrGluMetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSer 436
Db      361      ACCGAAATGGAAGAAAGAAATTAATCTCTCTCGATGAGCAACAGTTCCTTTTATCG 420

```

```

Qy 437 LysGluAsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArg 456
Db 421 AAAGGAACTGGAGCTAGAGGATCTAGGTATGAAAGTATGCAATTAATTAATCTTGAGG 480
Qy 457 SerPhePheGlnGluIleGluValIysSerGlyGlnThrTyrPheLysMetHisAspLeu 476
Db 481 TCTTCTTCCAAGAGATGAAAGTAAATCTGGTAAACTTAATTCAGATGCATGATCTC 540
Qy 477 IleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGlu 496
Db 541 ATCCATGATCTGGCTACATCTCTGTTACGGCAGCGCATCAAGCAATATATCCGTGAA 600
Qy 497 IleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysValValSerSer 516
Db 601 ATTAATGTAAAGGTTACCATATATGATGTGATTGGTTTCGCAAAAGTGTGTCTTCT 660
Qy 517 TyrSer 518
Db 661 TACTCT 666

```

Search completed: April 17, 2005, 04:46:11
 Job time : 6490 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using sw model

Run on: April 16, 2005, 01:05:58 ; Search time 178 Seconds
(without alignments)
2146.737 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFQLVLDNLTCFIGE.....EKIGEDMYKIAHPRVFIY 988

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5127	100.0	988	8	AdK98517 S Bulboca
2	5120	99.9	988	8	AdK98519 S Bulboca
3	5120	99.9	988	8	AdK98525 S Bulboca
4	4521.5	88.2	1003	8	AdK98521 S Bulboca
5	3798	74.1	979	7	AdF17766 Solanum b
6	3798	74.1	979	7	AdH51538 Plant inf
7	3787	73.9	979	8	AdH51541 Plant inf
8	3766.5	73.5	970	7	AdF17765 Solanum b
9	3766.5	73.5	970	8	AdH51537 S bulboca
10	3752.5	72.9	945	8	AdH51546 Plant inf
11	3736.5	72.8	992	7	AdH51543 Plant inf
12	3730.5	72.8	992	7	AdF17767 Solanum b
13	3730.5	72.8	992	8	AdH51539 Plant inf
14	3708.5	72.3	945	8	AdH51545 Plant inf
15	3654.5	71.3	945	8	AdH51542 Plant inf
16	3625	70.7	972	8	AdH51544 Plant inf
17	3542	69.1	1040	7	AdF17768 Solanum b
18	3542	69.1	1040	8	AdH51540 Plant inf
19	3369	65.7	1000	8	AdK98523 S Bulboca
20	1244	24.3	1266	2	AAW25157 Tomato im
21	1244	24.3	1266	3	AAW07754 Amino aci
22	1235	24.1	1240	2	AAW03665 I2C-2 pro
23	1176	20.3	1402	2	AAW03664 I2C-1 pro
24	1041.5	20.3	1402	5	AAW64150 Lettuce r
25	1041	20.3	1402	5	AAU95463 Lettuce p

26	969.5	18.9	784	2	AAW64151 Lettuce r
27	969.5	18.9	784	5	AAU95464 Lettuce p
28	937	18.3	1292	2	AAV39631 Zea mayr
29	937	18.3	1292	2	AAV39632 Zea mayr
30	910	17.7	1279	2	AAV39634 Zea mayr
31	904	17.6	1969	2	AAW72419 Rice bact
32	842	16.4	1294	2	AAV39633 Zea mayr
33	740	14.4	1282	8	AdI45253 Rice larp
34	736.5	14.4	979	8	AdI57168 Oryza mln
35	735.5	14.3	993	8	AdM72239 O. minuta
36	728.5	14.2	552	2	AAW64155 Lettuce r
37	728.5	14.2	553	2	AAU95468 Lettuce p
38	700.5	13.7	993	8	AdI57170 Oryza mln
39	685.5	13.4	342	3	AAW09957 Rice dise
40	685	13.4	1032	8	AdM72241 O. minuta
41	683	13.3	1031	8	AdI57172 Oryza mln
42	671	13.1	1032	8	AdM72245 O. minuta
43	665.5	13.0	1091	8	AdI57176 Oryza mln
44	657	12.8	901	2	AAW80251 An antiIdi
45	657	12.8	901	2	AAV01965 A protein

ALIGNMENTS

RESULT 1	ADK98517	ADK98517 standard; protein, 988 AA.
ID	ADK98517	
XX	ADK98517;	
AC		
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	S Bulbocastanum Sbul1 protein sequence SegID2.	
XX		
KW	plant disease resistance polypeptide; solanaceous plant; potato;	
KW	late blight disease; fungus; Phytophthora infestans;	
KW	conferring pathogen resistance; Sbul1.	
XX		
OS	Solanum bulbocastanum.	
XX		
PN	WO2004020594-A2.	
XX		
PD	11-MAR-2004.	
XX		
PF	28-AUG-2003; 2003WO-US027045.	
XX		
PR	29-AUG-2002; 2002US-0407100P.	
XX		
PA	(USDA) US SEC OF AGRIC.	
EA	(DRYC-) DRY CREEK LAB.	
XX		
PI	Osumi T, Belknap WR, Rockhold DR, Maccree MW;	
XX		
DR	WPI; 2004-239179/22.	
XX		
PT	N-PSDB; ADK98516.	
XX		
PT	New isolated Solanum bulbocastanum late blight resistance nucleic acid	
XX	molecule encoding a plant disease resistance polypeptide, useful for	
XX	conferring pathogen resistance to Phytophthora infestans in plants.	
PS	Claim 10; SEQ ID NO 2; 103bp; English.	
XX		
CC	This invention relates to a novel isolated nucleic acid molecule encoding	
CC	a plant disease resistance polypeptide. The preferred plant is a	
CC	solanaceous plant that is potato. The resistance is to late blight	
CC	disease, caused by the fungus Phytophthora infestans. The invention is	
CC	useful for conferring pathogen resistance in plants using a Solanum	
CC	bulbocastanum late blight resistance gene. The present sequence is the	
CC	protein encoded by the S bulbocastanum cDNA sequence of the invention.	
XX		
XX	Sequence 988 AA;	


```

QY 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGVPLAAKTLGSI 360
DB 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGVPLAAKTLGSI 360
QY 361 LRFKREBQWHEVHVDSEIWKLPQESSITLPAIRLSYHHLPLDLROCFYCAVFPDTEME 420
DB 361 LRFKREBQWHEVHVDSEIWKLPQESSITLPAIRLSYHHLPLDLROCFYCAVFPDTEME 420
QY 421 KGNLISLMAHGFILSKNLELVNENGVNENELVRSFQIEVKSQGYFPMHDLIHD 480
DB 421 KGNLISLMAHGFILSKNLELVNENGVNENELVRSFQIEVKSQGYFPMHDLIHD 480
QY 481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSRVNLSDIKLKQ 540
DB 481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSRVNLSDIKLKQ 540
QY 541 LPSSTIGDVLHRYNLNGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPKETSKLSLR 600
DB 541 LPSSTIGDVLHRYNLNGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPKETSKLSLR 600
QY 601 NLLDGCYGLTCMPRIGSLTCLKLSRFVVGIOKKSQGLGELRNLYGSIETHLERV 660
DB 601 NLLDGCYGLTCMPRIGSLTCLKLSRFVVGIOKKSQGLGELRNLYGSIETHLERV 660
QY 661 KNDMDAKENLSAKENLSLSMKWDDERPRIYESEKVELEALKPHSNLTCLTRGRFG 720
DB 661 KNDMDAKENLSAKENLSLSMKWDDERPRIYESEKVELEALKPHSNLTCLTRGRFG 720
QY 721 IRLPDMNHSVLYKNVYSIEIISCKNCSCLPPGELPCLKSELNMGSAEVEYVDSGFPTR 780
DB 721 IRLPDMNHSVLYKNVYSIEIISCKNCSCLPPGELPCLKSELNMGSAEVEYVDSGFPTR 780
QY 781 RRPFLRLKLTNREFNLTGKLLKKEBEOCPVLEIEICCPMFVPTLSSVYKLVSGDK 840
DB 781 RRPFLRLKLTNREFNLTGKLLKKEBEOCPVLEIEICCPMFVPTLSSVYKLVSGDK 840
QY 841 SDATGSSISNLMALTSLOIRYNKEDASLPBEMFKSLNLTNYNLFYFNKLPTSLAS 900
DB 841 SDATGSSISNLMALTSLOIRYNKEDASLPBEMFKSLNLTNYNLFYFNKLPTSLAS 900
QY 901 LNALKHLIHS CYALES LPBEGVKGLISLTQISITFCMLQCLPBGLOHLTALNLSVEF 960
DB 901 LNALKHLIHS CYALES LPBEGVKGLISLTQISITFCMLQCLPBGLOHLTALNLSVEF 960
QY 961 CPTLAKRCEKIGEBWYKIAHPRVFIY 988
DB 961 CPTLAKRCEKIGEBWYKIAHPRVFIY 988

```

RESULT 3

ADK98525 ID ADK98525 standard; protein; 988 AA.

AC ADK98525;

DT 03-JUN-2004 (first entry)

DE S Bulbocastanum Shu1 protein-related chimeric transgene protein Segid10.

KW plant disease resistance polypeptide; solanaceous plant; potato;

KW late blight disease; fungus; Phytophthora infestans;

KW conferring pathogen resistance; transgenic.

OS Solanum bulbocastanum.

XX Chimeric.

XX MO2004020594-A2.

XX 11-MAR-2004.

XX 28-AUG-2003; 2003WO-US027045.

```

PR 29-AUG-2002; 2002US-0407100P.
PR 20-AUG-2003; 2003US-00647268.
XX (USDA ) US SEC OF AGRIC.
PA (DRC-) DRY CREEK LAB.
PA Osuni T, Belknap WR, Rockhold DR, Maccree NM,
DR WPI; 2004-239179/22.
DR N-PSDB; ADK98524.
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
PT molecule encoding a plant disease resistance polypeptide, useful for
PT conferring pathogen resistance to Phytophthora infestans in plants.
XX Claim 10; SEQ ID NO 10; 103pp; English.
XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a plant disease resistance polypeptide. The preferred plant is a
CC solanaceous plant that is potato. The resistance is to late blight
CC disease, caused by the fungus Phytophthora infestans. The invention is
CC useful for conferring pathogen resistance in plants using a Solanum
CC bulbocastanum late blight resistance gene. The present sequence is that
CC of a protein encoded by a chimeric transgene of the invention.
XX
SQ Sequence 988 AA;

```

Query Match 99.9%; Score 5120; DB 8; Length 988;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 987; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MAEAFQVTLNLTNCFIAGEGLILGFDEFEKLTSTFTTIOAVLEDAQKKQLKDAIEN 60
DB 1 MAEAFQVTLNLTNCFIAGEGLILGFDEFEKLTSTFTTIOAVLEDAQKKQLKDAIEN 60
QY 61 WLQKLNAAVYADLDLDECKTEAPIRQKNKYGCYHNVITFRHKIGRMKKIMEKLDVI 120
DB 61 WLQKLNAAVYADLDLDECKTEAPIRQKNKYGCYHNVITFRHKIGRMKKIMEKLDVI 120
QY 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDCKDIIVKLLINNVSAQTLPLP 180
DB 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDCKDIIVKLLINNVSAQTLPLP 180
QY 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDCKDIIVKLLINNVSAQTLPLP 180
DB 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDCKDIIVKLLINNVSAQTLPLP 180
QY 181 ILGNGGLAKTTLAQMVFNDQVIEHFHPKVIWICSEDFNEKRLIKEIYESIEBKSLGMD 240
DB 181 ILGNGGLAKTTLAQMVFNDQVIEHFHPKVIWICSEDFNEKRLIKEIYESIEBKSLGMD 240
QY 241 LAPLOKRLDLLNGKRYLLVLDVWNEDQDMAKLRQYLKVGASGASVLTTRLEKVGSI 300
DB 241 LAPLOKRLDLLNGKRYLLVLDVWNEDQDMAKLRQYLKVGASGASVLTTRLEKVGSI 300
QY 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGVPLAAKTLGSI 360
DB 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGVPLAAKTLGSI 360
QY 361 LRFKREBQWHEVHVDSEIWKLPQESSITLPAIRLSYHHLPLDLROCFYCAVFPDTEME 420
DB 361 LRFKREBQWHEVHVDSEIWKLPQESSITLPAIRLSYHHLPLDLROCFYCAVFPDTEME 420
QY 421 KGNLISLMAHGFILSKNLELVNENGVNENELVRSFQIEVKSQGYFPMHDLIHD 480
DB 421 KGNLISLMAHGFILSKNLELVNENGVNENELVRSFQIEVKSQGYFPMHDLIHD 480
QY 481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSRVNLSDIKLKQ 540
DB 481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSRVNLSDIKLKQ 540
QY 541 LPSSTIGDVLHRYNLNGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPKETSKLSLR 600
DB 541 LPSSTIGDVLHRYNLNGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPKETSKLSLR 600
QY 601 NLLDGCYGLTCMPRIGSLTCLKLSRFVVGIOKKSQGLGELRNLYGSIETHLERV 660
DB 601 NLLDGCYGLTCMPRIGSLTCLKLSRFVVGIOKKSQGLGELRNLYGSIETHLERV 660

```

Db	601	NLLIDGCGYLTCMPPRIGSLTCLKTLSRFVVGIOKKSQCLGELRNLMNVGSIEITHLERV	660
Qy	661	KNDMDAKEANLSAKENHLSLSMKMDDDRPRRIYSEKEVLEALKPHSNLTCTLRGFRG	720
Db	661	KNDMDAKEANLSAKENHLSLSMKMDDDRPRRIYSEKEVLEALKPHSNLTCTLRGFRG	720
Qy	721	IRLPDMNHSVLYKNVSIIEIISCKNCSCLPPGGLPCLKSLFLMFGSAEVEYDSGFETR	780
Db	721	IRLPDMNHSVLYKNVSIIEIISCKNCSCLPPGGLPCLKSLFLMFGSAEVEYDSGFETR	780
Qy	781	RRPRLRLNLNREFPNLKGILKKEBEOCPVLEEIEIKCCPMFVPTLSSVKKLVVSGDK	840
Db	781	RRPRLRLNLNREFPNLKGILKKEBEOCPVLEEIEIKCCPMFVPTLSSVKKLVVSGDK	840
Qy	841	SDAIFSSISNIMALTSLQIRNKNEDASLPBEMFSLNLTXYLNI SFYFNLEKLP TSLAS	900
Db	841	SDAIFSSISNIMALTSLQIRNKNEDASLPBEMFSLNLTXYLNI SFYFNLEKLP TSLAS	900
Qy	901	LNALKHLIEHS CYALES LPBEGVKGLISITQISITYCEMLQCLPGLQHTLTALTVLSVF	960
Db	901	LNALKHLIEHS CYALES LPBEGVKGLISITQISITYCEMLQCLPGLQHTLTALTVLSVF	960
Qy	961	CPTLAKRCEKGGEDWYKIAHLPVFIY 988	
Db	961	CPTLAKRCEKGGEDWYKIAHLPVFIY 988	
RESULT 4			
ID	ADK98521	standard, protein, 1003 AA.	
XX	AC	ADK98521;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	S Bulbocastanum Sbul2 protein sequence SeqId6.	
XX	KW	late blight disease; fungus; Phytophthora infestans;	
XX	KW	conferring pathogen resistance; Sbul2.	
OS		Solanum bulbocastanum.	
PN		WO2004020594-A2.	
XX	PD	11-MAR-2004.	
XX	PF	28-AUG-2003; 2003WO-US027045.	
XX	PR	29-AUG-2002; 2002US-0407100P.	
XX	PR	20-AUG-2003; 2003US-00647268.	
PA		(USDA) US SEC OF AGRIC.	
PA		(DRYC-) DRY CREEK LAB.	
PI		Osunt T, Belknap WR, Rockhold DR, Macree MM;	
DR		WPI: 2004-239179/22.	
XX		N-PSDB; ADK98520.	
XX			
PT		New isolated Solanum bulbocastanum late blight resistance nucleic acid	
PT		molecule encoding a plant disease resistance polypeptide, useful for	
XX		confering pathogen resistance to Phytophthora infestans in plants.	
XX			
PS		Example; SEQ ID NO 6; 103bp; English.	
XX			
CC		This invention relates to a novel isolated nucleic acid molecule encoding	
CC		a plant disease resistance polypeptide. The preferred plant is a	
CC		solanaceous plant that is potato. The resistance is to late blight	
CC		disease, caused by the fungus Phytophthora infestans. The invention is	
CC		useful for conferring pathogen resistance in plants using a Solanum	
CC		bulbocastanum late blight resistance gene. The present sequence is the	
CC		protein encoded by the S bulbocastanum Sbul 2 gene sequence which was used	

CC	in the exemplification of the invention.
XX	Sequence 1003 AA;
50	Query Match 88.2%; Score 4521.5; DB 8; Length 1003; Best Local Similarity 88.0%; Pred. No. 0; Matches 883; Conservative 37; Mismatches 66; Indels 17; Gaps 2;
QY	1 MAEAFLOVLIDNLTCFIOGELGILGPKDEBEKQSFPTTIOATLEDAOKKOLMDAKIEN 60
DB	1 MAEAFLOVLIDNLTCFIOGELGILGPKDEBEKQSFPTTIOATLEDAOKKOLMDAKIEN 60
QY	61 WLQKLNAAAYEADIDLECKTEAPIRQKKNYGCYHNVIITFRHKIKRMKKIMEKLDVI 120
DB	61 WLQKLNAAAYEADIDLECKTEAPIRQKKNYGCYHNVIITFRHKIKRMKKIMEKLDVI 120
QY	121 AAERIKPHLDERTTEROVATROT-----GFTLNEPOVYGHDKKDEIVK 164
DB	121 AAERIKPHLDERTTEROVATROT-----GFTLNEPOVYGHDKKDEIVK 180
QY	165 ILINNVSAOQLPVLPILIGMGGLGKTTLAQWVNDQVIEHFNHKIMCVSEDENERKLI 224
DB	181 ILINIVSAOQLSVLPILIGMGGLGKTTLAQWVNDQVIEHFNHKIMCVSEDENERKLI 240
QY	225 KEIVSIEDEKSLGGMDLAPLOKKRLDILNGKKVLLVLDVNNEDQDQWAKLROYLKYVAS 284
DB	241 KEIVSIEDEKSLGGMDLAPLOKKRLDILNGKKVLLVLDVNNEDQDQWAKLREYLVKVAS 300
QY	285 GASVLTTRTRLEKVGSIINGTLOPYELSNLSQEDCWLFMQRAFQGOEELNVLVIGKEIV 344
DB	301 GASILTTRTRLEKVGSIINGTLOPYELSNLSQEDCWLFMQRAFQGOEELNVLVIGKEIV 360
QY	345 KKGCGVPLAAATLGGIILAFKREBEOWEVRPSEIMKPOEBSSTLPLALRLSYHNLPLDLR 404
DB	361 KKGCGVPLAAATLGGIILAFKREBEOWEVRPSEIMKPOEBSSTLPLALKLSYHNLPLDLR 420
QY	405 OCFTYCAVFPKOTEMKEKNLISLMMAHFLLSKNLELVNGEYVWELYLRSFFOEIEV 464
DB	421 OCFSICAVFPKOTKEKENLISLMMAHFLLSKNLELVNGEYVWELYLRSFFOEIEV 480
QY	465 KSGQTYFPMOHLIDHLATSLFSASTSSNIREIIVENYIMMSIGFTKVVSYSLSHQOK 524
DB	481 TYGKTYFPMOHLIDHLATSLFSASASSNNIREINVKGYPHMMSGIFAKVVSFYSSHPQK 540
QY	525 FVSLFVLNLSIDIKLQLPSSIGDLVHILRYNLISGNTSIRSLPNOLCTKQNLQTLDLHGCH 584
DB	541 FVSLFVLNLSIDIKLQLPSSIGDLVHILRYNLISGNTSIRSLPNOLCTKQNLQTLDLHGCH 600
QY	585 SLCCPKPKETSKLGSRLNLLDQCYELTQMPRIGSLTCLTSLREPVVGIQOKSCQGLER 644
DB	601 RLSCPKPKETSKLGSRLNLLDQCYELTQMPRIGSLTCLTSLREPVVGIQOKSCQGLER 659
QY	645 NLNLVGSIEITHLERVKNDMDAKEANLSAKENLHLSKMKDDDERPRLYESEKVEVLEAL 704
DB	660 NLNLVGSISTHLERVKNDMDAKEANLSAKENLHLSMIWEDERPHRYESBDEVELEAL 719
QY	705 KHSNULTCTITRGFRGILRPMNMHNSVLKYNVSIIEISCKNQCSCLPBGSLPCLSLSLM 764
DB	720 KHSNULTCTITIGFRGILRPMNMHNSVLKYNVSIIEISCKNQCSCLPBGSLPCLSLSLM 779
QY	765 RGSAAVEYVDSGFPRRRRPSPSLRKNIREFGNLKLKKEGEGQCPVLEIEIKCCPMFV 824
DB	780 RGSAAVEYVDSGFPRRRRPSPSLRKNIREFGNLKLKKEGEGQCPVLEIEIKCCPMFV 839
QY	825 IPTLSSVKKLVVSGDKSDAIGFSSISNIMATLSIOIRYNKEDASIPBEMFSLANLAKLIN 884
DB	840 IPTLSSVKKLVVSGESDAIGFSSISNIRALTSINISYNSSEATSPBEMFSLANLAKLIN 899
QY	885 ISPTYNLKLPTSLASLNAKLLETHSCYALBSLPBEGVKGILSTLOISITYCEMLQCLP 944
DB	900 IYFYNLKLPTNLASLNAKLLESCYALBSLPBEGVKGILSTLOISITYCEMLQCLP 959
QY	945 EGIQHTLALTNLSVEFCPTLAKRCKGIGEDWYKIAHPRPVI 987

[illegible][illegible]

KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
XX Solanum bulbocastanum.
OS US2003221215-A1.
PN 27-NOV-2003.
PD 07-FEB-2003; 2003US-00360522.
XX 07-FEB-2003; 2003US-00360522.
PR 07-FEB-2003; 2003US-00360522.
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PA Allefs JHM, Van Der Vossen EAG;
PI WPI, 2004-010903/01.
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX Example 7; SEQ ID NO 55; 98bp; English.
XX This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a protein which
CC was used for homology purposes in the exemplification of the invention.
XX Sequence 979 AA;
SQ
Query Match 74.1%; Score 3798; DB 8; Length 979;
Best Local Similarity 77.1%; Pred. No. 1.9e-304;
Matches 763; Conservative 75; Mismatches 139; Indels 12; Gaps 8;
QY 1 MAEAFLOVLLDNLTFQIGELGLIGFDEFEKLOSTFTTQAVLEDAQKQKDKAKEN 60
DB 1 MAEAFIOVLLDNLTFQIGELGLIGFDEFEKLOSTFTTQAVLEDAQKQKDKAKEN 60
QY 61 WLQKINAAAYEADDLIDECKTEAPTRQKKNKGYCYHPNVTFRHKTIGKMKIMEKLDVI 120
DB 61 WLQKINAAAYEADDLIDECKTKA-TRFQSEYGRVHPKVTIPRHVGVKRMQVMKKLNAI 119
QY 121 AAEIKFHLDEKTERQVATROTGFVLAINEPQVYGDKEKDEIVKLLINNVSAQTLPLPLP 180
DB 120 AAEIKFHLDEKTERQVATROTGFVLAINEPQVYGDKEKDEIVKLLINNVSAQTLPLPLP 179
QY 181 ILGWSGLGKTTAAOVFNDQRYIEHHPKIVTCSVEDNEFKRLIKEIVESIEKSLGGMD 240
DB 180 ILGWSGLGKTTAAOVFNDQRYIEHHPKIVTCSVEDNEFKRLIKEIVESIEKSLGGMD 239
QY 241 LAPLOKRLDLNGKKYLLVLDVNNEDQDKNAKLRQVLKVGASGASVLTTRLEKVGSI 300
DB 240 LAPLOKRLDLNGKKYLLVLDVNNEDQDKNAKLRQVLKVGASGASVLTTRLEKVGSI 299
QY 301 MGTLOPYELISNSQEDCWLLEWQARFGHQBIEINLVAIGKEIVKKGCVPLAATLGGI 360
DB 300 MGTLOPYELISNSQEDCWLLEWQARFGHQBIEINLVAIGKEIVKKGCVPLAATLGGI 359
QY 361 LRFKEERQWEHVRSEIKLPOESSILPRLSYHNLPLLBQCFYCAVFPKOTME 420
DB 360 LRFKEERQWEHVRSEIKLPOESSILPRLSYHNLPLLBQCFYCAVFPKOTME 419
QY 421 KGNLISLMAHGFILSKNLELENVGNENWELYLRSFQBIKVSQGTYPKQHLIHDL 480
DB 421 KGNLISLMAHGFILSKNLELENVGNENWELYLRSFQBIKVSQGTYPKQHLIHDL 480

DB 420 KENLIAFMMAHGFILSKNLELENVGNENWELYLRSFQBIKVSQGTYPKQHLIHDL 479
QY 481 ATSLFASSTSSNRREIIVENYIMMSIGFTKVAVSSYSLHLOKFSLRVNLSDIKKQ 540
DB 480 ATSLFASSTSSNRREINANDGYMMSIGFAEVSSYSPSLQKFSLRVNLNSNLNQ 539
QY 541 LPSSIGDLVHLRYNLNGTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSIGSLR 600
DB 540 LPSSIGDLVHLRYNLNGTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSIGSLR 599
QY 601 NLIDGCGYGLTQMPPIRGSLTCLTKLSRFVYVGIQKSCQGLGELFNILNGSIELTHERV 660
DB 600 NLIDGCGYGLTQMPPIRGSLTCLTKLSRFVYVGIQKSCQGLGELFNILNGSIELTHERV 657
QY 661 KNDWDKAEANLSAKENHSLSMKWDDDRPRIYSEKVEVLEALKPNSNLCTLTIRGRG 720
DB 658 KNDWDKAEANLSAKENHSLSMKWDDDRPRIYSEKVEVLEALKPNSNLCTLTIRGRG 713
QY 721 IRLPDMMNHSVLRKNVSIIEIISCKNCSCLPPFGLPCLKSLIELWRSABEVRY-DSGFP 779
DB 714 IRLPDMMNHSVLRKNVSIIEIISCKNCSCLPPFGLPCLKSLIELWRSABEVRY-DSGFP 772
QY 780 RRRPPLRKLNIRFPGNKGILKKEGBOCPVLEIEIKCPMVFVPTLSVKKLVSGD 839
DB 773 -GRPPSLRKLVIMDPNSMLKGLKKEGBOCPVLEIEIKCPMVFVPTLSVKKLVSGD 830
QY 840 KSDAIGFSSISNMLATLSQIRYKEDASLPDEMFKSLANLKYNISFYENLKELPSTLA 899
DB 831 -TDTVLRSLISNMLATLSQIRYKEDASLPDEMFKSLANLKYNISFYENLKELPSTLA 889
QY 900 SLNLKHLHLSCYALBSLPBEGVKGILSTQLSITYCEMLQCLPEGLQHLTALTNISVE 959
DB 890 SLNLKHLHLSCYALBSLPBEGVKGILSTQLSITYCEMLQCLPEGLQHLTALTNISVE 949
QY 960 FCPLTARCEGEGEDWYKIAHIRVFIY 988
DB 950 QCPVIFKRCERGIGEDWYKIAHIRVFIY 978
RESULT 7
ADHS1541
ID ADHS1541 standard; protein: 979 AA.
XX
AC ADHS1541;
XX
DT 25-MAR-2004 (first entry)
XX
DE Plant infection-related protein sequence Segid58.
XX
XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
XX Solanum bulbocastanum.
OS US2003221215-A1.
PN 27-NOV-2003.
PD 07-FEB-2003; 2003US-00360522.
XX 07-FEB-2003; 2003US-00360522.
PR 07-FEB-2003; 2003US-00360522.
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PA Allefs JHM, Van Der Vossen EAG;
PI WPI, 2004-010903/01.
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX Example 7; SEQ ID NO 58; 98bp; English.


```

Db      240 DLAPLQKQQLGELLNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTRLEKVG 299
Qy      300 IMGTLPYEISNLSEDCMLFMORAFGHOEINLVAIGKEIYKKGAVPLAKTIGL 359
Db      300 IMGTLPYEISNLSEDCMLFMORAFGHOEINLVAIGKEIYKKGAVPLAKTIGL 359
Qy      360 ILRFKREBROWEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTCYCAVPEKOTEM 419
Db      360 ILRFKREBROWEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTCYCAVPEKOTEM 419
Qy      420 EKGMLISLMAHAGFLSKGNLELVNGVENVNELYLSFPOEIEYKSGQTYFKMDLIHD 479
Db      420 EKGMLISLMAHAGFLSKGNLELVNGVENVNELYLSFPOEIEYKSGQTYFKMDLIHD 479
Qy      480 LATSLFSASTSSNNIREIIVENYIHMMSIGFTKVSSYSLSHLOKVSRLVNLSDILK 539
Db      480 LATSLFSASTSSNNIREIIVENYIHMMSIGFTKVSSYSLSHLOKVSRLVNLSDILK 539
Qy      540 QLPESIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSL 599
Db      540 QLPESIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSL 599
Qy      599 RNLLDGSGSLTCLMPPRIGSLTCLKTGQFVVG-RKKGYQLGELGNLNLVGSIKISHLER 657
Db      599 RNLLDGSGSLTCLMPPRIGSLTCLKTGQFVVG-RKKGYQLGELGNLNLVGSIKISHLER 657
Qy      660 VKNDMAKEANLSAKENHLSMKWDDERPRIYSESEVETLALKPHSNLTCLTINGFR 719
Db      660 VKNDMAKEANLSAKENHLSMKWDDERPRIYSESEVETLALKPHSNLTCLTINGFR 719
Qy      720 GIRLPDMNHSVLRKNVSIETISCKNSCLPPFGELPCLKSLLELRGSAEVEYVD----- 774
Db      720 GIRLPDMNHSVLRKNVSIETISCKNSCLPPFGELPCLKSLLELRGSAEVEYVD----- 774
Qy      775 --SGPPTRRPRLAKNIREFGNLKGLLKKKEBEOCVLEIEIKCCPMFVPIPLSSVK 832
Db      775 --SGPPTRRPRLAKNIREFGNLKGLLKKKEBEOCVLEIEIKCCPMFVPIPLSSVK 832
Qy      833 KLVVSGKSDAIGSSISNLMALTSLOIRYAKEDASLPBEMFKSLANIKYINISFYPLK 892
Db      833 KLVVSGKSDAIGSSISNLMALTSLOIRYAKEDASLPBEMFKSLANIKYINISFYPLK 892
Qy      934 LLSLAKIRGCPQLIRKCEKIGEDWMIKISHINVAIY 969
Db      934 LLSLAKIRGCPQLIRKCEKIGEDWMIKISHINVAIY 969

```

RESULT 10

```

ADH51546
ID ADH51546 standard; protein; 945 AA.
AC ADH51546;
XX
XX 25-MAR-2004 (first entry)
XX
XX Plant infection-related protein sequence SeqId3.
XX
XX plant diseases; oomycete infection; Phytophthora infestans; fungicide;
XX Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
XX
XX Solanum tuberosum.
XX
XX US2003221215-A1.
XX
XX 27-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360522.
XX

```

```

PR      07-FEB-2003; 2003US-00360522.
XX
XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Allele JHM, Van Der Vossen EAG;
XX
XX WPI; 2004-010903/01.
XX
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
XX for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX with resistance against oomycete infection.
XX
XX Example 7; SEQ ID NO 63; 98pp; English.
XX
XX This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
XX protein which may provide a plant or its progeny with at least partial
XX resistance against an oomycete infection caused by Phytophthora
XX infestans. The invention may be useful for the development of compounds
XX with a fungicide activity. The DNA sequence of the invention encodes an
XX Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX cell, protein or binding molecule is useful for providing a plant or its
XX progeny with resistance against an oomycete infection such as late blight
XX (a disease of major importance to production of Solanaceae such as potato
XX and tomato cultivars). The present sequence is that of a protein which
XX was used for homology purposes in the exemplification of the invention.
XX
XX Sequence 945 AA:

```

```

Query Match      73.2%; Score 3752.5; DB 8; Length 945;
Best local Similarity 76.6%; Pred. No. 1e-300;
Matches 745; Conservative 82; Mismatches 113; Indels 33; Gaps 7;

```

```

Qy      1 MAEAFVLVDNLTCFIOGELGLIFGRDEREKLQSTFTTQAVLEDAOKKOLDKAIEN 60
Db      1 MAEAFVLVDNLTCFIOGELGLIFGRDEREKLQSTFTTQAVLEDAOKKOLDKAIEN 60
Qy      61 WLOKLNAAVEADIDLECKTEAPIROKKNKVCYHNHNVITFRHIGKRMKIMEKLDVI 120
Db      61 WLOKLNAAVEADIDLECKTEAPIROKKNKVCYHNHNVITFRHIGKRMKIMEKLDVI 120
Qy      118 AKERTDHLHEKTIERQVAPBETSPVLTEPVYGRDKEDEIVKILINNVSNALESLVLP 177
Db      118 AKERTDHLHEKTIERQVAPBETSPVLTEPVYGRDKEDEIVKILINNVSNALESLVLP 177
Qy      181 ILGSGIGKTTLAQVNVNDQVIRHFRPKTIVCSBDFNEKRLKEIYESIEESLGMD 240
Db      181 ILGSGIGKTTLAQVNVNDQVIRHFRPKTIVCSBDFNEKRLKEIYESIEESLGMD 240
Qy      241 LAPLQKQQLGELLNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTRLEKVGSI 300
Db      241 LAPLQKQQLGELLNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTRLEKVGSI 300
Qy      298 MGTLQPYQLNLSQDDCMLFIOGAYRHQOEISPNLVAIGKEIYKKGAVPLAKTIGL 357
Db      298 MGTLQPYQLNLSQDDCMLFIOGAYRHQOEISPNLVAIGKEIYKKGAVPLAKTIGL 357
Qy      361 ILRFKREBROWEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTCYCAVPEKOTEME 420
Db      361 ILRFKREBROWEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTCYCAVPEKOTEME 420
Qy      421 KGNLISLMAHAGFLSKGNLELVNGVENVNELYLSFPOEIEYKSGQTYFKMDLIHD 480
Db      421 KGNLISLMAHAGFLSKGNLELVNGVENVNELYLSFPOEIEYKSGQTYFKMDLIHD 480
Qy      481 ATSLFSASTSSNNIREIIVENYIHMMSIGFTKVSSYSLSHLOKVSRLVNLSDILK 540
Db      481 ATSLFSASTSSNNIREIIVENYIHMMSIGFTKVSSYSLSHLOKVSRLVNLSDILK 540
Qy      541 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSLR 600
Db      541 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSLR 600
Qy      538 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSLR 597
Db      538 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSGLSLR 597

```

QY NLILDGCVGLTFCMPPRIGSLTCLTSLRFVVGIOKKSQCOLGELNINLYGSIIRITHLERV 660
DB 598 NLLHGHCHRLTRTPRIGSLTCLTSLGQFVVG-RKKGQOLGELNINLYGSIIRITHLERV 656
QY 661 KNDMDAKEANISAKENIHSLSMKWDDEPRRIYSEKYEVL EALKPHSNLTCLTIRGFRG 720
DB 657 KNDXBAKEANISAKENIHSLSMKWDDE-PRHYSEVEVEVLEALKPHSNLTCLTIRGFRG 715
QY 721 IRLDDMMNHSVLKNVVSIEIISCKNCSGLPPRGELPCIKSLIEMRGSAE-VYE-----VDS 775
DB 716 IRLDDMMNHSVLKNVVSIEIISCKNCSGLPPRGELPCIKSLIEMRGSAEVEVDIDVDS 775
QY 776 GPTRRRPPSLRKINIREFGNKGILKKEGEGQCVLEIEIKCCPMVPIPTLSSVKVLV 835
DB 776 GPTRRRPPSLRKINIREFGNKGILKKEGEGQCVLEIEIKCCPMVPIPTLSSVKVLV 826
QY 836 VSGDKSDAIGFSSISNLMALTSLOIRYNKEDASLPEEMFKSIANI KYINISFYENIKELP 895
DB 827 -----SNLKALTSINISDNKEATSPPEEMFKSIANIKYINISHPFKLAKELP 872
QY 896 TSLASINAKLHEIHSCTALSLPEEGYKGLISLTQLSITTCENIQCPLPEGQHLTALTN 955
DB 873 TSLASINAKLHEIHSCTALSLPEEGYKGLISLTQLSITTCENIQCPLPEGQHLTALTN 932
QY 956 LSVFCPTLAKRC 968
DB 933 VKINGCPOLIKRC 945

RESULT 11

ADHS1543
ADHS1543 standard; protein; 992 AA.

ADHS1543;
25-MAR-2004 (first entry)

Plant infection-related protein sequence Seg160.

plant disease; oomycete infection; Phytophthora infestans; fungicide;
Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.

Solanum bulbocastanum.

US2003221215-A1.

27-NOV-2003.

07-FEB-2003; 2003US-00360522.

07-FEB-2003; 2003US-00360522.

(KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

Allefs JHM, Van Der Vossen EAG;

WPI; 2004-010903/01.

New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
for providing members of the Solanaceae family e.g. Solanaceae tuberosum
with resistance against oomycete infection.

Example 7; SEQ ID NO 60; 989p; English.

This invention relates to a novel DNA sequence in the field of plant
disease, in particular oomycete infections. The DNA sequence encodes a
protein which may provide a plant or its progeny with at least partial
resistance against an oomycete infection caused by Phytophthora
infestans. The invention may be useful for the development of compounds
with a fungicide activity. The DNA sequence of the invention encodes an
Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
cell, protein or binding molecule is useful for providing a plant or its
progeny with resistance against an oomycete infection such as late blight

CC (a disease of major importance to production of Solanaceae such as potato
and tomato cultivars). The present sequence is that of a protein which
was used for homology purposes in the exemplification of the invention.

XX Sequence 992 AA;

Query Match 72.9%; Score 3736.5; DB 8; Length 992;
Best Local Similarity 74.8%; Pred. No. 2,4e-299;
Matches 747; Conservative 92; Mismatches 141; Indels 19; Gaps 8;

QY 1 MAEFLOYLDNLTCFIQSGELILGKDFEKLQSFPTTQAVLEDAOKKOLDKXKEN 60
DB 1 MAEFLOYLDNLTCFIQSGELILGKDFEKLQSFPTTQAVLEDAOKKOLDKXKEN 60
QY 61 WLOKLNAAVEADILDECKTEAPIRQKNKYGCYHNVTFRHKKRMKMEKLDVI 120
DB 61 WLOKLNAAVEADILDECKTEAPIRQKNKYGCYHNVTFRHKKRMKMEKLDVI 119
QY 61 WLOKLNAAVEADILDECKTEAPIRQKNKYGCYHNVTFRHKKRMKMEKLDVI 120
DB 61 WLOKLNAAVEADILDECKTEAPIRQKNKYGCYHNVTFRHKKRMKMEKLDVI 119
QY 121 AAEIRIKHLDERTTERQVARTQSGFVINEPQVYGRDXEKDEIVKILINNSNAQTLVPLP 180
DB 120 AAEIRIKHLDERTTERQVARTQSGFVINEPQVYGRDXEKDEIVKILINNSNAQTLVPLP 179
QY 181 ILMGGIGKTTLAQWVNDQVITHEHPKTMICVSEBDEKRLIKETIESTEEKSLGMD 240
DB 180 ILMGGIGKTTLAQWVNDQVITHEHPKTMICVSEBDEKRLIKETIESTEEKSLGMD 239
QY 241 LAPLOKKLRDLNKGKTYLVLDVWNEDODKAKLRQVLKVGASGASVLTTRLEKYSI 300
DB 240 LAPLOKKLRDLNKGKTYLVLDVWNEDODKAKLRQVLKVGASGASVLTTRLEKYSI 299
QY 301 MGTLOPYELSNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGCI 360
DB 300 MGTLOPYELSNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGCI 359
QY 361 LRFKREEROMHAYVDSSEIKWLPQDESSILPALTSTYHNLPLDIAOCFTYCAVPPKDTME 420
DB 360 LRFKREEROMHAYVDSSEIKWLPQDESSILPALTSTYHNLPLDIAOCFTYCAVPPKDTME 419
QY 421 KGNLISLMAHGFILSKGNLELVNGBEVMNLELARSFQREIEVKSQTYFKMDLIHDL 480
DB 420 KGNLISLMAHGFILSKGNLELVNGBEVMNLELARSFQREIEVKSQTYFKMDLIHDL 479
QY 481 ATSLPESASTSSNIREI-----IVENYHMSIGFTKVVSYSLSLQKRVSLRV 530
DB 480 ATSLPESASTSSNIREI-----IVENYHMSIGFTKVVSYSLSLQKRVSLRV 539
QY 531 LNLSDIKLQKPPSSIGDLVHLRYNLISGNISIRSLPNQCLQNLQTLDLHGHSLCLCP 590
DB 530 LNLSDIKLQKPPSSIGDLVHLRYNLISGNISIRSLPNQCLQNLQTLDLHGHSLCLCP 598
QY 591 KETSKLGLSLRNLLDGCYGLTFCMPPRIGSLTCLTSLRFVVGIOKKSQCOLGELNINLYG 650
DB 590 KETSKLGLSLRNLLDGCYGLTFCMPPRIGSLTCLTSLRFVVGIOKKSQCOLGELNINLYG 656
QY 651 SIEITHLERVKNDMDAKEANISAKENIHSLSMKWDDEPRRIYSEKYEVL EALKPHSNL 710
DB 651 SIEITHLERVKNDMDAKEANISAKENIHSLSMKWDDEPRRIYSEKYEVL EALKPHSNL 713
QY 711 TCLYTRGFRGRLDDMMNHSVLKNVVSIEIISCKNCSGLPPRGELPCIKSLIEMRGSAEV 770
DB 710 TCLYTRGFRGRLDDMMNHSVLKNVVSIEIISCKNCSGLPPRGELPCIKSLIEMRGSAEV 773
QY 771 EYV-DGPTRRRPPSLRKINIREFGNKGILKKEGEGQCVLEIEIKCCPMVPIPTLS 829
DB 771 EYV-DGPTRRRPPSLRKINIREFGNKGILKKEGEGQCVLEIEIKCCPMVPIPTLS 833
QY 830 SVKKLIVSGDKSDAIGFSSISNLMALTSLOIRYNKEDASLPEEMFKSIANI KYINISFY 889
DB 830 SVKKLIVSGDKSDAIGFSSISNLMALTSLOIRYNKEDASLPEEMFKSIANI KYINISFY 892
QY 890 NUKELPISLAINAKLHEIHSCTALSLPEEGYKGLISLTQLSITTCENIQCPLPEGQHL 949
DB 890 NUKELPISLAINAKLHEIHSCTALSLPEEGYKGLISLTQLSITTCENIQCPLPEGQHL 952

QY 950 LTAATNLNLSVEFCPTLAKRCCKGIGEDWYKIAHIPRVIY 988
DB 953 LTTLTSLKIRGCPOLIKRCCKGIGEDWYKISHIPRVIY 991

RESULT 12
ADFL7767 standard; protein; 992 AA.
XX ADF17767;
AC ADF17767;
XX 12-FEB-2004 (first entry)
DT 12-FEB-2004 (first entry)
XX Solanum bulbocastanum RGCL-blb protein sequence.
DE Solanum bulbocastanum RGCL-blb protein sequence.
XX RGCL-blb; Rpi-blb gene cluster; growth regulator; oomycete infection;
KM introgression breeding; plant; late blight.
XX Solanum bulbocastanum.
OS Solanum bulbocastanum.
XX Key Location/Qualifiers
FT Misc-difference 143
FT Misc-difference 143 /note= "Encoded by GT"
XX EP1334979-A1.
XX 13-AUG-2003.
PD 13-AUG-2003.
XX 08-FEB-2002; 2002EP-00075565.
PP 08-FEB-2002; 2002EP-00075565.
XX 08-FEB-2002; 2002EP-00075565.
PR 08-FEB-2002; 2002EP-00075565.
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PA Van Der Vossen BAG, Allefs JHM;
PI Van Der Vossen BAG, Allefs JHM;
XX WPI: 2003-714439/68.
DR N-PSDB: ADF17762.
DR N-PSDB: ADF17762.
XX New resistance gene conferring resistance against an oomycete pathogen,
PT useful for producing plants, especially potatoes and tomatoes, resistant
PT against oomycete pathogens such as Phytophthora infestans.
XX Example 5; SEQ ID NO 43; 86bp; English.
PS Example 5; SEQ ID NO 43; 86bp; English.
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-blb) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-blb, RGCL-blb and RGCL-blb, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum RGCL-blb protein
XX of the invention.
SQ Sequence 992 AA;

Query Match 72.8%; Score 3730.5; DB 7; Length 992;
Best Local Similarity 74.7%; Pred. No. 7.4e-299;
Matches 746; Conservative 92; Mismatches 142; Indels 19; Gaps 8;

QY 1 MAAEFLQVLLNLTNCFIGELGILGFDPEKOSTTTTQVLEDAQKQKDAIEN 60
DB 1 MAAEFLQVLLNLTNLTFFIGELGILGFDPEKOSTTTTQVLEDAQKQKDAIEN 60
QY 61 WLQKLNAAAYEADDLIDCKTEAPIRQKKNKYGVHNVITFRHKIGKMKMKIKDLVI 120

DB 61 WLQKLNAAAYEADDLIDCKTEA-ARFQAVLGHYHPTITFCYKVGKMKMKIKDLVI 119
QY 121 AAERIKPHLDERTIERQVATPOTGFVINEPOVYARDKEDIKVILINNVAQTLPTLP 180
DB 120 AAERIKPHLDERTIERQVATPOTGFVINEPOVYARDKEDIKVILINNVAQTLPTLP 179
QY 181 ILGNGGLGKTTLAQMFVNDQEVIEHFPKTIQVSEDFNEKRLIKEIYESIEKSLGMD 240
DB 180 ILGNGGLGKTTLAQMFVNDQEVIEHFPKTIQVSEDFNEKRLIKEIYESIEKSLGMD 239
QY 241 LAPLOKTLQELNKRFLVLDVWNNEDQKMAKROYLKVAGSASVLTTRLEKSGI 300
DB 240 LAPLOKTLQELNKRFLVLDVWNNEDQKMAKROYLKVAGSASVLTTRLEKSGI 299
QY 301 MGLTQVLESLNLSQEDCMLFMORAFOHOBENLNLVAIGEIVYKGGVPLAKTIGI 360
DB 300 MGLTQVLESLNLSQEDCMLFMORAFOHOBENLNLVAIGEIVYKGGVPLAKTIGI 359
QY 361 LRFGRSEMEHVDSEIWKLPQESSILPALRLSYHHLPLDLRQCFYCAVPKDTME 420
DB 360 LRFGRSEMEHVDSEIWKLPQESSILPALRLSYHHLPLDLRQCFYCAVPKDTME 419
QY 421 KGNLISLMAHGFILSKGNILENVGNWNELYLSFPQEIYKSGQTYFKMDLIHDL 480
DB 420 KGNLISLMAHGFILSKGNILENVGNWNELYLSFPQEIYKSGQTYFKMDLIHDL 479
QY 481 ATSLFASSTSSNTRFET-----IYENVHMSIGFTKVVSVSLSLQKPVSLRV 530
DB 480 ATSLFASSTSSNTRFET-----IYENVHMSIGFTKVVSVSLSLQKPVSLRV 529
QY 531 LNLSDIKLKQDPSISGLVHLRYLNLGNTSIRSLPNOLCQNLQTLDLHGCSLCLP 590
DB 530 LNLSDIKLKQDPSISGLVHLRYLNLGNTSIRSLPNOLCQNLQTLDLHGCSLCLP 589
QY 590 LNLNSFEPQLPSSVGVVHLRYLNLGNTSIRSLPNOLCQNLQTLDLHGCSLCLP 656
DB 590 LNLNSFEPQLPSSVGVVHLRYLNLGNTSIRSLPNOLCQNLQTLDLHGCSLCLP 655
QY 651 SIETTHLEKYNQMDAKENANISAKENHSLSMKDDDERPRIYSEKVEVLEAKPHSNL 710
DB 650 SIETTHLEKYNQMDAKENANISAKENHSLSMKDDDERPRIYSEKVEVLEAKPHSNL 709
QY 711 TCTLRGPRGRLPDMNHSVLTKNVSIIEIISCKNGSCLPFGELPCKLSLELRGSAEV 770
DB 710 TCTLRGPRGRLPDMNHSVLTKNVSIIEIISCKNGSCLPFGELPCKLSLELRGSAEV 769
QY 771 EYV-DSGFPTRRRPPSLRKINIREFGNLIKGLKKEGEOCPVLEIEIKCCPMFVPTLS 829
DB 770 EYV-DSGFPTRRRPPSLRKINIREFGNLIKGLKKEGEOCPVLEIEIKCCPMFVPTLS 828
QY 830 SVKLVVSGDKSADIGSSISNLMALTSLOIRYNKEDASLEEMFKSLANLKYINISFYF 889
DB 830 SVKLVVSGDKSADIGSSISNLMALTSLOIRYNKEDASLEEMFKSLANLKYINISFYF 888
QY 890 NIKELPTSLASLNLKLEIHSYALSLPEEGKGLISTQSLITYCEMLQCPREGLOH 949
DB 890 NIKELPTSLASLNLKLEIHSYALSLPEEGKGLISTQSLITYCEMLQCPREGLOH 948
QY 950 LTAATNLNLSVEFCPTLAKRCCKGIGEDWYKIAHIPRVIY 988
DB 953 LTTLTSLKIRGCPOLIKRCCKGIGEDWYKISHIPRVIY 991

RESULT 13
ADH51539 standard; protein; 992 AA.
ID ADH51539
XX ADH51539;
AC ADH51539;
XX 25-MAR-2004 (first entry)
DT 25-MAR-2004 (first entry)
XX Plant infection-related protein sequence SeqId56.

XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
 KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
 XX Solanum bulbocastanum.
 OS
 XX US2003221215-A1.
 PN
 XX 27-NOV-2003.
 PD
 XX 07-FEB-2003; 2003US-00360522.
 PF
 XX 07-FEB-2003; 2003US-00360522.
 PR
 XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
 PA
 XX Allefs JHM, Van Der Vossen EAG;
 PI
 XX WPI, 2004-010903/01.
 DR
 XX
 XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.
 CC
 XX Example 7; SEQ ID NO 56; 98bp; English.
 PS
 XX This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector, or
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of a protein which
 CC was used for homology purposes in the exemplification of the invention.
 CC
 XX
 SQ Sequence 992 AA;
 Query Match 72.8%; Score 3730.5; DB 8; Length 992;
 Best Local Similarity 74.7%; Pred. No. 7.4e-299;
 Matches 746; Conservative 92; Mismatches 142; Indels 19; Gaps 8;

QY 421 KGNLISIMAHGFLSKGNLELVNGEVNNEVLYLSFQGEIVKSGQTYFKKHDLIHDL 480
 DB 420 KEYILIAMMAHSPFLSKGNNELELVNGEVNNEVLYLSFQGEIVKSGQTYFKKHDLIHDL 479
 QY 481 ATSLFSASTSSNIREL-----IVENYIHMSIGFTKVSSYSLHLOKFSLYR 530
 DB 480 ATSMFSAASRSRIRQINVKDDEDMFIVNYNDMSIGFSEVSSYSPBLFKFVSLRV 539
 QY 531 LNLSDIKLOLPSSIGLVHLRYLNLSCNTSIRSLPNQLCKLQNLQTLDLHGCHSLCCLP 590
 DB 540 LNLNSFSEQLPSSVGLVHLRYLNLSCN- KIGCLPRLCKLQNLQTLDLNLQCSLCLP 596
 QY 591 KETSKGLSLNLLDGCYGLTQMPRIIGSLTCLKTLSPFVVGIOKSCQUGELNMLNYG 650
 DB 599 KQTSKLSLRNLVLDHC-PLTSMPPRIGLTLCKTLGLFVVG-ERKGYOLGELNMLNYG 656
 QY 651 SLEITHLERYKQMDAEANLSAKENLSLSMKWDDDERPRIYSEKVEVLEALKPSNL 710
 DB 657 AISTHLERYKQMDAEANLSAKANLSLSMSWD--RPRYSEEVKYLEALKRPNL 713
 QY 711 TCLTRGFRGRLPDMNHSVLKNVYSIEIISCKNCSCLPPFGLPCLKSLLEWRGSAEV 770
 DB 714 KYLEIIPFCGCLPDMNHSVLKNVYSILSGCNGSCLPFGELPCLSELELDGGSVEV 773
 QY 771 EYV-DSGPPTRRPRLKLNIREGNLKGILKKEBQCPVLEIHKCPMVFITLS 829
 DB 774 EYVEDSGFLTRRPRLKLNIREGNLKGILKKEBQCPVLEIHKCPMVFITLS 833
 QY 830 SVKLVVSGKSDALGSSISNLMLNLQIRNKEDASLPEEMFKSLANKYINISFYF 889
 DB 834 SVKLEIHWG-ADAGGLSSISNSTLSLKFSSHVTYSLLEEMFKNLEMLIYLSVFL 892
 QY 890 NLKELPTSLASINALKHELIHSCYALLESPLDEEYKGLISLTOLSTYCEMLQCLPEGLQH 949
 DB 893 NLKELPTSLASINLNLKCLDIRCYCALSLPEEGLEGLSTLELVHCHNMLKCLPEGLQH 952
 QY 950 LPTALNLSVEFCPTLAKRCCEKIGEDMYKTAHPRVITY 988
 DB 953 LTTLTSLKIRGCPOLIKRCEKIGEDMWHKISHIPNVIY 991

RESULT 14
 ADH51545
 ID ADH51545 standard; protein, 945 AA.
 XX
 AC ADH51545;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Plant infection-related protein sequence SeqId62.
 XX
 KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
 KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
 XX
 OS Solanum bulbocastanum.
 XX
 PN US2003221215-A1.
 XX
 PD 27-NOV-2003.
 XX
 PF 07-FEB-2003; 2003US-00360522.
 PR
 XX 07-FEB-2003; 2003US-00360522.
 PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
 PI Allefs JHM, Van Der Vossen EAG;
 DR WPI, 2004-010903/01.
 XX
 PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.

XX Example 7; SEQ ID NO 62; 98bp; English.

PS This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a protein which
CC was used for homology purposes in the exemplification of the invention.

XX Sequence 945 AA:

Query Match 72.3%; Score 3708.5; DB 8; Length 945;
Best Local Similarity 75.8%; Pred. No. 4.5e-297;
Matches 738; Conservative 82; Mismatches 120; Indels 33; Gaps 7;

QY 1 MAEAFQVLLDNLTGFIQELGILGFKDEPERKQSTFTTIOAVLEDAQKQKDKAIEN 60
DB 1 MAEAFIQVLLDNLTGFIQELGILGFKDEPERKQSTFTTIOAVLEDAQKQKDKAIEN 60
QY 61 WLOKLNAAVEADDIIDCEKTEAPIRKQKKGCVHPVITFRHKGKMKIMEKLDVI 120
DB 61 WLOKLNAAVEADDIIDCEKTEAPIRKQKKGCVHPVITFRHKGKMKIMEKLDVI 120
QY 121 AAEIRIKFLDERTIERQVATQGFVLENEPOVYGRKDEKDEIVKLLNNVNAQTLPLVP 180
DB 121 AAEIRIKFLDERTIERQVATQGFVLENEPOVYGRKDEKDEIVKLLNNVNAQTLPLVP 180
QY 118 AKERTDFLHKETIERQVARETGFVLEPOVYGRKDEKDEIVKLLNNVNAQTLPLVP 177
DB 118 AKERTDFLHKETIERQVARETGFVLEPOVYGRKDEKDEIVKLLNNVNAQTLPLVP 177
QY 181 ILGNGGIGKTTLAQVFPDQVIEHFHFKIWCSEDENEKRLKEIYESIEBKSLGMD 240
DB 181 ILGNGGIGKTTLAQVFPDQVIEHFHFKIWCSEDENEKRLKEIYESIEBKSLGMD 240
QY 178 ILGNGGIGKTTLAQVFPDQVIEHFHFKIWCSEDENEKRLKEIYESIEBKSLGMD 237
DB 178 ILGNGGIGKTTLAQVFPDQVIEHFHFKIWCSEDENEKRLKEIYESIEBKSLGMD 237
QY 241 LAPLOKRLDLNGKKYLLVDVWNEPDQKAKRQVLYKYGASGLVLTTRLEKYSI 300
DB 241 LAPLOKRLDLNGKKYLLVDVWNEPDQKAKRQVLYKYGASGLVLTTRLEKYSI 300
QY 238 LASFOKQLQQLNGKRYLLVDVWNEPDQKAKRQVLYKYGASGLVLTTRLEKYSI 297
DB 238 LASFOKQLQQLNGKRYLLVDVWNEPDQKAKRQVLYKYGASGLVLTTRLEKYSI 297
QY 301 MGTLOPYELSNLSQBDCLFMORAFGHOEINLVAIGKEIVKCGVPLAAKTLSGI 360
DB 301 MGTLOPYELSNLSQBDCLFMORAFGHOEINLVAIGKEIVKCGVPLAAKTLSGI 360
QY 298 MGTLOPYELSNLSQBDCLFMORAFGHOEINLVAIGKEIVKCGVPLAAKTLSGI 357
DB 298 MGTLOPYELSNLSQBDCLFMORAFGHOEINLVAIGKEIVKCGVPLAAKTLSGI 357
QY 361 LRFREERQWEHVDSEIWKLPQBESSITLPAIRLSYHHLPLDLNQCFTYCAVPRDTEME 420
DB 361 LRFREERQWEHVDSEIWKLPQBESSITLPAIRLSYHHLPLDLNQCFTYCAVPRDTEME 420
QY 421 KGNLISLMAGFLSKNLELVNENVEWVMEVLYRSFQIEVKSQGTFRMDLIDHL 480
DB 421 KGNLISLMAGFLSKNLELVNENVEWVMEVLYRSFQIEVKSQGTFRMDLIDHL 480
QY 418 KKKVYISLMAGFLSKNLELVNENVEWVMEVLYRSFQIEVKSQGTFRMDLIDHL 477
DB 418 KKKVYISLMAGFLSKNLELVNENVEWVMEVLYRSFQIEVKSQGTFRMDLIDHL 477
QY 481 ATLSFASSTSSNIREIYENYIHMMSIGFTKWSVSYSLHOKFVSLRVNLSDIKLKO 540
DB 481 ATLSFASSTSSNIREIYENYIHMMSIGFTKWSVSYSLHOKFVSLRVNLSDIKLKO 540
QY 478 ATLSFASSTSSNIREIYENYIHMMSIGFTKWSVSYSLHOKFVSLRVNLSDIKLKO 537
DB 478 ATLSFASSTSSNIREIYENYIHMMSIGFTKWSVSYSLHOKFVSLRVNLSDIKLKO 537
QY 541 LPSISIGLVHLRYNLGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPRETSKLSLR 600
DB 541 LPSISIGLVHLRYNLGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPRETSKLSLR 600
QY 538 LPSISIGLVHLRYNLGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPRETSKLSLR 597
DB 538 LPSISIGLVHLRYNLGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPRETSKLSLR 597
QY 601 NLILDDGCGYGLTCLPRTIGSLTCLTSLRFFVVGIOKSSQLGELRNANLYSGEITHLERV 660
DB 601 NLILDDGCGYGLTCLPRTIGSLTCLTSLRFFVVGIOKSSQLGELRNANLYSGEITHLERV 660
QY 598 NLILHGGCHRLTRTPRIGSLTCLTSLRFFVVGIOKSSQLGELRNANLYSGEITHLERV 656
DB 598 NLILHGGCHRLTRTPRIGSLTCLTSLRFFVVGIOKSSQLGELRNANLYSGEITHLERV 656
QY 661 KNDMDAKEANTSAKENLSLSMKMDDDERPRIYSEKVEVLEALXPHSNLCTLRIGPRG 720
DB 661 KNDMDAKEANTSAKENLSLSMKMDDDERPRIYSEKVEVLEALXPHSNLCTLRIGPRG 720
QY 657 KNDMDAKEANTSAKENLSLSMKMDDDERPRIYSEKVEVLEALXPHSNLCTLRIGPRG 715
DB 657 KNDMDAKEANTSAKENLSLSMKMDDDERPRIYSEKVEVLEALXPHSNLCTLRIGPRG 715
QY 721 IRLPDMNHSYLVKXVNSIEIISCKNCSGLPPFGLPCLKSLLELRGSAE-VEY----VDS 775
DB 721 IRLPDMNHSYLVKXVNSIEIISCKNCSGLPPFGLPCLKSLLELRGSAE-VEY----VDS 775
QY 716 IRLPDMNHSYLVKXVNSIEIISCKNCSGLPPFGLPCLKSLLELRGSAE-VEY----VDS 775
DB 716 IRLPDMNHSYLVKXVNSIEIISCKNCSGLPPFGLPCLKSLLELRGSAE-VEY----VDS 775

QY 776 GPTRRRPPSLRKLNIREFNGNLKGLKKGEQCPVLEIEIRIKCCPMFVITLSVKLV 835
DB 776 GPTRRRPPSLRKLNIREFNGNLKGLKKGEQCPVLEIEIRIKCCPMFVITLSVKLV 835
QY 776 GPTRRRPPSLRKLNIREFNGNLKGLKKGEQCPVLEIEIRIKCCPMFVITLSVKLV 826
DB 776 GPTRRRPPSLRKLNIREFNGNLKGLKKGEQCPVLEIEIRIKCCPMFVITLSVKLV 826
QY 836 VSGKSDAIGSSISNLTSLQIRNKEDASLPEEMFKLANUKYINISFYFLKLP 895
DB 836 VSGKSDAIGSSISNLTSLQIRNKEDASLPEEMFKLANUKYINISFYFLKLP 895
QY 827 -----PNKALTSLNISNKEATSPPEEMFKSLANUKYINISFYFLKLP 872
DB 827 -----PNKALTSLNISNKEATSPPEEMFKSLANUKYINISFYFLKLP 872
QY 896 TSLASLNALKHLIEHSCYALFSLPEEGVKGILSTOLITVCEMLQCLPEGLOHUTALTN 955
DB 896 TSLASLNALKHLIEHSCYALFSLPEEGVKGILSTOLITVCEMLQCLPEGLOHUTALTN 955
QY 873 TSLASLNALKHLIEHSCYALFSLPEEGVKGILSTOLITVCEMLQCLPEGLOHUTALTN 932
DB 873 TSLASLNALKHLIEHSCYALFSLPEEGVKGILSTOLITVCEMLQCLPEGLOHUTALTN 932
QY 956 LSVFECPTLAKRC 968
DB 956 LSVFECPTLAKRC 968
QY 933 LKINGCPQLIKRC 945
DB 933 LKINGCPQLIKRC 945

RESULT 15
ADHS1542
ID ADHS1542 standard; protein; 945 AA.

AC ADHS1542;
XX 25-MAR-2004 (first entry)
DE Plant infection-related protein sequence SegID59.

KM plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.

XX Solanum bulbocastanum.

XX US2003221215-A1.

XX 27-NOV-2003.

XX 07-FEB-2003; 2003US-00360522.

XX 07-FEB-2003; 2003US-00360522.

XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

XX Allefs JHM, Van Der Vossen EAG;

XX WPI; 2004-010903/01.

XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.

XX Example 7; SEQ ID NO 59; 98bp; English.

PS This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a protein which
CC was used for homology purposes in the exemplification of the invention.

XX Sequence 945 AA:

Query Match 71.3%; Score 3654.5; DB 8; Length 945;
Best Local Similarity 75.3%; Pred. No. 1.3e-292;
Matches 730; Conservative 72; Mismatches 142; Indels 25; Gaps 5;

QY 1 MAEAFQVLLDNLTGFIQELGILGFKDEPERKQSTFTTIOAVLEDAQKQKDKAIEN 60

```

Db      1 MAEAFIVLIDNLTSPFLKGLVLLPFGONEROLRSLSTIFSTIQAVLEDAQOKLNDKPLEN 60
Qy      61 WLOKLNAAAYEADDILDECKTEAPIRQKKNKYCYHPNVITFRHKIGKRMKIMEKLDVI 120
Db      61 WLOKLNAAAYEVDDILDEYKTKA -TRFSQAYAGRHPKVIIPFRHKYGRMDQVKKLNAI 119
Qy      121 AAEIRIKHLDERTIEROVATROTGFVLANEPQVYGRDKKDEIVKILINNVSNAOTLPVLP 180
Db      120 AAEIRKHFHLEKIERQAVRETSGVLTEPQVGRDKDEIVKILINNVSNAOTLPVLP 179
Qy      181 ILGWSGKTKTAAQVFNDOQVIEHHPKVIWCVSEDENERKLIKEIYESIEEKS -LGSM 239
Db      180 ILGWSGKTKTAAQVFNDOQVIEHHPKVIWCVSEDENERKLIKEIYESIEEKS -LGSM 239
Qy      240 DIAPLQKKLBDLNGKXYLLVLDVWNEODQKMAKROVLKVGASGASVLTTRLEKVG 299
Db      240 DIAPLQKKLQGLNGKRYFLVLDVWNEODQKMAKRAVLKVGASGAFVLTTRLEKVG 299
Qy      300 IMGTLOPYELSNLSQEDCMLPMDQAFGHQHEINLVAIGKETVKKGGVPLAKTLGG 359
Db      300 IMGTLOPYELSNLSQEDCMLPMDQAFGHQHEINLVAIGKETVKKGGVPLAKTLGG 359
Qy      360 ILRFKREEROMEHYVDSIEIWKLPQESSILPALRLSYHHLPLDLROCFYCAVPKOTEM 419
Db      360 ILRFKREERAMEHYVDSIEIWKLPQESSILPALRLSYHHLPLDLROCFYCAVPKOTEM 419
Qy      420 EKGNIISLMAHGFILSKNLELENVGNEVWNEVYLRSPFOEIEVKSQTYFKWHLIHD 479
Db      420 EKEKLIISLMAHGFILSKNLELENVGNEVWNEVYLRSPFOEIEVKSQTYFKWHLIHD 479
Qy      480 IATSLFASSTSSNREITVENYTHMSIGTKVVSYSLSHLOKFSRLVNLSDIKLK 539
Db      480 IATSLFASSTSSNREITVENYTHMSIGTKVVSYSLSHLOKFSRLVNLSDIKLK 539
Qy      540 QLPSSIGLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGS 599
Db      540 ELSSSIGLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGS 599
Qy      600 RNLIDGCGYGLTQMPRIIGSLTCLKTLRFPVVGIOKSCQJGELNMLYGSIEITHLER 659
Db      600 RNLFPHGCEDEINSMPPRIGSLTFLTKWICCGI -KKGYLGKLDVNLVYGSIEITHLER 658
Qy      660 VKNDMDAKEANISAKENHSLSMKWDDEPRPIYSEKVEVLEALKPSNLTCLTIRGFR 719
Db      659 VKNVMDAKEANISAKENHSLSMKWDDEPRPIYSEKVEVLEALKPSNLTCLTIRGFR 717
Qy      720 GIRLPDMNHSVYKXVVSIEIISCHNCSCLPPFGEIPLCKSLLEWRGSAEVEYVDSGFP 779
Db      718 GFRPFEMNHSVYKXVVSIEISCHNCSCLPPFGEIPLCKSLLEWRGSAEVEYVDSGFP 777
Qy      780 RRRPFLKRLNIREFGNLTGKLLKKGEBQCPVLEIEIKCCPMFYIPLISSYKXLVSGD 839
Db      778 RRRPFLKRLNIREFGNLTGKLLKKGEBQCPVLEIEIKCCPMFYIPLISSYKXLVSGD 832
Qy      840 KSDAIGFSSISLMLTSLQIRYNKEDASLPEEMFSLANLKYLNISFYFNKELPTSLA 899
Db      823 -----YTTLSNFRALTSLSHSHNBEATSLPEEIRKSPANLKYLKISLFPYNKELEPSSLA 876
Qy      900 SINALKHLEIHSQVLESLEBQVKGSLSLTQISITYCEMLQCLPEGLQHLTALTNLSVE 959
Db      877 CUNAKTEIHSQVLESLEBQVKGSLSLTQISITYCEMLQCLPEGLQHLTALTNLSKLR 936
Qy      960 FCPYLAIRC 968
Db      937 RCPOLIKRC 945

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 01:07:49 ; Search time 45 Seconds
(without alignments)
1638.962 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFQLVDLNLTCFIQGE.....EKIGEDMYKIAHPRVFIY 988

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	24.2	1240	3	US-08-930-996A-4
2	1198	23.4	1220	3	US-08-930-996A-2
3	1041	20.3	1402	3	US-09-004-838-11
4	969.5	18.9	784	3	US-09-004-838-12
5	729.5	14.2	553	3	US-09-004-838-16
6	609.5	11.9	1255	3	US-08-947-823-3
7	606	11.8	920	3	US-08-930-996A-8
8	575.5	11.2	1206	4	US-09-245-928A-19
9	575.5	11.2	1253	4	US-09-245-928A-17
10	575.5	11.2	1257	4	US-09-245-928A-18
11	571.5	11.1	1257	3	US-08-947-823-5
12	550.5	10.7	905	3	US-09-360-166-3
13	550.5	10.7	905	4	US-09-864-680A-3
14	528	10.3	234	4	US-09-803-286A-8
15	526.5	10.3	1205	3	US-09-330-330-1
16	521	10.2	1247	4	US-09-803-286A-7
17	518	10.1	250	4	US-09-803-286A-2
18	512.5	10.0	909	2	US-08-310-912A-142
19	512.5	10.0	909	3	US-09-301-085-142
20	512.5	10.0	909	5	PCT-US95-04589-142
21	510	9.9	885	2	US-08-310-912A-2
22	510	9.9	885	3	US-08-841-089-2
23	510	9.9	885	3	US-09-301-085-2
24	510	9.9	885	5	PCT-US95-04589-2
25	510	9.9	885	5	PCT-US95-04589-2
26	505.5	9.9	907	3	US-08-930-996A-7
27	473.5	9.2	1824	2	US-08-680-327-3

28	473.5	9.2	1824	3	US-09-228-246-2	Sequence 2, Appli
29	454	8.9	412	2	US-08-414-938A-4	Sequence 4, Appli
30	436.5	8.5	345	3	US-09-004-838-13	Sequence 13, Appli
31	436.5	8.5	928	4	US-09-336-946B-2	Sequence 2, Appli
32	436.5	8.5	928	4	US-09-336-946B-2	Sequence 58, Appli
33	431.5	8.4	928	4	US-09-336-946B-4	Sequence 4, Appli
34	394	7.7	1890	3	US-09-004-838-88	Sequence 88, Appli
35	386	7.5	1074	3	US-09-004-838-111	Sequence 111, Appli
36	385	7.5	1366	3	US-09-004-838-82	Sequence 22, Appli
37	378	7.4	1144	3	US-08-930-996A-9	Sequence 9, Appli
38	377	7.4	1854	3	US-09-004-838-108	Sequence 108, Appli
39	374	7.3	1805	3	US-09-004-838-92	Sequence 92, Appli
40	373	7.3	1222	3	US-09-004-838-119	Sequence 119, Appli
41	367	7.2	1143	2	US-08-310-912A-108	Sequence 108, Appli
42	367	7.2	1143	3	US-09-301-085-108	Sequence 108, Appli
43	367	7.2	1143	5	PCT-US95-04589-108	Sequence 108, Appli
44	367	7.2	1144	1	US-08-261-663A-2	Sequence 2, Appli
45	367	7.2	1144	1	US-08-261-663A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-4
Sequence 4, Application US/08930996A
Parent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUOR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naom
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930, 996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-4
Query Match 24.2%, Score 1240; DB 3; Length 1240;
Best Local Similarity 28.6%; Pred. No. 1.66-100;
Matches 359; Conservative 211; Mismatches 378; Indels 306; Gaps 39;
QY 6 LQVLLDNLTCFIQGE---FEKLOSTFTTQAVLVEDAKKQKQKALENW 61
DB 16 LNVLFRLA--PNDLLNMFRRKHQDHYVLLKKLQWTLRGVQIVLSDANKQASNPVSVDW 73

QY	62	QOKMAAAYEADDIIDEKTEPARIOKKNKYCYNP-----VTPPHKIG	108
Db	74	INELRDADVASANLLEEVNVEA-----LRKVEGQONBSETSNQOVSDPEFFINIDKLED	129
QY	109	RMKKIMEKIDVVAARIKPHLDERTIEROVATROGCVLANEPQVGRDKEXEIKVILIN	168
Db	130	TIETIKDIOEQIGLLGKLEYFPOSTKLETRPSTPST---LIDEDDINGROSEIEDLIDRLLS	186
QY	169	NVSNAGTLPVPLITMGIGIKTTLAQMFPNDORVLEHHPKWICVSDPEKELIKEIV	228
Db	187	EGASRKNITVBEIVEMGGIGKTTAKAAYNDESVXNHPDLKMFCSVSEYNAFRITTKGL	246
QY	229	ESIEEKSLGMDLAPLOKKLRDLNKGKYLVLVDVNMNDOOKMAKLOVLKVASGASV	288
Db	247	QEIGSIDLVDDNQLNOQYKLERLKEKFEYLVLDDVWMDNRYMBELKRVNVPQSIGSKI	306
QY	289	LTTTRLEKVSIMGTLPQPELSNLSQEDCWLIFMOPAF-----GHQEBINILVAIGKE	342
Db	307	IVTTRKSDVVALMGMNQ--ISMGNLSTESWSLFOHRAEFNMPMGHSE-----LEEVGRQ	360
QY	343	IVKKGQVPIAKTGLGILRPFREEROWENHVDSSIMKLPQESSILPALRSTYHNLPLD	402
Db	361	IAAKKGRLALAKITLAGMIRKSEVEBWKCIJRSEIMEL--RDNDILPLMLSTYNDLPAH	418
QY	403	LROCFYCAVPEPKDMEEMKGNLISLMMHGFILSKNLELVNENVEMLTYSFPFOEI	462
Db	419	LKRCSPCAIFPKDVPFRBEQVTHIMIANGLVPEDEI-IDOLGNQFLELSSRSJLFRV	477
QY	463	EYKSG---QYTPKMDLHDLATSLFS-----ASTSSNRREITVENYIHMSIGTK	512
Db	478	PNPSSGNIKELFELMDLVNDLAQIASSKLCIRLEBSQGSNHLEQORHLSTYSNGYDGEEK	537
QY	513	VVSYSLSHLOKFV-----SLRVNLSDIKLKOLPSSIG	546
Db	538	LTPLYKLEQRLRLTPTCSSVNFVFNPLTKRVLHNLPLTLRSIRALSLHYKMEELPNLF	597
QY	547	-DVLHRLYINSGNTSIRSLPNOLCKLONLOTLDHGHSICLPKXETKSGSLNLLD	605
Db	598	IKLKLRLEPLDIS-RTNIKRLPDSICVLNLETLILSSC-KLEELPLQMEKJINLRHLDIS	655
QY	606	GCYGLTCMPRIRGSLTCKLT--SRFVVGIOKSCQLGELNMLYGSILETHLERYKND	663
Db	656	NTMHLK-MPLHSIRKSLQVLGAKFVLGVWRME-DLGEAQ--NLYGSLSVKLENVDR	711
QY	664	MDAKEANLSAKENHLSLSMKWDDDERPIYSEKVEVLZALKPHSNLCTLTIRGGRJRL	723
Db	712	REAVPEPKREKRNHVEOLSLWSESISANSQGER-DIIDEPLRPHKNIOEVKIIIGRGTFN	770
QY	724	PDMNHSLVKNVUSLEIISCKNCSGLPRFGELPCLSLELRGSALEVYVDSGF---PT	779
Db	771	FNWVADPLPLKVLKUSLKNCKDCSLPLAGQPCIKFELSV-KGMHGIRVTVBEFGRUSS	829
QY	780	RRRPEPSLRK-----INIRBEFNLKGL-----LKKEGEE	807
Db	830	KKPFCNCEKLEFEDMTWKOMHAGIGFPLTEKLSINCPELSLEIRIOPSLSKRPFV	889
QY	808	QCPV-----LEBEIKCC-----PMFVPLTSSVKKLVVSG-----	838
Db	890	GCPLVVFYDOVLRSQLBGMKOIEEIIYIRDNSVTSFPISILPT-TLKTIDISGGPKJL	947
QY	839	-----DKSDAIGFSSINL	852
Db	948	EAPVCEKSMFLBESVBEBCGVSPBELPTABELRIGNCHNVRFLPTATETLHIRNCNV	1007
QY	853	-----MA-----LTSLOIRYNKEDASLE-----	871
Db	1008	EKLSMACGAQTLTSDISIGCKKLKCLPELRLPKLEQLTNCPEIPEGELPNNLOKLYTRD	1067
QY	872	-----EMF-----KSLAN	879
Db	1068	CKKLNGRKEMHLORLKLYLYIHDSODEDIEHMBLPGSITRLEVFNNLITSSQHKLSITS	1127

```

QY      880 LKYNISFYNNKELP-----TSLASLNALKHLEHSCALSLPBEVKGILSTOLSI 934
DB      1128 LÖYICID--NLSLPISÖGQISSFSHLSLTÖLQIWNFNHNLSSLSAPLS--SLSÖLETI 1183

QY      935 TYCEMLQCLP-EGIÖHLTALTNVSFCPLAKRCEKGEOMYKIAHPRVFI 987
DB      1184 FHCNLOSPLNGMP--SLISKLLISGCPLTLPLEFPGGEYWPQIAHPTILI 1235

RESULT 2
US-08-930-996A-2
; Sequence 2, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLOHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PAPAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-2

Query Match      23.4%; Score 1198; DB 3; Length 1220;
Best Local Similarity 29.0%; Pred. No. 8,6e-97;
Matches 359; Conservative 208; Mismatches 379; Indels 230; Gaps 39;

QY      6 LOYLLNLNLTFCIGE-IGLILGFKDE---FEKLQSTFTTIOAVLEDAQKOLKDKALIEHW 61
DB      16 LNVLFRLA--PQGLDLMNFRKHTDVELFEKLGDIILSLQVLSDANKKASNQFQSQW 73

QY      62 LQKLNAAAYEADDILDE-----CKTEAPIRÖKKNKYGCYHPNVYTRFHKIGRMMKKIM 114
DB      74 LHKLQVAVDAENLIRQVNYEALRLKVFETSNQVSDNLCLSD---PFLNIKKKLEDTI 130

QY      115 EKLDVIAARIKXHLDERTEREQVATR-OTGVVLANEPQVYGRDKEDKIVKILINNNSNA 173
DB      131 KKLVEVLEKQIGRGLKEHPISTKQETRPSTSLVDDSGIFGKKEIENLVGRLLSMPTKR 190

QY      174 QTLPVPLIGMGGLGKTTLAQWVNDQVYIEHFHFKIMICVSEDPENEGRLIKEIVESIEE 233
DB      191 KNLAVPVIVGGMGKTLAKAVNIDERYQKIFGLTAMFCVSEAYDARIKIGLLOETIGS 250

QY      234 KSLGGMD-----LAPLÖKCLRDLNLNGKYILVLDVWNEDDQMKAKLRÖVL 279

```

```

Db 251 TDLDKADNLDNQVYTLKADNDLNQVYTLKXETLNKRFVLVUDVDVNDYNEPMDLRLPLF 310
Qy 280 KVGASGASVLTTRLEKVGSIWGTLOPYELSNLSGEDCMLFMORAFGHQOE E1NLNIVA 338
Db 311 LQGDIGSKIIVTTRKESVALMMDSGAIY-MGILSESDWALFKRSHLEKPKKEPFEER 369
Qy 339 IGKEIVKCGGVPLAATKLGLIRKREBERQWENHRDSEIWLPOBESSIIPALRLSTH 398
Db 370 VGOQIADCKGJPLALKALAGLRKSEVEDENRNLREIHELPCSGNGILLPALMLSTND 429
Qy 399 LPLDRQCFYCAVPEPKDTEMEKGLI5LMMHGFILSKNMLELVNNGVWENELYSRF 458
Db 430 LPLHKKQCLATCAITPKDYQPRKEQVITHMLANGV-----HOPHSNQPIELRBSL 483
Qy 459 FOEIEVKSQGY--FKMHLIHLATLSFSASTSSNR-----EIVENVYHM-MSIG 509
Db 484 FEMASEPSERDVEEPLMHDLVNDLA-----QIASSNHCIRLDNKSGSHMLEOCRHMSYSIG 539
Qy 510 ----FTKVSSYSLSHLQFV-----SIRVNLSDIKLKQ 540
Db 540 QDGEBEKKSKSEFKSEBQRLTLLPIDIOFHYSKLSKRVLANILLPTLRSLSTHYQIEV 599
Qy 541 LPSISG-DVHLRYNLNSGNTSIRSLPNOLCKLQIOTLDHGHSLCCLPRESKGLS 599
Db 600 LPNDIFYTKLIRFLDLS-ETSIYTKLPDSIFVYLNLETLSSCYBELPQEKLN 658
Qy 600 RNLLLDGCGYGLTCMPEPRIGSLTCLKTL--SRFVVGIOQKSCOLGELRYMLNLYSIEITHL 657
Db 659 RHLDISNTRRK-IPHLISRLKSLQVLVAGAFVGVGMME-YLGGAP--NLYGSLSIEL 714
Qy 658 ERVKNDDAKAANTSAKENLHLSMKWDDEPRRIYSEKQVYELALKPHSNLTCLTIRG 717
Db 715 ENVVDRRRAVAKAKREKNHVEQLSLEWSEBSISADNSQTER-DIIDELPHKNIKAVEITG 773
Qy 718 FRGIRLPPMWHASHVLKXNVYSIEIISCKNCSCLPRNGELPCLSLELMGSAEVEYVDSGF 777
Db 774 YRGINFPFWMADPLFVKVLVHLNRCNKDCYSLPALGQPLCELFYST-RGMHGRVYVEEF 832
Qy 778 PTR-----RRPSLRKLNIR-----EFGNL 797
Db 833 YGRLLSKKPFNSLVKLAREPDMPEWKQHTLIGEPFTEKLSIKNCPBELSLPIQFBSL 892
Qy 798 KGL-----LKKE--GB-----806
Db 893 KRLDIOCKSVTSFPFSILPTLLKRIKISGCPKLTLEAPVGMFEYLVIDCGVDIS 952
Qy 807 -EQCPVLEIEIKC--PMFVIRP-----827
Db 953 PEPLPTARQSLIENCHNVTRFLIPATESLHIRNCEKLSMACGAAQUTSLINWCKKJK 1012
Qy 828 ----LSSVKKL-----VSGDKSDAIGFSSISNLMALT 856
Db 1013 CLPELBPBLKRLRLTCEIBEGLRPNQIIDIRCKGLVNGRKE-----WHLQRLT 1064
Qy 857 SLQIRYNKD-----ASLPEMEKSIANLYT-----NISFYNLK 892
Db 1065 ELMTWKDSDEHIEHWELPSSIQRLFIPLNKLTLISQHLKSLTSIQFLRIVGNLSQFQSG 1124
Qy 893 ELPLPSLASLNLKHLHISCTALBESLPREGVKGLISLTQLSITYCEMLQCP-EGLOHUT 951
Db 1125 QL-SSFSHLTSLQTLQIWNFNLTOSLPESAPLS--SLSHLISNCPNQLSPLKGM--S 1179
Qy 952 ALTNLSVEFCPTLARCKEKGIGEDPYKIAHPRVEI 987
Db 1180 SLSTLSISKCPULPLLEFDDKGEYWEIYAHPIITQI 1215

```

```

1 APPLICANT: Michelmores, Richard W.
2 APPLICANT: Shen, Kathy
3 APPLICANT: Meyers, Blake
4 TITLE OF INVENTION: Procedures and Materials for
5 TITLE OF INVENTION: Confering Pest Resistance in Plants
6 NUMBER OF SEQUENCES: 140
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Townsend and Townsend and Crew LLP
9 STREET: Two Embarcadero Center, Eighth Floor
10 CITY: San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94111-3834
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentin Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/004,838
21 FILING DATE: 09-JAN-1998
22 CLASSIFICATION: 800
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/781,734
25 FILING DATE: 10-JAN-1997
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Einhorn, Gregory P.
28 REGISTRATION NUMBER: 38,440
29 REFERENCE/DOCKET NUMBER: 023070-078810US
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (415) 576-0200
32 TELEFAX: (415) 576-0300
33 INFORMATION FOR SEQ ID NO: 11:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 1402 amino acids
36 TYPE: amino acid
37 STRANDNESS:
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 FEATURE:
41 NAME KEY: -
42 LOCATION: 1..1402
43 OTHER INFORMATION: /note= "RLGIA amino acids"
44 US-09-004-838-11

```

Query Match 20.3%; Score 1041; DB 3; Length 1402;
Best Local Similarity 29.3%; Pred. No. 9.6e-83;
Matches 311; Conservative 180; Mismatches 395; Indels 174; Gaps 28;

DY 1 MAE-----AFQVLLDLNLTCTFGELGLILGFKDFEFKLSTFTTIOAVLBAOKKOLDK 56
 ||| | | | | | | : : : | | | | | | | : : : :
DB 367 MAEVLSAFLTVVEFKLAHEMLKKIIVSKRIESELEKIKETLIDTOILLNDASCKEYNE 426
 AIEHWLOKLNAAAAYEADIIIDECKTEAPIRKKNKYGCYNHV-----ITFRKI 106
DY 57 AIENWLOKLNAAAAYEADIIIDECKTEAPIRKKNKYGCYNHV-----ITFRKI 106
 ||| | | | | | | : : : | | | | | | | : : : :
DB 427 AVKRWLNDQLHVAVIDDLDLDXATEAVXRRELTREGGASSMVBKLIIPSCCTSFSQSIRM 486
 AKRWMNLNDQLHVAVIDDLDLDXATEAVXRRELTREGGASSMVBKLIIPSCCTSFSQSIRM 486
DY 107 GKRRKIMTELGDVIAARIRKHLDERTIEROVARROGCVPLINEQVYGRDRDEKEIVAIL 166
 :: | | : : : | | | | : : : : : : : : : : : : : : : : : : :
DB 487 HAKULDIATIRIQELIVEAKNNLGSLVTYEKPRTERYEASTDESGETVGEDDKTKLLEKL 546
 I--NNVNNAOTLPVLPIITMGGLGKTTLTAQVFNDORYIEHFHKIWICVEDENFEKILI 224
DY 547 LGEDVDSEGSGNFSPVIIVMGGVAGVKTTLARLLYBEKVYKHFFELRAWVCSDSEPSVRNIS 606
 :
DY 225 KEIVESITEESLGGMDIAPLOKKLRJLDLNGKCYLVLDVWNEDODKMAKLRYVLKGAS 284
 :
DB 607 RVIQSVTYGEKKEPEDINLLQEALKERKLRMQLFIVLDVVASESGBWEKLCVPFLAGSP 666
 GASVLTTRLEKXSINGTIQPYEISLNSGEDCWLFMQRAFGHQE-EINLNVAIAGEKI 343
DY 285 GASVLTTRLEKXSINGTIQPYEISLNSGEDCWLFMQRAFGHQE-EINLNVAIAGEKI 343
 GSRIIMTRYEQILRKRGFHSQHDPEBGSDDALSLFAQHAFGVPNFDSPHTLRPHGLELF 726

```

OY 344 VKCGVPLAKTIGLIRFREROMEHVDSBIWKLPOESSILPALRSTYHHLPLDL 403
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 727 VKKDDGLPLARTIGRLRLRTDEQWEKELDSEIWRIGKSD-ELVPLRLSYNDLSXKL 785
OY 404 RQCTTCYAVFPDTEMKGNLISLMAHGF-LSKGNILELVNGEVNNEIYLSFFOEI 462
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 786 KILFAYCSLFPKDYEFDEKEELILMMAEGFLHQPTXNKSOKRLGLEVEKELLSRFPQ-- 843
OY 463 EVKSGQYFKNHDLIHLATSLFSASTSSSN--REIIVENYIHM----- 505
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 844 HAPNKSLLFVHDLMDLDTFVAGEFFRDLDEMKEFRMSLEHHRMSFVCEXYIYK 903
OY 506 -----MSIGFTKVVSYSLSH-----LQKFVSLRYNLSDIKLKQDPS 543
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 904 XFEPRGAKNLTPLALSVGVVEDMKFVLSKVLNDLQDPLRLVXLLXIXYXPX 963
OY 544 SIGDLVHLRYNLSGNTSIRSLPNOLCYLQTLDLHGCHSLCCLPRETSKLSRLNL 603
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 964 XVGSMXHLRYNLIS-XTXITHLPEXKCNLYMLQTLIVSGCYLVXLPPTFSXLKXLFHD 1022
OY 604 LDGCYGLTQMPPRIGSLTCLKTLRSFVYIOKKSQGLBELNLT-NLVGSIETHLERVKN 662
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1023 MRYTPXLMPLXIGELKKLQTLF-XNIGI-----AITELKNLXNLHGKXCIIGLGMEN 1076
OY 663 DMDAKENI,SAKENIHSISM-----KWDDEPRRIYSESEKVEVLEALKPHSNL-T 711
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1077 AVGCTLSLSEVKKVXXXXXNWXGXIXCPKK-----BHLKKXSMMX 1119
OY 712 CL-----TIRGRGIRLDPWNHVSUKVNSIETISCKNCSCLPPFGLPCLKSL-- 761
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1120 CLIMWLAKKPKYIMSIGIEFPWVGSILRVSETRVDVFWYEK--KCTYFHOSPSCKMIF 1177
OY 762 -----ELMRGSA-----EVEVY-DSGPTRRRFPRLKLTREFGNLGL 800
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1178 SGXTDEMRGMIGKIGAVEBISHSCHNEIRYLMSEBAASKVLNWKLDJGECNVL 1237
OY 801 LKKEGEE-----QCPVLEIEIETKCP-----MEVPIPTLSVKLV 835
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1238 GEKEDNNINSGSLTFRRRLNVRKNSLHCR--CPDSWENLYMHGCSXVSFPT 1294
OY 836 VSGDKSDAIGPSSISNLMTLSLQIRYNKEDASLPEBPKSIAN-----LKTINISFTFN 890
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1295 GGGQK-----IKSLITTDCKLSEBELGGERETRVLINSMQMLSEVDIRNPN 1343
OY 891 LKELPTSLASLNALKHLHSCYALESLPEBVGKGLISLT 930
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 1344 LKSL-SELSCPTIHLNRLYISNCPXKSPDDELFWLTSLT 1382

```

```

RESULT 4
US-09-004-838-12
; Sequence 12, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michellmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Confering Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Binhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 784 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..784
; OTHER INFORMATION: /note= "R1G1B amino acids"
US-09-004-838-12

```

```

Query Match 18.9%, Score 969.5; DB 3; Length 784;
Best Local Similarity 34.7%; Pred. No. 8,2e-77;
Matches 242; Conservative 131; Mismatches 265; Indels 59; Gaps 12;

OY 1 MAEAPLOYLDNLTCFIQELGLIGFQDEPEKIQSTFTTQAVLEDAQKQKLDKAIEN 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 97 LGSAPFAVFFPEKLSAELKRVACSKVIDKELEKLNSSXINIKALINASQKSEKAYKE 156
OY 61 WLQKMAAAYADLDLDECKTEAPLRQKXKYG-----CYHPNVTFRHKGK 108
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 157 WLNALQHLPYIDLDLGLATKALHKKFSESEYGTINKVRKLTSCPSLSST---KGRN 213
OY 109 RMKIMEKLDVIAERIKFHLDERTIEROVATROGFVLANP-QVYGRDEKDEIVKILI 167
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 214 KIHNTSLQGLLEBRNNLIGCEIGESKLNRRSESYKLDPSISVGRDTDKEALLLY 273
OY 168 NNVNSAQTLPYLPIIWMGGLGKTTLAQWVENDQYIEHFHFKIMICVSEDENEKRLKEI 227
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 274 EPCD--RNFSILPIVGMGLDKTTLGRLLYDMQVKHFEKAWCVSDEPDIGISKTI 331
OY 228 VESTIEKSLGMDLAPLOKXLRDLNGKKYLVLDVWNEDQDKAKIROYLKVGSAGAS 287
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 332 FESIEGNGQEFKDLNLQVALKEKISKRRFLVLDVWSESYYTWEILERFPLAGAPSG 391
OY 288 VLTTRLEKVGSIINGTLOPYELSNLSQEDCWLTFMORAFG-HQBEININLVAIGKEIVK 346
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 392 VIITTRKSLNLOJHQDPYQSLDSHNMALSCQNAFGVNSPDHPIILKPHGGLVEK 451
OY 347 CGGVPLAKTIGLIRFREROMEHVDSBIWKLPOESSILPALRSTYHHLPLDLRQC 406
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 452 CDGLPLIALIGRLRTGRDEEWKELINSIRWIRGKRD-BIIPXRLSYNDLSASXKL 510
OY 407 FTYCAVFPKDEMKNLISLMAHGFILSKG-NLELVNGEVNNEIYLSFFOEIVK 465
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 511 FAYCSLFPKDYFVNEKILILMMAEGFLHPLANENTNKSMEKLETFDLSRFPQ--HAL 568
OY 466 SGQYFKNHDLIHLATSLFSASTSSSN--REIIVENYIHM----- 505
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 569 DDKSLFVHDLMDLNDLTSVADYFLRLDIENKKEALEKRYMSFVCSYVWYKFEPEPG 628
OY 506 -----MSIGFTKVVSYSLSH-----LQKFVSLRYNLSDIKLKQDPSIGDLVH 550
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 629 AKKLTFLAMPVGMKSWTTFYLSKNVLDLHLHELPLRLVLSLSTSLKEVPEIIGNLKH 688
OY 551 LRYNLNSGNTSIRSLPNOLCYLQTLDLHGCHSLCCLPRETSKLSRLNLDDGCYGL 610
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 689 LRYNLIS-HTSITHLPENVCNLYMLQTLILCGCCFTYKFPNNFLKXLRHLSDTDFGL 747

```


Qy 611 TCMPPRIGSLTCLTSLRFRVGIQKSCOLGELRYLN 647
Db 748 KKMSSGIGELKNLHTLSLIIIGENRNLKNLQNLH 784

RESULT 5

US-09-004-838-16
Sequence 16, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Binhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY:
LOCATION: 1..553
OTHER INFORMATION: /note= "R16f amino acids"
US-09-004-838-16

Query Match 14.2%; Score 729.5; DB 3; Length 553;
Best Local Similarity 35.0%; Pred. No. 9.5e-56;
Matches 165; Conservative 102; Mismatches 181; Indels 23; Gaps 8;

Qy 30 EPEKLGSTFTTQAVLEDDAKKQKLAENWLOKNAAYEADDIDDECKTEA----- 83
Db 43 ELKLLKSLIIRSLYNDASEKISDEAVKEMNLQSLDIDDLDLATETMHRRLT 102
Qy 84 -----PIROKKNKYCYHPNVITFRHKIGKRMKKIMEKLDVIAERIKFHLDEKTERQ 137
Db 103 TDLBPFPACKKDNPTCC---TDFSLSSIKRMKLDNITIKQLVLVEKONLGLSYVGSBPX 159
Qy 138 VATR--QCGPVLNREYVGRDKEKDEIVKILLNVSNGTLPVLPITLGMGGLGKTTAQM 195
Db 160 HTNRRLQTSLV-DASSIIGREGDKDALLKHLLEDPDSRNRSIVITVGMGSGKTTARL 218
Qy 196 VFNDQVIEHFHPKIKVICSEDFNEKRLIKEIVSIEEKSIGMDLADLOKKDLNDLNGK 255

Db 219 LYDEMOEKDHRELKAWVCVSDFDIFNISKVIFOSIGGKQXQEFYDNLMLQVAVKEXISKX 278
Qy 256 KYLLVLDVNMEDDQKAKLRQVLKVGASGASVLTTRLEKVGSIKMTLOPYELSNLSQE 315
Db 279 RELVLDVMSSEYTEMETLARPLAGAPGSKIITTRKLSLTLTGNGPNLSVLSHD 338
Qy 316 DCMLLFMOARFHOE-EINLNLVAIGKEIVKCGVPLAATLGILRFKEERQMEHVR 374
Db 339 NALSLFOHALGENPDSHPFLKXGESIVKCDGLPLALALGRILKXTDDEEMKEVL 398
Qy 375 DSEIKWLPQESSILPALRSLYHHLPLDLRCFTYCAVPPTDMEKGNLSLMAHGPI 434
Db 399 NSIWMGSKGD-EIVPALKLSYNDLSASIKKLFAYCSIFPDVYFDEKELLILWMAEGFL 457
Qy 435 -LSKGNLELVNGEVNVELYRSFQEIYKSGQTYKMDLHDLATSL 484
Db 458 HQTTSKSMERLHGHPDELRSFPQ--HAPDAKSMFVMDLMDLNTSV 506

RESULT 6

US-08-947-823-3
Sequence 3, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isagoubi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baerlian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-947-823-3

Query Match 11.9%; Score 609.5; DB 3; Length 1255;
Best Local Similarity 27.0%; Pred. No. 1.7e-44;
Matches 259; Conservative 144; Mismatches 384; Indels 173; Gaps 37;

```

QY 5 FLQVLDNLTCFIOGELGLIGFKDFEKLQSTFTTIOAVEDAKQKQKDAIENMLQK 64
D 390 FMHLHLHLNDLSDNNAVSIALIKKEIEIVKQDLKFIKSPVDAKQGLYKDL-----VARV 445
QY 65 LMAAYEADDILDECKTEAPIRQKKNKCGCHPANTIFRHIG-KRMKIMKEDV----- 119
D 446 LD-VAYEKADVIDS-----IIVRON-GLIH--LIFSLPTTKKIKLKEEISALDEN 493
QY 120 IAAER--IKFHLDEKTERQVATRGTFVLINEPOUYGDKDEIVKLLINNVAQTLF 177
D 494 IPRKRGILVNSPKKPVKRSKLT-----TDKITVGEFEETNILLRGL-----TGSADLD 543
QY 178 VLPITGAGLQKTTIAQNVENDQVIEHFHPKIMCVSEDNREKRLIYEIVSEIKSLG 237
D 544 VISITGMGSGKTTIAYKAVYNDKSVSRFDIIRAMCTVQOGDEKRLMTITISQVSDSK 603
QY 238 GMDLAPLOKRLDNLNGKKYLLVLDVNNEDQDKAKLROYLVKVGASGASVLTTRLEKV 297
D 604 LSENIDVADKRLKQKPKRKYLIVLDVW--DITTWDELTRPPSKKGSRIILITTR-EKE 660
QY 298 GSIMGTL--OPEYLSNLQSOEDCMLFMORAFGHOEINLNIWAIGKEIVKCGVPLAAK 355
D 661 VALHKNTATDPLDLRLRPDSMELLEKRAFQCN-ESCPDELLDVGEKIAENCKGLPLVAD 719
QY 356 TLGGILFRREERQ-WEHYROSEIKYKLPQEBESSILPALRLSYHNLPLDLQCFYCAVFP 414
D 720 LIAGVIAGREKRRKRWLEVOSSISFIIINSEVEVKKVIELSDHLPHHLKPLCLFYASF 779
QY 415 KOTEMEKNLISLMAHGFILSKNLEENGVNEVNEIYLSRF--FOEIEVKSQCYTF 471
D 780 KOTSLITYELANYFAGSEFVGKTEWNSMEVVKITMDLIYSVLICNEIGYALN---F 836
QY 472 KMHDLIHD-----LATSLSFASSTSSNIREIIV---ENYIHMSIGCFYVSSY 517
D 837 QIHDLVHDPCLIKARKENLFDQIRSSAPSDLLPQIITIDCEBEHFGNFWFEDSKKH 896
QY 518 SLISHQKFSVLNVLSDIKLKQPLSSIGDLVHLAYLN-----LSQNTSI---RSLPNOL 569
D 897 SKKH---YSLRITIG-----DQLDSDVADAFHLHLRLVLDLHTSTFWKDSLMEI 947
QY 570 CGLONIQTLDLHGCHSLCCLPKETSKLGSRLNMLLDGCGYGLTCMPRIGSLTCLTLGRF 629
D 948 CMLNHLRYTISD--IQVKLPISPSNLMWJESLFWSTNRSLIIVLPRILDLVKLVLS-- 1003
QY 630 VVGIOKKSQGLGELRNLMNLYSIEITHLERVKNDMDAKANLSAK---ENHLSMKWD 685
D 1004 -----VDACSF-----FMDADESILIAEDTYKLEMLRILT--- 1033
QY 686 DDERPRIYSEKVENLEALKPHSNLTCLTRGFRGRLPDMNHSVLKKNVSIIRIISCKN 745
D 1034 -----ELLISYKQDKNIFKRPENQL-----LSFELKESMD 1065
QY 746 CSCLPF-FGELPCLKSLE-LMRGSAEVEYVDSGF-----PYRRRPS-LRKLNIREFGN 796
D 1066 YSTEQMFBELDFLTLELTLSGFKSSNNDGSSVATRRPMDHPSPULKILMLREFPL 1125
QY 797 LKGLLKKEGEOCPVLEIEIKCCPMFYPTLSVYKVLVSGDKSDADIFSSISNMLMT 856
D 1126 TSDSLSTIA--RLPNIEEL-----SLHTIIGHBENWMEGDEDFEENIKFLN 1169
QY 857 SIQIRNKEDASLPEEMFKSIANLKYLNISFYFNKLEPTSLASINALKLEIHSQYALE 916
D 1170 FNOVSIKWEVG--EESF--PMLKDLKRGCHKEIPPSFGDIYLSLSIKIVASPOL 1224

```

RESULT 7
 US-08-930-996A-8
 ; Sequence 8; Application US/08930996A
 ; Patent No. 6100449
 ; GENERAL INFORMATION:
 ; APPLICANT: FLUHR, Robert
 ; APPLICANT: ESHED, Yuval

```

; APPLICANT: ORI, Naomi
; APPLICANT: PAPAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 920 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-8

```

Query Match 11.8%; Score 606; DB 3; Length 920;
 Best Local Similarity 22.8%; Pred. No. 2,1e-44;
 Matches 250; Conservative 176; Mismatches 371; Indels 300; Gaps 40;

```

QY 1 MAEAPLOVLDNLTCFIOGELGLIGFKDFEKLQSTFTTIOAVLEDAQK-----KQLK 54
D 1 MASATVDFGIRISLIVENETLLISGVHGEI-KMKKELLNWSFLEDTNKHGNGSTTTT 59
QY 55 DKATEINMLQKNAAYEADDILDECKTEAPIRQKKNKGYCYH-----PN 98
D 60 TQLFQTFVANTRDLAIVQIEDLDE-----FG-YHIGYNSCAKIMRAPHPRR 105
QY 99 VITFRHKIGKMKKIMEKLDVIAERIKFH-----LDEKTERQVATRGQFV 146
D 106 YMAARHSIAQGLGVNVAIQISIDSMKRYHSENYOALLPPIIDGDAKWNNTISESSLF 165
QY 147 LNEPOVYRDKERQBEIVKLLINNVSNNQTLFVPLILGAGLGTTLAQMVFNDQVIEHF 206
D 166 FSEKSLVIGIDAPKCKLIGRLIS--PEPQRI-VVAVVGSGSKTTLISNIFKSGSVRRHF 222
QY 207 HPKIMCVSEDF-----NEKRLIYEIVSEIEEK-----SLGMDLAPLOKRLDNLNGKK 256
D 223 ESYAWTISKSYVIEDVRKIMKEFYKADQIAPALYSIGYREL--EGLVRYLQSKR 279
QY 257 YLVLDVNNEDQDKAKLROVLKVGASGASVLTTRLEKYGSI--MGTIQPYELNLS 313
D 280 YIVLVLDVMT--TGLMRISIALPDGIVGSRVMMITRDMNVASPPYIGGSTR-HEIELLK 336
QY 314 QEDCMLFMORAFGHOE--INLNIWAIGKEIVKCGVPLAAKTLGGILFRKREEROME 371
D 337 BDEAWVLFSNKAFPASLEQCRQTNLEPIARKLVERC-GLPALIASLSGMSMTKTFESNKK 395
QY 372 HYRDESEIKYKLPQEBESSILPALRLSYHNLPLDLQCFYCAVFPKOTEMEKNLISLMM 429
D 396 KYVSTLMEINNNHKLKIVRSIMPLSPFNDLVPPLKRCGLYCSLFPVNVYMRKRLIRMM 455

```

```

QY 430 AHGFLSKGNLELVNGEVENNELYLRSPFOEI-----EVKSGQTYFPMADLIHDLATS 483
Db 456 AGRFVEPIRGVAAEYADSYLNEVLVYRNMLQVILNMPGRPRXA-----FMDVIVEIMALS 511
QY 484 -----LFSASTSSNIREIIVENY-----IHMSIGFTKVSS--Y 517
Db 512 VSKLERPCDVYDDSDGDDAAE--TWENYGSRLCIQKEMTPSIRATNINSHSLVCSAKH 570
QY 518 SLSHLQKFSVLNLSIDIKLQKQPSIGDLVHLRYLNSGNTSIRSLPNOLCKLQNTQT 577
Db 571 KWEILLPSLNLARALDLBSSISKLPDCLVTMNLKINLS--KTQVKEIPKHNKXVNIET 629
QY 578 LDHCHGS--LCLPKEYSKLSRLNLDGCGYGLTQMPRIGSLTCLKTLNR----- 628
Db 630 LNTK--HSKIEELPLGMMMLKKLRVLI-----TFRRNEGHDSNW 666
QY 629 -FVVG--LOKSCOLGELRNMLVGSIEI-----TLERYKNDMAKE-----ANLS 672
Db 667 NYVLGTRVVPKIMQKLDQWDCFNEDELKMLGCMTQLTRISLVYVRREHGRDLCDSL 726
QY 673 AKENLHSLSMKWDDEPRRIYSEKEVEVLKPKHSNLTCLTIRGFRGIRLPMNNHSLV 732
Db 727 KIKRIFSLTSLSDDEBPLEIDDLATASIEKFLAGKLE-----RVPSWEN----- 772
QY 733 KNVVSIEIISCNCSCLPPFGEPLCLKSLLEWRGSAEVEYVDSGFPTRRRPPLRKLNIR 792
Db 773 ----- 772
QY 793 EFGNLKGLLKEGEBOCYVLEIEIKCCPMFVPTLSSVKLVSGDSDAIGFSSISNL 852
Db 773 -----TLOMLTYLGLGSQLQENALISITL 798
QY 853 MALTSIQIRYNKEDASLPEEMF--KSLANIKYLNISFYFNLEKLPSTLASLNLKHLBIHS 911
Db 799 PRVLWLSF--YANVMG--FRLRPAQGFQNLKILIEIYQMGHLREVAEDAMELQCLYRA 855
QY 912 CYALESLEPEGVKGLISLTQUSITYCEMLQCLPBGLOHLTALTNLSVEPCPTLAKRCEKG 971
Db 856 CRGLEEYV--RGIEMLINLQEL-----HLIHVSQNLVERI-----RG 890
QY 972 IGEDMYKLAHPRVITY 988
Db 891 EGSVDSRV-HIPIAKHY 906

```

RESULT 8
US-09-245-928A-19
Sequence 19, Application US/09245928A
Patent No. 6613962
GENERAL INFORMATION:
APPLICANT: KEYGENE N.V.
TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
FILE REFERENCE: 960-35
CURRENT APPLICATION NUMBER: US/09/245, 928A
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: PCT/EP97/04340
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: EP96401764.4
PRIOR FILING DATE: 1996-08-09
PRIOR APPLICATION NUMBER: EP97401101.7
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 1206
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: ORF2 encoded
US-09-245-928A-19

Query Match 11.2%; Score 575.5; DB 4; Length 1206;

Best Local Similarity 26.3%; Pred. No. 1.7e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;

```

QY 5 FLOYLDNLGCEIIGELGILGKDEPEKLTSTFTTQAVLEDDOKQL--DKDAIENMLQ 63
Db 339 FPHLHMLNDLNSMAYSLIKEIEIYVSGEELFISFFGDAAEQGLYD---IYAR 394
QY 64 KLNAAVEADDLDECKTEAPIRQKNKYGCYHPNVITFRHKIG--KRMKKIMEKLDV--- 119
Db 395 VLD--VAEAKVIDS-----IIVRDN--GLLH--LIFSPLITIKIKLKEISALDE 442
QY 120 -IAER--IKFHLDBRTIEROVATRGTFVLANEPQVYGRDKEDEIYKILINNVSMAQT 176
Db 443 NIPDRGLIVNSPKKVEPKSLT-----TDKIIYGFEEETMLIIRKL---TSGPADL 492
QY 177 FVLPLIGLGLGKTTLAQMVNDQRVIEHFPKIMICSEBDFNKRKILKEIVESIEERSL 236
Db 493 DVISITGMPGSKTTLKAVKYNDKSVSRHFDLRAMCTVDQGYDQKLDLDTIFSGVSGSDS 552
QY 237 GGMDLAPLOKKLRDLNLGKTYLLVLDVWNEDQDKMAKLROVLKVGASGASVLTTRLEK 296
Db 553 NLSNIDVADKLKRLQKRGKRLIVDDVW--DTTLDLITRPFPEAKKGSRIILITTR--EK 609
QY 297 VGSIMGTIL--QVELSNISQEDCWLFMQRAFGHQBIEINLVAIGKEIYKKGCGVPLAA 354
Db 610 EVALHGKINTDPLRLRLRPDESWELEKRTFG--ESCPDELDVGEIAENCKGLPLVA 668
QY 355 KTLGGIARFKREERQ--WEHRDSEIKWLPQESSILRALRSLNHLPLDLRQCTYCAVF 413
Db 669 DLGAVIAGREKRKSWLEVOSSLSFSLNSEVMVKEIETSLYHPLPHLKPCLLHFPASW 728
QY 414 PKOTEMERGNLISLMAHGFILSKNLELVNGEVENNELYLRSPF---FOEIEVKSQTY 470
Db 729 PKOTFPLITLYLVLAGBGFVETKEMKIEVYKIMDDLSSLVLCFNEI---GDILN 785
QY 471 FKMDLIHDLA-----TSLF---SASTSSNIREIIV-----ENYIHMSIGFTKVS 515
Db 786 FOIHDVLVDFCLIKARKNLFDRISSAPSDLPRQRTIIDVEDEEHFGILFVFDNSKK 845
QY 516 SYSLSHLQKVSLEVLNLSIDIKLQKQPSIGDLVHLRYLNSGNTSIR-----SLPN 567
Db 846 RHSGKHL---YSLR-----INGQDDSVSDAFLHLRLIRVLDLPSLIWVNDLNL 896
QY 568 QLCQLQNLQTLDLHGCHSLCCLPKETSKLSRLNLDGCGYGLTQMPRIGSLTCLKTL 627
Db 897 EICMLNHLRIYLR--TQVKYLPSPSNLWNLBSLFPNSKGSILVLLPRIIDLKLVLS 954
QY 628 RFVVGIOKSCQOLGELRNMLVGSIEITHDERVKNMDAKEANLSAK-----ENLHSLSMK 683
Db 955 ---VG---ACSF-----FMDADDESILIAOTYLENRLIG-- 984
QY 684 WDDDERRIYSEKEVEVLKPKHSNLTCTIRGFRGIRLPMNNHSLVKNVVSIEIISC 743
Db 985 -----ELIISYKDTMNIKRPFNQVLO---FELKESGDSYTEOHM----- 1023
QY 744 KNGSCLPFGEPLCLKSL--LMRG--SAEVEYVDSGFPTR---RPSLRKLNIREFGN 796
Db 1024 -----FKLDCLTELETLVGFKSSNTNHGSSVATNRKPMDFHPS-----N 1065
QY 797 LKGLLKEGEBOCYVLEIEIKCCPMFVPTLSSVKL-----VSGDKSDAIGFSSISN 851
Db 1066 LKELL-----LYDFPLTDSLSLTARLPLNLSLYDTLIOGEEHNMGBEDTFEN 1115
QY 852 LMAITSIQIRYNKEDASLPEEMFKSLANIKYLNISFYFNLEKLPSTLASLNLKHLBIHS 911
Db 1116 LKFLNLRLLTSLKWEVG--EESFPNLEKLIQBCG--KLEIIPSPGDIYSIKFIKIVK 1170
QY 912 CYALE 916
Db 1171 SPQLE 1175

```

RESULT 9

US-09-245-928A-17
; Sequence 17, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1243
; TYPE: PRT
; ORGANISM: M1 resistance gene deduced amino acid
US-09-245-928A-17
Query Match 11.2%; Score 575.5; DB 4; Length 1243;
Best Local Similarity 26.3%; Pred. No. 1.8e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;
QY 5 FLQVLLDNLTCPFOGELGLIGFQDEFEKLOSTFTTQAVLEDAQKOL-KDKAIENWLQ 63
DB FPHLLHMLNDLDSNAYSISLKEIEIVSQLEFIRSFQDAEQQLYKD---IWAR 431
QY 64 KLNAAAYEADDLDECKTEAPIRQKKNKGCYHNPVITFRHIG-KRMKKIMEKLDV--- 119
DB 432 VLD-VAYEAKVDIS-----IIVRDN--GLIH---LIFSLEPTTKIKLKEEISALDE 479
QY 120 -IAAER--IKFHLDERTIERQVATROTGFVINEPQVYGRDKEDIVKILINNVSNQTL 176
DB 480 NIPKRGILVNSPKKPYERSKLT-----TDKIIVGEETNLIIRKL--TSGPADL 529
QY 177 PVLPIILMGIGIKTTLAQVNDQVIVHFRPKVICVSEDENEKRLKEIVSEIEEKS 236
DB 530 DIVSITGMPSGKTTLAKYVNDKSVSRHFDLRACVTDQGDGDKLDTTFSQVSGSDS 589
QY 237 GGMDLAPLOKKLRDLNKGKTYLVLDVWNEEDQDKMAKLRQVLAKGASGASVLTTRLEK 296
DB 590 NUSENIVADKLRKOLFGRKYLIIVLDVW--DTTLDLDELTRPPEAKKGSRIILITTR-EK 646
QY 297 VGSIMGTL--QPYELSNLSQEDCWLIFMQRAGHQBELINLVAIGKEIVKKGCVPLAA 354
DB 647 EYALHGKLTNDPLDLRLRPDSWELERKTFGN-ESCPDELIDVGEIAENCKGLPIVA 705
QY 355 KTLGGILFRKREERO-WEHVARDSEIWKLPQESSIILPALRLSYHNLPLDLRCFTYCAVF 413
DB 706 DLIAGIAGREKKRSYWEVOSLSFPIINSEVEWVYELSYDHLPHILKQCLLHFAFASW 765
QY 414 PKOTEMKENLNLISWMAHGFILSKGNLEENYGENEVMNELYRSF---FOEIEVKSQTY 470
DB 766 PKOTPLTYLLTVYIGAGSEFVEKTEMKGIEEVYKIMYMDLISSSVATCNEI---GDILN 822
QY 471 FKMHDLIHDLA-----TSLF-----SASTSSSNIREIIV-----ENYIHMSIGFTKVS 515
DB 823 FQIHDLVHDFCLIKARKENLFDRISSAPSDLLPRQITIDYEEBEHFGFLNMFEDSNK 882
QY 516 SYSLSHLOQFVSLRVNLSDIKLOLPSIGDLYHRYNLNGNSIR-----SLPN 567
DB 883 RSHSGKL---YSLR-----INGDQDLDSDVDAFHRLRLRLRVLDLEPSLIMVNDSLN 933
QY 568 QLCCKLONLQTLDHGCHSLCPKETSGLSLNLLDGCYGLTQMPRIIGSLTCLIKTIS 627
DB 934 EICMLNHLHYLIR--TQYKYLPRFSNLMNLESFLVSKNGSILVLLPRILDLVLRVLS 991
QY 628 RRVVGIQKSKCOLGELRNINLYGSIEITHLERVKNMDMAKANLSAK---ENHLSLNMK 683

DB 992 ---VG-----ACSF-----FMDADESILLIAKOTKLENLRILG-- 1021
QY 684 WDDDERPRIYSEKEVLEALKPHSNLTCITIRGFRIGRLPDMWNHSHVKNVYSIEIISC 743
DB 1022 -----ELLISYKDTWNIKRFEPNLOVQ-----FELKESMDYSTEQH----- 1060
QY 744 KNCSCLPPEGLPCLASLE-LWRG--SAEVEYVDSGFPYTR---RPSLRKLNIREFGN 796
DB 1061 -----FKDCLDTLELTLCYGFSSNTHGSSVATNRPMDFHPPS-----N 1102
QY 797 LKGLLKEGBEQCVLEIEIKCCPMFVITLSSVKL-----VSGDKSDAIGFSSISN 851
DB 1103 LKELL-----LVDPLTSDLSSTIARLPNLNLSYDTLIOGEWMMGEEDTFEN 1152
QY 852 LMAITSQIRYNKEDASLPREMFKSLANLYKLNISFYENKELPTSLASINALKHEIHS 911
DB 1153 LKFLNRLTLTSKWEVG--BESFPNLEKLOQECG--KLEIIPPSGDIYSLKFIKIVK 1207
QY 912 CYALE 916
DB 1208 SPQLE 1212
RESULT 10
US-09-245-928A-18
; Sequence 18, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF1 encoded
; OTHER INFORMATION: polypeptide
US-09-245-928A-18
Query Match 11.2%; Score 575.5; DB 4; Length 1257;
Best Local Similarity 26.3%; Pred. No. 1.8e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;
QY 5 FLQVLLDNLTCPFOGELGLIGFQDEFEKLOSTFTTQAVLEDAQKOL-KDKAIENWLQ 63
DB 390 FPHLLHMLNDLDSNAYSISLKEIEIVSQLEFIRSFQDAEQQLYKD---IWAR 445
QY 64 KLNAAAYEADDLDECKTEAPIRQKKNKGCYHNPVITFRHIG-KRMKKIMEKLDV--- 119
DB 446 VLD-VAYEAKVDIS-----IIVRDN--GLIH---LIFSLEPTTKIKLKEEISALDE 493
QY 120 -IAAER--IKFHLDERTIERQVATROTGFVINEPQVYGRDKEDIVKILINNVSNQTL 176
DB 494 NIPKRGILVNSPKKPYERSKLT-----TDKIIVGEETNLIIRKL--TSGPADL 543
QY 177 PVLPIILMGIGIKTTLAQVNDQVIVHFRPKVICVSEDENEKRLKEIVSEIEEKS 236
DB 544 DIVSITGMPSGKTTLAKYVNDKSVSRHFDLRACVTDQGDGDKLDTTFSQVSGSDS 603
QY 237 GGMDLAPLOKKLRDLNKGKTYLVLDVWNEEDQDKMAKLRQVLAKGASGASVLTTRLEK 296
DB 604 NUSENIVADKLRKOLFGRKYLIIVLDVW--DTTLDLDELTRPPEAKKGSRIILITTR-EK 660

```

QY 297 VGSIMGTU--OPEYLSNLSOEDCMLFMORAFGHOEINLNLVAIGEIVKKGCVPLAA 354
D6 661 EVALHGKLNTPDLRLRPRDESWELKRTFGN--ESCPDELDDVGKEIENCKGLPLVA 719
QY 355 KTLGGILRFRKBERO--WEHVRDSEIWKLPQEBSSILPALRLSYHNLPLDLROCFYCAVF 413
D6 720 DLINGVIAGRKKSQVLEVOSSLSFINSSEVEMKVEISYDLPHHLKPCLLHFAFW 779
QY 414 PKOTEMKGNLSLMAHGFILSKGNLEENGVNMEIYLSRF--FOEIVKSGQY 470
D6 780 PKOTPLTYLLTVYGAEGFEKTEMKGIEEVVKIYMDLLSSSLVICFNEI--GDILN 836
QY 471 FKMDLHDLA-----TSLF-----SASTSSNIREIIV-----ENYIHMMSIGFTYVS 515
D6 837 FOIHDLVHPCFLIKARKENLFDRISSAPSDLLPRQITIDYDEEBHFGALFWFMSDKK 896
QY 516 SYSLSHLOKFSVLRVNLSDIKLQLPSSIGDLVHLRYNLSGNTSIR-----SLPN 567
D6 897 RHSGKHL---YSLR-----INGDQLDSDVSDAFHLRLRLRVLDLPSLIMVDSILN 947
QY 568 OLCKLONLQTLIDHGHCHSLCCLPKETSKLSLRLNLLDGCYGLTCMPRIGSLTCLTKLS 627
D6 948 EICMLNHLRYLRIR--TQVKYLPSSFSNLMNLESLEFVSNKGSILVLLRLLDLVLRVLS 1005
QY 628 RFVVGIOKKSFCOLGELRLNLYGSIETHLERVKNDMDAKEANLSAK-----ENLHLSMK 683
D6 1006 ---VG---ACSF-----FDMAHDSILIAKOTKLENLRLG-- 1035
QY 684 WDDERPRIYSEKVELEALKPHSNLCTLRGFRGRLRPMNMHSLKXNVSIETISC 743
D6 1036 -----ELLISYSKDTWNIPFRFPNLQVLQ-----FELKESMDYSTEGHW----- 1074
QY 744 KNCSCLPFGSLPCLKSLLE-LMRG--SAVEYVDSGFTRR-----REPSLAKNIRERGN 796
D6 1075 -----FPLDCLTELETCVGFSSNTNHCSSVATNRPWDFHPS-----N 1116
QY 797 LKGLLKEGEBOCPVLEIEIKCPMFIPTLSVYKL-----VVSGBDASIGFSSISN 851
D6 1117 LKELL-----LYDFPLTSDSLSTIARLPNLENLSYDTIIQGEEMNMBEDTREN 1166
QY 852 LMAITSLQIRYKNDASLPBEMFYSLANLYKYNISFYENKELPTSLASLALNKLHLS 911
D6 1167 LKFLNLRLLTSLKNEVG--EESFPLBKLQOEGC--KLEIIPSPFSDIYSLKRIKIVK 1221
QY 912 CYALE 916
D6 1222 SPOLE 1226

```

RESULT 11

```

US-08-947-823-5
; Sequence 5, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kaloehian, Isagouni
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Confering
; NUMBER OF INVENTION: Pest Resistance in Plants
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baetian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-947-823-5

Query Match 11.1%; Score 571.5; DB 3; Length 1257;
Best Local Similarity 26.3%; Pred. No. 4,1e-41;
Matches 254; Conservative 149; Mismatches 380; Indels 183; Gaps 42;

5 FLOVLDNLNFCFIGELGLILGFPOEFKLOSTFTTIOAVLEDAQKOL--KDKAIENMLQ 63
D6 390 FMHLHNLHNDLDSNAYSLIKEIEIVSGELEFIRSPFGDAEGLYND----IWAR 445
QY 64 KLNAAVEADDIIDECKTEADIRQKNKYGCTHPNVITFRHIG--KRMKIMKLDV-- 119
D6 446 VLD--VAEAKVIDS-----IIVRDN--GLH--LIFSIPITIKIKIKEISALDE 493
QY 120 -IAER--IKHDLERTIERQVATROGTVLNEQVYGRDKEKEIYKILINNVMNQTL 176
D6 494 NIPDRGLIVNSPKKVERKSLT-----TDKIVGFEEETVLILRK--TSQADL 543
QY 177 PVLPILGGLGKTTLQWYFNDOVIEHPFKIMICVSEDFNKRILIKEIVSIEEKS 236
D6 544 DVISITGPPSGKTTLLKYKYNDSVSRHFDLRMCCTVDOGCTDCKLIDTIFSOVSGSD 603
QY 237 GMDIAPLOKKLRDLNGKTYLLVLDVWNEODDKMAKLROVLKVGASGAVLTTRLEK 296
D6 604 NLSNIDVADKLARKQLGKRYLIVLDVW--DTTLDELTRPPEAKKGSRIILITTR--EK 660
QY 297 VGSIMGTU--OPEYLSNLSOEDCMLFMORAFGHOEINLNLVAIGEIVKKGCVPLAA 354
D6 661 EVALHGKLNTPDLRLRPRDESWELKRTFGN--ESCPDELDDVGKEIENCKGLPLVA 719
QY 355 KTLGGILRFRKBERO--WEHVRDSEIWKLPQEBSSILPALRLSYHNLPLDLROCFYCAVF 413
D6 720 DLINGVIAGRKKSQVLEVOSSLSFINSSEVEMKVEISYDLPHHLKPCLLHFAFW 779
QY 414 PKOTEMKGNLSLMAHGFILSKGNLEENGVNMEIYLSRF--FOEIVKSGQY 470
D6 780 PKOTPLTYLLTVYGAEGFEKTEMKGIEEVVKIYMDLLSSSLVICFNEI--GDILN 836
QY 471 FKMDLHDLA-----TSLF-----SASTSSNIREIIV-----ENYIHMMSIGFTYVS 515
D6 837 FOIHDLVHPCFLIKARKENLFDRISSAPSDLLPRQITIDYDEEBHFGALFWFMSDKK 896
QY 516 SYSLSHLOKFSVLRVNLSDIKLQLPSSIGDLVHLRYNLSGNTSIR-----SLPN 567
D6 897 RHSGKHL---YSLR-----INGDQLDSDVSDAFHLRLRLRVLDLPSLIMVDSILN 947
QY 568 OLCKLONLQTLIDHGHCHSLCCLPKETSKLSLRLNLLDGCYGLTCMPRIGSLTCLTKL 627

```



```

Db 7 ASLMRTIESLTFNSPMOSLSCDHREELCALREKVSLEFVFNKPNKNNVGEWTDVEVE 66
Qy 60 NMLQCLNAAAYE-----ADDIDECKTEAPIRQKNKRYGCHPNVITFRHKGKMKIM 114
Db 67 -VRBASAAETIQRLTGTGKNGKS-----QKGA-----RRRROSLQOVA 109
Qy 115 EKLDTVAERIKFHLDERTEREQVATROTGFVANE-----POVGRDKKEIKVILINN 169
Db 110 EDMDHIMKESKTIQDKQKQVSKEISLVHDFSSTNDILAKKNNMVGDRDQKQLDLRLRS 169
Qy 170 VSNMOTLVLPLNGMGLGKTTLAQWVFNDOVIEHFNPKIWCISDFNKRILKEIVE 229
Db 170 YSGEP--KPIPVGMGIGKTTLAKVYNDESILCRFVHAWATISQHNKKEILGLLH 227
Qy 220 SI-----BEKSGMDLAP-LOKRLDNLNGKCYLLVLDVWNEODQKMAKRLQVLA-K-G 282
Db 228 STIKMDVAKMIGELMADMLQKSLK---RRYIIVADDIS--CEWWDGVRRCPPED 281
Qy 283 ASGASVLTTRLEKVSIMGTLO-PYELSNTSQEDCMLFMQARFHOEINLNLVAIGK 341
Db 282 NAGSRILLTRNDEVACYAVENFSLRMSFMDQBSWLSFKSAVS--SEALPYEPETVGK 340
Qy 342 EIVKCGGVPLAATLGLILPKREEROMEHVR---DSIWKLPQESSILPALRLSTH 398
Db 341 QIABECHGLPLTIVVAGILSKRTIEDMKTVAKDVKSFTVNDPDERCS--RVLGLSYDH 398
Qy 399 LPDLROCFYCAVFPKOTEMEKNLISLMAHGFILSKNLELNENGVNENLYLSF 458
Db 399 LTRDCKTLHLFGIFPESDILPVKNLMSWMAHGLKLENDGEH-----VEKC 447
Qy 459 FOEI-----EYKSGOTYFKMHLIHLIATSLFSASTSSNIREIIVENY 502
Db 448 LQELVDRCLVLSKSRDGTKRS---CKVHDLTYDC-----VREQGRANI 491
Qy 503 IHMSIGF-----510
Db 492 FIMNDIYLDVSVBECSCYLQMKMOPKREVTGDEINVCYGLYRALLTEVNRQLRDHNN 551
Qy 511 ---TKVVSYSYL-----SHLOKPVSLRYANLSDIKLQKLPSSIGDLVHLRYLNL- 556
Db 552 LKRTSHVSFRHLEPLVYVLSSEVHFYKLKVLBEHRQIDGFPREIISLWRLYLSLPS 611
Qy 557 SGNTSIRSLPNQCLQNLQTLDLHGHS--LCCLPKETSRLSLNLLDGCYGLTCMP 615
Db 612 YGNPQV---PPEICLWMLQTFIVQFRPSDIIIFAEIEMELQRLHLKLPRLYLPDCSG 668
Qy 616 RIG-----SLTCLKTLG-----RNVVGIQKSCQGLBELRNILYGSIEITHLERYK 661
Db 669 SVDKGRHLDPNLTQITISYSPRCTKEVIMGIONVK-KLGISGNKDDYKSPDSGLPN-- 725
Qy 662 NDMAKKANLSAKENLHLSM-KWDDDRPRYSEKVEVLEALKPHENLCTLTRGRG 720
Db 726 ---NLVYLOQLLEILSLSVYSLPVIISAKAPRATLKLUKERTYLS----- 771
Qy 721 IRLPDMNHSYLKONVSIETISCKNCS-----LPPGELPCL-----KSLIELMRGSA 768
Db 772 ---WVYLDIIAEIPNLEVLKMDACCGEEMHPIVWGFRLKLLIKYSEFLKWKKA-- 824
Qy 769 EREVVDGSPFTRRRPRLKLNIREFGLKGLLKEGEGQCV-----LEEIRIKCCP 821
Db 825 ---TNDNPPVLERLIRSKNMLK-----EIPIEPADIHITLQIELRSCP 865

```

```

RESULT 14
US-09-803-286A-8
; Sequence 8, Application US/09803286A
; Patent No. 6664447
; GENERAL INFORMATION:
; APPLICANT: Tankeley, Steven D.
; APPLICANT: Brommonschenkel, Sergio H.
; TITLE OF INVENTION: PLANT GENE CONFERRING RESISTANCE TO TOSPOVIRUSES
; FILE REFERENCE: 19603/3201
; CURRENT APPLICATION NUMBER: US/09/803,286A

```

```

; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/188,356
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Lycopersicon var.
US-09-803-286A-8

```

```

Query Match 10.3%; Score 528; DB 4; Length 234;
Best Local Similarity 45.6%; Pred. No. 1.8e-38;
Matches 110; Conservative 42; Mismatches 75; Indels 14; Gaps 4;

```

```

Qy 176 LPVPIIIMGGLGKTTLAQWVFNDOVIEHFNPKIWCISDFNKRILKEIVSEIEKS 235
Db 2 LTVPIVGMGIGKTTLAKAVYNDESIVKNHFDLAKFVSAVNAFRITKILQELIGSID 61
Qy 236 LGMDLAPLQKRLDNLNGKCYLLVLDVWNEODQKMAKRLQVLA-KVSGASVLTTRLE 295
Db 62 LVDDNLNLQVYKLERLKEKKEFLVLDVWNDNNEDELNVFVQSDIGSKIITTRKD 121
Qy 296 KVGSIIMGTLOPYELSNISQEDCMLFMQARF-----GHOEININLVAIGKEIVKCGG 349
Db 122 SVALLMGNBQ-ISMGNISTEASWLSLFQHAFFENMDPMHSE-----LEEVGRQIANKCG 175
Qy 350 VPLAKTLGILRKREEROMEHVRDSIWKLPQESSILPALRLSTHNLPLDLROCFY 409
Db 176 LPLALTLAAGMLRSKEVEEWKTLRSEIWL--RNDILPALMLSTNDLPAHLFRCSF 233
Qy 410 C 410
Db 234 C 234

```

```

RESULT 15
US-09-330-330-1
; Sequence 1, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Utao
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FaastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:

```



```

Db      1 MAEAFIQVLDNLNLSFLKGEVLVLFQDEFORLSMSFSTIQAVALDAQOKOLDKPLEN 60
Qy      61 WLOKLNAAAYEADILDECKTEAPIRQKKNYGCYCHPNVITFRHKIGRMKIMKLDVI 120
Db      61 WLOKLNAAAYEADILDECKTEAPIRQKKNYGCYCHPNVITFRHKIGRMKIMKLDVI 119
Qy      121 AAEIRKTHLDBERTTERQVATRTQGFVLNEPQVYGRDKEDEIVKILNNVNAQTLPLVP 180
Db      120 AAEIRKTHLDBERTTERQVATRTQGFVLNEPQVYGRDKEDEIVKILNNVNAQTLPLVP 179
Qy      181 ILGWGIGKTTLAQVFNVDORVIEHFPKIMICVSEDFNEKRLIKEIYESIEEKSIGMD 240
Db      180 ILGWGIGKTTLAQVFNVDORVIEHFPKIMICVSEDFNEKRLIKEIYESIEEKSIGMD 239
Qy      241 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKXGASGASVLTTRLEKYSI 300
Db      240 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKXGASGASVLTTRLEKYSI 299
Qy      301 MGTLOPYELSNLSOEDCMLFMQRAFGHQBIEINLVAIGKEIYKKGCGVPLAAKTLGGI 360
Db      300 MGTLOPYELSNLSOEDCMLFMQRAFGHQBIEINLVAIGKEIYKKGCGVPLAAKTLGGI 359
Qy      361 LRFREERQWHEVDSSEIWKLPQESSILPALRSYHHLPLDLROCFYCAVFPKOTEME 420
Db      360 LRFREERQWHEVDSSEIWKLPQESSILPALRSYHHLPLDLROCFYCAVFPKOTEMA 419
Qy      421 KGNLISLMAHGFILSKNLELVNGVNMELVRSFQELIEVSGKTYFRMDLIHDL 480
Db      420 KGNLISLMAHGFILSKNLELVNGVNMELVRSFQELIEVSGKTYFRMDLIHDL 479
Qy      481 ATSLFASSTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKFSRLVNLSDIKLQ 540
Db      480 ATSLFASSTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKFSRLVNLSDIKLQ 539
Qy      541 LPSSTIGDVLHRYLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCSLCLPKETSKLGSIR 600
Db      540 LPSSTIGDVLHRYLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCSLCLPKETSKLGSIR 599
Qy      601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQOLGELRNLYGSIETHLERY 660
Db      600 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQOLGELRNLYGSIETHLERY 657
Qy      661 KNDMDAKEANLSAKENLHSLSMKWDDBRPRITYSEKVEVLKALPKHSNLTCLTIRGRG 720
Db      660 KNDMDAKEANLSAKENLHSLSMKWDDBRPRITYSEKVEVLKALPKHSNLTCLTIRGRG 713
Qy      721 LRLPDMNHSLVKNVYSIRISCKNCSCLPPRGEPLCKSLFLWFGSAERYV-DSGFPT 779
Db      720 LRLPDMNHSLVKNVYSIRISCKNCSCLPPRGEPLCKSLFLWFGSAERYV-DSGFPT 772
Qy      779 RRRPESLAKNIRERGNLKGILLKEGEOCPVLEIEIKCCPMFYITLTSVYKLVSGD 839
Db      778 RRRPESLAKNIRERGNLKGILLKEGEOCPVLEIEIKCCPMFYITLTSVYKLVSGD 830
Qy      839 KSDAIGFESSISNLMALTSIQIRYNKEDASLPEEMFKSLANLKYINISFYFNKLKELPTSIA 899
Db      838 KSDAIGFESSISNLMALTSIQIRYNKEDASLPEEMFKSLANLKYINISFYFNKLKELPTSIA 889
Qy      899 SLNALKHLHSHCYALLESIPBEGVKGILSLTOLSTTYCEMLQCLPEGIQHLTALNLSVE 959
Db      898 SLNALKHLHSHCYALLESIPBEGVKGILSLTOLSTTYCEMLQCLPEGIQHLTALNLSVE 949
Qy      959 FCPTLAKRCEKGIQGDWYKIAHPIPVFIY 988
Db      958 FCPTLAKRCEKGIQGDWYKIAHPIPVFIY 978

```

RESULT 2
US-10-360-522-58

; Sequence 58, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.

```

; APPLICANT: Vossen v. d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT FILING DATE: 2003-02-07
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 979
; TYPE: PR
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; OTHER INFORMATION: RGAG-b1b
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(979)
US-10-360-522-58

```

Query Match 73.9%; Score 3787; DB 15; Length 979;

Best Local Similarity 76.9%; Pred. No. 4.3e-286;

Matches 761; Conservative 76; Mismatches 140; Indels 12; Gaps 8;

```

Qy      1 MAEAFIQVLDNLNLSFLKGEVLVLFQDEFORLSMSFSTIQAVALDAQOKOLDKPLEN 60
Db      1 MAEAFIQVLDNLNLSFLKGEVLVLFQDEFORLSMSFSTIQAVALDAQOKOLDKPLEN 60
Qy      61 WLOKLNAAAYEADILDECKTEAPIRQKKNYGCYCHPNVITFRHKIGRMKIMKLDVI 120
Db      61 WLOKLNAAAYEADILDECKTEAPIRQKKNYGCYCHPNVITFRHKIGRMKIMKLDVI 119
Qy      121 AAEIRKTHLDBERTTERQVATRTQGFVLNEPQVYGRDKEDEIVKILNNVNAQTLPLVP 180
Db      120 AAEIRKTHLDBERTTERQVATRTQGFVLNEPQVYGRDKEDEIVKILNNVNAQTLPLVP 179
Qy      181 ILGWGIGKTTLAQVFNVDORVIEHFPKIMICVSEDFNEKRLIKEIYESIEEKSIGMD 240
Db      180 ILGWGIGKTTLAQVFNVDORVIEHFPKIMICVSEDFNEKRLIKEIYESIEEKSIGMD 239
Qy      241 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKXGASGASVLTTRLEKYSI 300
Db      240 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKXGASGASVLTTRLEKYSI 299
Qy      301 MGTLOPYELSNLSOEDCMLFMQRAFGHQBIEINLVAIGKEIYKKGCGVPLAAKTLGGI 360
Db      300 MGTLOPYELSNLSOEDCMLFMQRAFGHQBIEINLVAIGKEIYKKGCGVPLAAKTLGGI 359
Qy      361 LRFREERQWHEVDSSEIWKLPQESSILPALRSYHHLPLDLROCFYCAVFPKOTEME 420
Db      360 LRFREERQWHEVDSSEIWKLPQESSILPALRSYHHLPLDLROCFYCAVFPKOTEMA 419
Qy      421 KGNLISLMAHGFILSKNLELVNGVNMELVRSFQELIEVSGKTYFRMDLIHDL 480
Db      420 KGNLISLMAHGFILSKNLELVNGVNMELVRSFQELIEVSGKTYFRMDLIHDL 479
Qy      481 ATSLFASSTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKFSRLVNLSDIKLQ 540
Db      480 ATSLFASSTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKFSRLVNLSDIKLQ 539
Qy      541 LPSSTIGDVLHRYLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCSLCLPKETSKLGSIR 600
Db      540 LPSSTIGDVLHRYLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCSLCLPKETSKLGSIR 599
Qy      601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQOLGELRNLYGSIETHLERY 660
Db      600 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQOLGELRNLYGSIETHLERY 657
Qy      661 KNDMDAKEANLSAKENLHSLSMKWDDBRPRITYSEKVEVLKALPKHSNLTCLTIRGRG 720

```

Db 658 KKDSDAKANLSAKANLHSLCSDWLDGKHR-YDS--EVLEALKPHSNLKYLETINGGG 713
Qy 721 IRLPDMNHSVLANVSIIEISCKNCSCLPPGEIPCLKSLLEAMGSAVEYV-DSGPT 779
Db 714 IRLPDMNHSVLANVSIIRIRGCNCSCLPPGEIPCLKSLLEAMGSAVEYV-DSGPT 772
Qy 780 RRRPPLKLNIRERGNLKGILKKEGEOCPVLEIEIKCCPMFVITLSSVYKLVSGD 839
Db 773 -GRFPLSLKLVIMWDSNKLKGLKKEGEOCPVLEIEIKCCPMFVITLSSVYKLVIA 830
Qy 840 KSDAIGFSSISNLTSLQIRYNKEDASLPREMKSLANLKYINISYFNKELPTSLA 899
Db 831 -TDAVLRSISNLTSLQIRYNKEDASLPREMKSLANLKYINISYFNKELPTSLA 889
Qy 900 SLNALKHLEHSCVLALESIPREVGKGLISTOLSTTYCEMLQCPGLQHLTALNLSVE 959
Db 890 SLNALKSLKFEKCNLESIPREVGKGLISTOLSTTYCEMLQCPGLQHLTALNLSVE 949
Qy 960 FCPTLAKCEKIGEDWYKIAHPRVFIY 988
Db 950 QCPVIFKRCERGIGEDWYKIAHPRVFIY 978

RESULT 3

US-10-360-522-54
; Sequence 54, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 970
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: deduced
; OTHER INFORMATION: Rpl-D1b protein sequence domain A, B and C
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(970)
US-10-360-522-54

Query Match 73.5%; Score 3766.5; DB 15; Length 970;
Best Local Similarity 75.6%; Pred. No. 1.7e-284;
Matches 753; Conservative 78; Mismatches 130; Indels 35; Gaps 8;

Qy 1 MAEFLOYLDNLTCFIOGELGILGFODEBKLOSTTTTQAVLEDAQKQKQKALEN 60
Db 1 MAEFLOYLDNLTCFIOGELGILGFODEBKLOSTTTTQAVLEDAQKQKQKALEN 60
Qy 61 WLOGLNAAAYEADDIIDECCTEAPIRQKNKYGCCHPVVITFRHKIGKRMKIKEDVI 120
Db 61 WLOGLNAAAYEADDIIDECCTEAPIRQKNKYGCCHPVVITFRHKIGKRMKIKEDVI 119
Qy 121 AAEIRKFLDERTTERQVATQGFVINEPOVYGRDKEKDEIVKILINNVAATLPLVP 180
Db 120 AAEIRKFLDERTTERQVATQGFVINEPOVYGRDKEKDEIVKILINNVAATLPLVP 179
Qy 181 ILGNGGAGKTTLAQWVENDQVIVHFHFKIIVCSSEDFNEKRLIKEIVESTEEKS-IGQM 239
Db 180 ILGNGGAGKTTLAQWVENDQVIVHFHFKIIVCSSEDFNEKRLIKEIVESTEEKS-IGQM 239

Qy 240 DLAPLOKKRLDNLNGKTYLLVLDVWVEDQDKAKLQVLRVKGASGASVLTTRLEKVS 299
Db 240 DLAPLOKKRLDNLNGKTYLLVLDVWVEDQDKAKLQVLRVKGASGASVLTTRLEKVS 299
Qy 300 IMGLTQPELSNLQOEDCMLFMQARFQHEINLNLVAIKEIYKCKGVPPLAKTIG 359
Db 300 IMGLTQPELSNLQOEDCMLFMQARFQHEINLNLVAIKEIYKCKGVPPLAKTIG 359
Qy 360 ILRFRERQHEHVRDSEIWMLEPOESSILPALRSTYHHLPLDIRQCTYCAVPPKOTEM 419
Db 360 ILRFRERQHEHVRDSEIWMLEPOESSILPALRSTYHHLPLDIRQCTYCAVPPKOTEM 419
Qy 420 EKNGLISLMAHGFILSKNLELNANGNEVNNELYLRSFPOEIEYKSGQTYFKMHLIHD 479
Db 420 EKNGLISLMAHGFILSKNLELNANGNEVNNELYLRSFPOEIEYKSGQTYFKMHLIHD 479
Qy 480 LATSLSFASSTSSNIREIYENYTHMNSIGFTKYVSSYSLHLOKPYSLRVLANSIDYK 539
Db 480 LATSLSFASSTSSNIREIYENYTHMNSIGFTKYVSSYSLHLOKPYSLRVLANSIDYK 539
Qy 540 QLPESIGDLVHLRYLNLNGNLSIRSLPNOCLQNLQTLQTLQTLQTLQTLQTLQTLQTL 599
Db 540 QLPESIGDLVHLRYLNLNGNLSIRSLPNOCLQNLQTLQTLQTLQTLQTLQTLQTLQTL 598
Qy 599 RNLDDSGSLTQMPPIRIGSLTCLKTLSPFVVGIOKSCQGLRNLNLYGSIETHLER 659
Db 599 RNLDDSGSLTQMPPIRIGSLTCLKTLSPFVVGIOKSCQGLRNLNLYGSIETHLER 657
Qy 660 VKNDMAKLANLAKENHLSISMKDDERPRIYESKEVLEALKPHSNLTCTLTNGFR 719
Db 660 VKNDMAKLANLAKENHLSISMKDDERPRIYESKEVLEALKPHSNLTCTLTNGFR 716
Qy 720 GIRLPMNHSVLANVSIIEISCKNCSCLPPGEIPCLKSLLEAMGSAVEYV-DSGPT 774
Db 720 GIRLPMNHSVLANVSIIEISCKNCSCLPPGEIPCLKSLLEAMGSAVEYV-DSGPT 774
Qy 775 --SGPPTRRPPLSLKLNIRERGNLKGILKKEGEOCPVLEIEIKCCPMFVITLSSV 832
Db 775 --SGPPTRRPPLSLKLNIRERGNLKGILKKEGEOCPVLEIEIKCCPMFVITLSSV 830
Qy 833 KLVVSGKSDAIGFSSISNLTSLQIRYNKEDASLPREMKSLANLKYINISYFNK 892
Db 833 KLVVSGKSDAIGFSSISNLTSLQIRYNKEDASLPREMKSLANLKYINISYFNK 873
Qy 893 ELPTSLASLNAKLEHSCVLALESIPREVGKGLISTOLSTTYCEMLQCPGLQHLT 952
Db 893 ELPTSLASLNAKLEHSCVLALESIPREVGKGLISTOLSTTYCEMLQCPGLQHLT 933
Qy 953 LTNLSVEFCPTLAKCEKIGEDWYKIAHPRVFIY 988
Db 934 LTNLSVEFCPTLAKCEKIGEDWYKIAHPRVFIY 969

RESULT 4

US-10-360-522-63
; Sequence 63, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63

```

; LENGTH: 945
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(945)
US-10-360-522-63

```

```

Query Match      73.2%; Score 3752.5; DB 15; Length 945;
Best Local Similarity 76.6%; Pred. No. 2e-283;
Matches 745; Conservative 82; Mismatches 113; Indels 33; Gaps 7;

```

```

QY 1 MAEAFLOVLNLTGFCIGELGILGFDEBEKLOSTTTTQAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFLOVLNLTGFCIGELGILGFDEBEKLOSTTTTQAVLEDAQKQKLDKAIEN 60
QY 61 WLQKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 120
DB 61 WLQKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 117
QY 121 AAERIKPHLDERTTERQVATQGTGVLNEPQVYGRDKKDEIVKLLINNSNAQTLPVLP 180
DB 118 AKERTDFHHEKLIERYARPETGVLTEPQYGRDKKDEIVKLLINNSNAQTLPVLP 177
QY 181 ILGMGGLGKTTLAQWVENDQVIEHFHFKIWI CVSEDENEKRLIKEIYESIEKSLGMD 240
DB 178 ILGMGGLGKTTLAQWVENDQVIEHFHFKIWI CVSEDENEKRLIKEIYESIEKSLGMD 237
QY 241 LAPLOKRLDLNGKKYLLVLDVWNEEDQKMAKRLROYLAKGASGVLTTRLEKYSI 300
DB 238 LASFOKRLQOLNGKRYLLVLDVWNEEDQKMDNIRAYLAKGASGVLTTRLEKYSI 297
QY 301 MGTLOPYELSLNSQEDCWLTFMORAFGHOEINLNLVAIGKEIVKCGGVPLAAKTLGSI 360
DB 298 MGTLOPYOLSLNSQEDCWLTFIQRAYRHOEISPLNLVAIGKEIVKCGGVPLAAKTLGSI 357
QY 361 LRFKREEROMEHVHDSIWKLPQOESSILPALRLSYHHLPLDLRQCFTYCAVFPDTEME 420
DB 358 LRFKREEROMEHVHDSIWKLPQOESSILPALRLSYHHLPLDLRQCFTYCAVFPDTEME 417
QY 421 KGNLSIMWAGFSLSKNLELVNGEYVWNLVYRSPFOEIEVSGQTYFPMHDLIDL 480
DB 418 KKVAVSLWAGHGFSLSKNLELVNGEYVWNLVYRSPFOEIEVSGQTYFPMHDLIDL 477
QY 481 ATSLPSASTSSNIREIIVENYIHMSIGFTYVSSYSLSHLQKFVSLRVNLSDIKLKQ 540
DB 478 ATSLPSASTSSNIREIIVENYIHMSIGFTYVSSYSLSHLQKFVSLRVNLSDIKLKQ 537
QY 541 LPSISIGDLVHLRYLWLSGNTSIRSLPNQICLQNTQTLDHGCHSLCCLPRETSGLSIR 600
DB 538 LPSISIGDLVHLRYLWLSGNTSIRSLPNQICLQNTQTLDHGCHSLCCLPRETSGLSIR 597
QY 601 NLLLDGCGYGLTQMPRIGSLTCLKTLSPRVVGIQKKSCLGELRYMLNTYGSIEITHLEBY 660
DB 598 NLLLDGCHSLTTPRIGSLTCLKTLGQFVVG-RKKGYOLGELSLNLYGSIKISHLEBY 656
QY 661 KNDMDAKEANLSAKENLSLSMKWDDERPRIYSEKYEVLBALPMSNLCTLRGFRG 720
DB 657 KNDMDAKEANLSAKENLSLSMKWDDER-PHRYSEBEVVLBALPMSNLCTLRGFRG 715
QY 721 IRLPMMWNSVTKANVSTIISCKKNSCLPPEGELPCLKSLLEMGSAE-VRY----VDS 775
DB 716 IRLPMMWNSVTKANVSTIISCKKNSCLPPEGELPCLKSLLEMGSAE-VRY----VDS 775
QY 776 GPPTRRRPFLSKRLNIRBGNLKGILLKKEGECQPLVEIEIKCPMFVITPLSSYKLV 835
DB 776 GPPTRIRPFLSKRLCTCKFDNLKGLVKGEGEOPVLEMEIRYCP---IFPLS----- 826
QY 836 VSGKSDAIGFSSISNLMLTSLQIRYNKEDASLPREMFKSLANTKYLINISFYFNILKELP 895
DB 836 VSGKSDAIGFSSISNLMLTSLQIRYNKEDASLPREMFKSLANTKYLINISFYFNILKELP 895

```

```

DB 827 -----SNKALTSINISDNKEATSPREMFKSLANTKYLINISHFKNLKEP 872
QY 896 TSLASLNALKHLIHSQYALLESIPREGVKGLISITQSTIYCEMLQCLPGLQHLTALTN 955
DB 873 TSLASLNALKSLKIQWCCALLESIPREGVKGLISITELIVFCMLKCLPGLQHLTALTR 932
QY 956 LSVFCEPTLAKRC 968
DB 933 VKIWCPCQLIKRC 945

```

```

RESULT 5
US-10-360-522-60
; Sequence 60, Application US/10360522
; Publication No. US20030221215A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT FILING DATE: US/10/360,522
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 992
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(992)
US-10-360-522-60

```

```

Query Match      72.9%; Score 3736.5; DB 15; Length 992;
Best Local Similarity 74.8%; Pred. No. 3.9e-282;
Matches 747; Conservative 92; Mismatches 141; Indels 19; Gaps 8;

```

```

QY 1 MAEAFLOVLNLTGFCIGELGILGFDEBEKLOSTTTTQAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFLOVLNLTGFCIGELGILGFDEBEKLOSTTTTQAVLEDAQKQKLDKAIEN 60
QY 61 WLQKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 120
DB 61 WLQKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 119
QY 121 AAERIKPHLDERTTERQVATQGTGVLNEPQVYGRDKKDEIVKLLINNSNAQTLPVLP 180
DB 118 AKERTDFHHEKLIERYARPETGVLTEPQYGRDKKDEIVKLLINNSNAQTLPVLP 179
QY 181 ILGMGGLGKTTLAQWVENDQVIEHFHFKIWI CVSEDENEKRLIKEIYESIEKSLGMD 240
DB 180 ILGMGGLGKTTLAQWVENDQVIEHFHFKIWI CVSEDENEKRLIKEIYESIEKSLGMD 239
QY 241 LAPLOKRLDLNGKKYLLVLDVWNEEDQKMAKRLROYLAKGASGVLTTRLEKYSI 300
DB 240 LAPLOKRLDLNGKKYLLVLDVWNEEDQKMDNIRAYLAKGASGVLTTRLEKYSI 299
QY 301 MGTLOPYELSLNSQEDCWLTFMORAFGHOEINLNLVAIGKEIVKCGGVPLAAKTLGSI 360
DB 300 MGTLOPYOLSLNSQEDCWLTFIQRAYRHOEISPLNLVAIGKEIVKCGGVPLAAKTLGSI 359
QY 361 LRFKREEROMEHVHDSIWKLPQOESSILPALRLSYHHLPLDLRQCFTYCAVFPDTEME 420
DB 360 LRFKREEROMEHVHDSIWKLPQOESSILPALRLSYHHLPLDLRQCFTYCAVFPDTEME 419

```

Qy 421 KGNLSIMAHGFLISKGNLELVNGVNMELYLRSFQOIEYKSGQTYFKMDLJIDL 480
Db 420 KEYLIALMAMHAFILSKGNMELVDGNEVMNELYLRSFQOIEYKSGQTYFKMDLJIDL 479
Qy 481 ATSLFSASTSSNIREI-----IVENYIHMSIGFTKVSSYSLSLQKVSRLV 530
Db 480 ATSMFSASASRSRJRQINVKDDEDMFIVTNYKDMMSIGFSEVSSYSPSIFKRVSLRV 539
Qy 531 LNLSDIKLKOPSSIGDLVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 590
Db 540 LNLNSEREOQPSVGDVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 598
Qy 591 KETSKLGSRLNLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQCLGELRLNLYG 650
Db 599 KQTSKLGSLRLVLDHC-PLTSMRPRIGLTLCTKLGLGFVVG-ERKGYQLGELRLNLYG 656
Qy 651 SIEITHLERVKNDDAKANISAKENHLSLSKMDDEPRPRIYSEKYEVLAKPHSNL 710
Db 657 AISITHLERVKNDDAKANISAKANHLSLSMSWD---RPRRYSEEVKVLAKPHSNL 713
Qy 711 TCLTIRGFRGRLPDMNHSVLKNVSIETISCKNCSCLPPRGLPCLKSLRLMRSAY 770
Db 714 KYLEIIFDGCCLPDMNHSVLKNVSIETISCKNCSCLPPRGLPCLKSLRLMRSAY 773
Qy 771 EYV-DSGFPTRRRPPSLRKLNIRFNGNLKGLKKEGEOCVLEIEIKCCPMFVPTLS 829
Db 774 EYVEDSGFLTRRRPPSLRKLNIGFCNLKGLQRMKGEOQFVLEBMKISDCPMVPTLS 833
Qy 830 SVKLVVSGDKSDAIGFSSISNLMAJLSLQIRYNKEDASLPEMFKSLANIKYINISYF 889
Db 834 SVKLEIWMGE-ADAGGSSISNLSTLTKIFSNHTVLSLEEMFKNENIYLSVSFL 892
Qy 890 NLKELPTSLASLNKLEIHSYALSLPREGVGLSLTOLSTYCEMLQCLPEGIOH 949
Db 893 NLKELPTSLASLNKLEIHSYALSLPREGVGLSLTOLSTYCEMLQCLPEGIOH 952
Qy 950 LTLATNLVSECPPLAKRCEKIGEDWYKIAHPRVFIY 988
Db 953 LTLTSLKIRGCPOLIKRCEKIGEDWYKISHIPVNIY 991

RESULT 6

US-10-360-522-56
; Sequence 56, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360, 522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 992
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; OTHER INFORMATION: RGL1-b1b
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(992)
US-10-360-522-56

Query Match 72.8%; Score 3730.5; DB 15; Length 992;
Best Local Similarity 74.7%; Pred. No. 1.1e-281;

Matches 746; Conservative 92; Mismatches 142; Indels 19; Gaps 8;

Qy 1 MAEAFLOVLIDNLVCFIOGELGLILGFKDPEFKLQSTFTTIQAVLEDAQKKQKOKALEN 60
Db 1 MAEAFLOVLIDNLVCFIOGELGLILGFKDPEFKLQSTFTTIQAVLEDAQKKQKOKALEN 60
Qy 61 WLQKLNAAVYBADDILDECKTEADIRQKNRYGCYHPNVITFRHKGIRMKIMEKLDVI 120
Db 61 WLQKLNAAVYBADDILDECKTEA-ARFKQAVLGRYHPRTITFCYKVGKRMKEMEKDAI 119
Qy 121 AAEIKTHLDEKTERQVATQGTQVLANEPOVYGRDKEDIVKILINNVNAQTLPLP 180
Db 120 AAEIRNFILDERIIRERQARQGTQVLEPRYGRKEDEDIKILINNVYSEKVPALP 179
Qy 181 ILGNGGLGKTLAQMVPNDORVIEHPHKIWCYSEBDEKRLIKELIESIEKSLGMD 240
Db 180 ILGNGGLGKTLAQMVPNDORITHEFNKIVWCYSDPDEKRLIKALIESIEKSLGMD 239
Qy 241 LAPLOKLRDLNKGKYLVLVDVWNEBQDKMAKLRQVLKYGASAVLITTRLEKVGSI 300
Db 240 LAPLOKLRDLNKGKYLVLVDVWNEBQDKMDLRAVLKIGAGASLITTRLEKVGSI 299
Qy 301 MGTLOPYELSLSGEDCMLFMQRAFGHQBENLNVAIGEYIKKCGVPLAKTLCGI 360
Db 300 MGTLOPYELSLSGEDCMLFMQRAFGHQBENLNVAIGEYIKKCGVPLAKTLCGI 359
Qy 361 LRFREEROMEVHVDSEIWMKPOESSITPLRLSYHNLPLDLNOCFTYCAVPFDTEME 420
Db 360 LRFRESEMEVHVDSEIWMKPOESSITPLRLSYHNLPLDLNOCFTYCAVPFDTEME 419
Qy 421 KGNLSIMAHGFLISKGNLELVNGVNMELYLRSFQOIEYKSGQTYFKMDLJIDL 480
Db 420 KEYLIALMAMHAFILSKGNMELVDGNEVMNELYLRSFQOIEYKSGQTYFKMDLJIDL 479
Qy 481 ATSLFSASTSSNIREI-----IVENYIHMSIGFTKVSSYSLSLQKVSRLV 530
Db 480 ATSMFSASASRSRJRQINVKDDEDMFIVTNYKDMMSIGFSEVSSYSPSIFKRVSLRV 539
Qy 531 LNLSDIKLKOPSSIGDLVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 590
Db 540 LNLNSEREOQPSVGDVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 598
Qy 591 KETSKLGSRLNLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQCLGELRLNLYG 650
Db 599 KQTSKLGSLRLVLDHC-PLTSMRPRIGLTLCTKLGLGFVVG-ERKGYQLGELRLNLYG 656
Qy 651 SIEITHLERVKNDDAKANISAKENHLSLSKMDDEPRPRIYSEKYEVLAKPHSNL 710
Db 657 AISITHLERVKNDDAKANISAKANHLSLSMSWD---RPRRYSEEVKVLAKPHSNL 713
Qy 711 TCLTIRGFRGRLPDMNHSVLKNVSIETISCKNCSCLPPRGLPCLKSLRLMRSAY 770
Db 714 KYLEIIFDGCCLPDMNHSVLKNVSIETISCKNCSCLPPRGLPCLKSLRLMRSAY 773
Qy 771 EYV-DSGFPTRRRPPSLRKLNIRFNGNLKGLKKEGEOCVLEIEIKCCPMFVPTLS 829
Db 774 EYVEDSGFLTRRRPPSLRKLNIGFCNLKGLQRMKGEOQFVLEBMKISDCPMVPTLS 833
Qy 830 SVKLVVSGDKSDAIGFSSISNLMAJLSLQIRYNKEDASLPEMFKSLANIKYINISYF 889
Db 834 SVKLEIWMGE-ADAGGSSISNLSTLTKIFSNHTVLSLEEMFKNENIYLSVSFL 892
Qy 890 NLKELPTSLASLNKLEIHSYALSLPREGVGLSLTOLSTYCEMLQCLPEGIOH 949
Db 893 NLKELPTSLASLNKLEIHSYALSLPREGVGLSLTOLSTYCEMLQCLPEGIOH 952
Qy 950 LTLATNLVSECPPLAKRCEKIGEDWYKIAHPRVFIY 988
Db 953 LTLTSLKIRGCPOLIKRCEKIGEDWYKISHIPVNIY 991

RESULT 7

US-10-360-522-62

```
/ Sequence 62, Application US/10360522
/ Publication No. US20030221215A1
/ GENERAL INFORMATION:
/ APPLICANT: Vossen v.d.; Edwin A.G.
/ TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
/ TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
/ FILE REFERENCE: U 014413-9
/ CURRENT APPLICATION NUMBER: US/10/360,522
/ PRIOR FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: EP 02075565.8
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: PCT/NI03/00091
/ PRIOR FILING DATE: 2003-02-07
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 62
/ LENGTH: 945
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: alignment
/ FEATURE:
/ OTHER INFORMATION: SH20-tub
/ NAME/KEY: SITE
/ LOCATION: (1)..(945)
/ US-10-360-522-62
```

```
Query Match 72.3%; Score 3708.5; DB 15; Length 945;
Best Local Similarity 75.8%; Pred. No. 5,5e-280;
Matches 738; Conservative 82; Mismatches 120; Indels 33; Gaps 7;
```

```
QY 1 MAEAFQVILNLTCTFIOGELILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
DB 1 MAEAFQVILNLTCTFIOGELILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
QY 61 WLOKNAAYEADDLDECKTEAPIRQKNKYGCHPVNITFRHKGKMKIMEKLDVI 120
DB 61 WLOKNAAYEADDLDECKTEAPIRQKNKYGCHPVNITFRHKGKMKIMEKLDVI 117
QY 121 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 180
DB 121 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 177
QY 118 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 177
DB 118 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 177
QY 181 IIGMGLGKTTTAAQVAVNDQVTEHHPKIKWTCSVEDPFEKRLIKEIVESTIEKSLGMD 240
DB 181 IIGMGLGKTTTAAQVAVNDQVTEHHPKIKWTCSVEDPFEKRLIKEIVESTIEKSLGMD 240
QY 178 IIGMGLGKTTTAAQVAVNDQVTEHHPKIKWTCSVEDPFEKRLIKEIVESTIEKSLGMD 237
DB 178 IIGMGLGKTTTAAQVAVNDQVTEHHPKIKWTCSVEDPFEKRLIKEIVESTIEKSLGMD 237
QY 241 LAPLOKRLDLNGKKYLLVLDVNNBEDQDKWAKLROYLVKVGASGVLTTRLEKVGSI 300
DB 241 LAPLOKRLDLNGKKYLLVLDVNNBEDQDKWAKLROYLVKVGASGVLTTRLEKVGSI 300
QY 238 IASFOKLLQOLNGKRYLLVLDVNNBEDQDKWAKLROYLVKVGASGVLTTRLEKVGSI 297
DB 238 IASFOKLLQOLNGKRYLLVLDVNNBEDQDKWAKLROYLVKVGASGVLTTRLEKVGSI 297
QY 301 MGTLOPYELSNLSQEDCWLLEFQARFGHQBESILPALRLSTVHNLPLRQCFNYCAVFPDTEME 420
DB 301 MGTLOPYELSNLSQEDCWLLEFQARFGHQBESILPALRLSTVHNLPLRQCFNYCAVFPDTEME 417
QY 298 MGTLOPYELSNLSQEDCWLLEFQARFGHQBESILPALRLSTVHNLPLRQCFNYCAVFPDTEME 357
DB 298 MGTLOPYELSNLSQEDCWLLEFQARFGHQBESILPALRLSTVHNLPLRQCFNYCAVFPDTEME 357
QY 361 IAPKKEERQWERYRSEIYKLEQOESSILPALRLSTVHNLPLRQCFNYCAVFPDTEME 420
DB 361 IAPKKEERQWERYRSEIYKLEQOESSILPALRLSTVHNLPLRQCFNYCAVFPDTEME 417
QY 358 IAPKKEERQWERYRSEIYKLEQOESSILPALRLSTVHNLPLRQCFNYCAVFPDTEME 417
DB 358 IAPKKEERQWERYRSEIYKLEQOESSILPALRLSTVHNLPLRQCFNYCAVFPDTEME 417
QY 421 KGNLISLMAAHGFLSKGNLELVNNGEVENNELYLRSFQOELIVKSGQTYFPMHDLIHD 480
DB 421 KGNLISLMAAHGFLSKGNLELVNNGEVENNELYLRSFQOELIVKSGQTYFPMHDLIHD 477
QY 481 ATSLFSASTSSNIREIIVENYTHMMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 540
DB 481 ATSLFSASTSSNIREIIVENYTHMMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 478 ATSLFSASTSSNIREIIVENYTHMMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
DB 478 ATSLFSASTSSNIREIIVENYTHMMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 541 LRSSTGDLVHLAYNLSTGTSRSLPNOICXKONOTLHLGCHSLCCLPKESKXLSLR 600
DB 541 LRSSTGDLVHLAYNLSTGTSRSLPNOICXKONOTLHLGCHSLCCLPKESKXLSLR 600
QY 538 LRSSTGDLVHLAYNLSTGTSRSLPNOICXKONOTLHLGCHSLCCLPKESKXLSLR 597
DB 538 LRSSTGDLVHLAYNLSTGTSRSLPNOICXKONOTLHLGCHSLCCLPKESKXLSLR 597
QY 601 NILLDGCGYGLTGWPPRIGSLTCLKTLISRFVVGIOKSCOLGELRNINLVGSIETHLERV 660
DB 601 NILLDGCGYGLTGWPPRIGSLTCLKTLISRFVVGIOKSCOLGELRNINLVGSIETHLERV 660
```

```
DB 598 NILDHGHRILTRPPRIGSLTCLKTLIGQSVK-RKKGYQLGELGSLNIGSIXISHLERY 656
QY 661 KNDMDAKENALSAKENIHSIMKWDDEDRIRIESKEVLEALXPHSNLTCLTIGFPG 720
DB 661 KNDMDAKENALSAKENIHSIMKWDDEDRIRIESKEVLEALXPHSNLTCLTIGFPG 715
QY 657 KNDKEAKENALSAKENIHSIMKWDDE-PRHSESEVEVLEALXPHSNLTCLTIGFPG 715
DB 657 KNDKEAKENALSAKENIHSIMKWDDE-PRHSESEVEVLEALXPHSNLTCLTIGFPG 715
QY 721 IRLPDWNNHSLVKNVYSIEIISCKNCSCLPPFEGELPCLSLBIRMSAB-VEX-----VDS 775
DB 721 IRLPDWNNHSLVKNVYSIEIISCKNCSCLPPFEGELPCLSLBIRMSAB-VEX-----VDS 775
QY 776 GFTTRRRPRLKRLNIREPNLKLKKGEBQCPVLEIEIKCCPMFVPLTSSVKKV 835
DB 776 GFTTRRRPRLKRLNIREPNLKLKKGEBQCPVLEIEIKCCPMFVPLTSSVKKV 826
QY 776 GFTTRRRPRLKRLNIREPNLKLKKGEBQCPVLEIEIKCCPMFVPLTSSVKKV 826
DB 776 GFTTRRRPRLKRLNIREPNLKLKKGEBQCPVLEIEIKCCPMFVPLTSSVKKV 826
QY 836 VSGKSAIGFSSSNLMATLSQIRNKEADSLPEEMFSLNMLKYINISFYFNKELP 895
DB 836 VSGKSAIGFSSSNLMATLSQIRNKEADSLPEEMFSLNMLKYINISFYFNKELP 872
QY 827 -----PINKALTSINISDNKEATSPPEEMFSLNMLKYINISFYFNKELP 872
DB 827 -----PINKALTSINISDNKEATSPPEEMFSLNMLKYINISFYFNKELP 872
QY 896 TSLASLNAKLHLEHSCYALSPPEBGVGLISLTQSYTYCEMLQCLPGLQHTALYN 955
DB 896 TSLASLNAKLHLEHSCYALSPPEBGVGLISLTQSYTYCEMLQCLPGLQHTALYN 932
QY 873 TSLASLNAKLHLEHSCYALSPPEBGVGLISLTQSYTYCEMLQCLPGLQHTALYN 932
DB 873 TSLASLNAKLHLEHSCYALSPPEBGVGLISLTQSYTYCEMLQCLPGLQHTALYN 932
QY 956 LSVFCEPTLAKC 968
DB 956 LSVFCEPTLAKC 945
QY 933 LKINGCPQLIKRC 945
DB 933 LKINGCPQLIKRC 945
```

```
RESULT 8
US-10-360-522-59
```

```
/ Sequence 59, Application US/10360522
/ Publication No. US20030221215A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Vossen v.d.; Edwin A.G.
/ TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
/ TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
/ FILE REFERENCE: U 014413-9
/ CURRENT APPLICATION NUMBER: US/10/360,522
/ PRIOR FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: EP 02075565.8
/ PRIOR FILING DATE: 2002-02-08
/ PRIOR APPLICATION NUMBER: PCT/NI03/00091
/ PRIOR FILING DATE: 2003-02-07
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 59
/ LENGTH: 945
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: alignment
/ FEATURE:
/ OTHER INFORMATION: SH10-tub
/ NAME/KEY: SITE
/ LOCATION: (1)..(945)
/ US-10-360-522-59
```

```
Query Match 71.3%; Score 3654.5; DB 15; Length 945;
Best Local Similarity 75.3%; Pred. No. 9e-276;
Matches 730; Conservative 72; Mismatches 142; Indels 25; Gaps 5;
```

```
QY 1 MAEAFQVILNLTCTFIOGELILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
DB 1 MAEAFQVILNLTCTFIOGELILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
QY 61 WLOKNAAYEADDLDECKTEAPIRQKNKYGCHPVNITFRHKGKMKIMEKLDVI 120
DB 61 WLOKNAAYEADDLDECKTEAPIRQKNKYGCHPVNITFRHKGKMKIMEKLDVI 119
QY 121 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 180
DB 121 AAEIKFHLDEKTERIOVATROTGFVLNBPQVYGRDKEDEIVKILINNVSNAQTLPLY 179
```

```

Qy 181 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKS-IGGM 239
Db 180 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKS-IGGM 239
Qy 240 DLAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 299
Db 240 DLAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 299
Qy 300 IMGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 359
Db 300 IMGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 359
Qy 360 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 419
Db 360 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 419
Qy 420 EKGNIISLMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 479
Db 420 EKGNIISLMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 479
Qy 480 LATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 539
Db 480 LATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 539
Qy 540 QLPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Db 540 QLPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Qy 600 RNLFFHGCDELNSMPRIGSLTFLKTLKMICCGI-KKGYQGLKRDVNLVYSIEITHLER 658
Db 600 RNLFFHGCDELNSMPRIGSLTFLKTLKMICCGI-KKGYQGLKRDVNLVYSIEITHLER 658
Qy 660 VKNDMAKEANLSAKENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGRFR 719
Db 660 VKNDMAKEANLSAKENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGRFR 719
Qy 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAEVEYDSGPT 779
Db 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAEVEYDSGPT 779
Qy 748 RRRPPLSRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCPMFVITPLSSVKLVVSGD 839
Db 748 RRRPPLSRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCPMFVITPLSSVKLVVSGD 839
Qy 840 KSDAIGSSSISNLMALTSLOIRYNKEDASLPBEMFKLANIKYINISFYMKELPSTLA 899
Db 840 KSDAIGSSSISNLMALTSLOIRYNKEDASLPBEMFKLANIKYINISFYMKELPSTLA 899
Qy 900 SLNALKHLIHSYALBSLPBEGVGLSLTQLSITYCEMLQCLPEGLQHLTALTNLSVE 959
Db 900 SLNALKHLIHSYALBSLPBEGVGLSLTQLSITYCEMLQCLPEGLQHLTALTNLSVE 959
Qy 960 FCPTLAKRC 968
Db 960 FCPTLAKRC 968
Qy 937 RCPQLIKRC 945
Db 937 RCPQLIKRC 945

```

```

; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 61
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; NAME/KEY: SITE
; LOCATION: (1)..(972)
; US-10-360-522-61

Query Match 70.7%; Score 3625; DB 15; Length 972;
Best Local Similarity 74.2%; Pred. No. 1.9e-273;
Matches 726; Conservative 92; Mismatches 143; Indels 18; Gaps 7;

Qy 1 MAEAFLOVLDNLTCFTIGELIGLGFKEPEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
Db 1 MAEAFLOVLDNLTCFTIGELIGLGFKEPEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
Qy 61 WLQTLNAAVEADDIIDECKTEADIROKKNGCYHPNVITFRHKIGKMKKIMEKLDVI 120
Db 61 WLQTLNAAVEADDIIDECKTEADIROKKNGCYHPNVITFRHKIGKMKKIMEKLDVI 120
Qy 121 AAERIKHDEBRTERVOATROGCVLNEPOVGRDKEKEIVKILINNNAQTLPLP 180
Db 121 AAERIKHDEBRTERVOATROGCVLNEPOVGRDKEKEIVKILINNNAQTLPLP 180
Qy 120 ABERRNHDEBRTERVOATROGCVLNEPOVGRDKEKEIVKILINNNAQTLPLP 179
Db 120 ABERRNHDEBRTERVOATROGCVLNEPOVGRDKEKEIVKILINNNAQTLPLP 179
Qy 181 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKSIGMD 240
Db 181 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKSIGMD 240
Qy 180 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKSIGMD 239
Db 180 ILGNGGLGKTTLAQVFNDOQVIEHFPKINI CVSEDFENKRLIKEIVESIEEKSIGMD 239
Qy 241 LAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 300
Db 241 LAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 300
Qy 240 LAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 299
Db 240 LAPLOKRLDLNGKRYFLVLDVWNEODQKMAKLOVLYKVGASGAVLTTRLEKVS 299
Qy 301 MGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 360
Db 301 MGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 360
Qy 300 MGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 359
Db 300 MGTLOPELISNLSEDCWLLFMORAFGHOEININVAIGKEIYKKGGLVLAAXTLG 359
Qy 361 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 420
Db 361 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 420
Qy 360 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 419
Db 360 ILRFKREEROMEHVDSEIWLKPOEESILPALRLSYHHLPLDLRQCFTYCAVFPKOTEM 419
Qy 421 KGNILSLMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 480
Db 421 KGNILSLMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 480
Qy 420 KEYILALMMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 479
Db 420 KEYILALMMAHGFILSKGNELENGNEVWNEIYLSRFOEIEVKSQTYFKMHDLIHD 479
Qy 481 ATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 530
Db 481 ATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 530
Qy 480 ATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 529
Db 480 ATSLFASSTSSSNIREIYVNIYHMSIGFTKVSSSYSLHLOKQVSLRVLNLSIDTLK 529
Qy 531 LNLSDIKLOPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLP 590
Db 531 LNLSDIKLOPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLP 590
Qy 540 LNLSDIKLOPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLP 598
Db 540 LNLSDIKLOPSSIGDLVHLRYLNLGNTSIRSIPNOLCKLQNLQTLDLHGCHSLCCLP 598
Qy 591 KETSIGLSTLNLGCGYGLTCLKTLTSLRFPVVGIOKSCQGLGELRLNLVYG 650
Db 591 KETSIGLSTLNLGCGYGLTCLKTLTSLRFPVVGIOKSCQGLGELRLNLVYG 650
Qy 599 KOTSICLSTLNLVLDHSCPLTSMPPRIGLTLCTLTGAFVVG-BRKGYQGLGELRLNLVYG 657
Db 599 KOTSICLSTLNLVLDHSCPLTSMPPRIGLTLCTLTGAFVVG-BRKGYQGLGELRLNLVYG 657
Qy 651 SIEITHLERKYNMDAENALSAENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGR 710
Db 651 SIEITHLERKYNMDAENALSAENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGR 710
Qy 658 AISTHLERKYNMDAENALSAENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGR 714
Db 658 AISTHLERKYNMDAENALSAENHSLSMKDDDERPRIYSESEVLEALPKHSNLTCTITGR 714
Qy 711 TCTITGRFGRIBLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAE 770
Db 711 TCTITGRFGRIBLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAE 770
Qy 715 KYLEIIDPFGCLPDMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAE 774
Db 715 KYLEIIDPFGCLPDMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLLEMRGSAE 774
Qy 771 EYV-DSEFPTRRRPPLSRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCPMFVITPLS 829
Db 771 EYV-DSEFPTRRRPPLSRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCPMFVITPLS 829

```



```

Db 775 EYEDSGCLTRRRPPLSLKHLIGFPCNLKGLQRMKGAQFVVLPEMKISDCPMFVPTLS 834
Qy 830 SVKTLVWVGDXSDAIGFSSISNLMLATSLQIRYNKEDASLEPEMFKSIANKYINISFYF 889
Db 835 SVKLEIWE-ADAGGASSISNLSTLTKIFSNHTVSLLEEMFKNENLIYISVSFLE 893
Qy 890 NLKELPTSLASLNALKHLIEHSVCYALBESLPEGVKGLISLQOLSTYCEMLQCLPEGLOH 949
Db 894 NLKELPTSLASLNALKHLIDIRCYALESLEPEBGLSLSTLELFEVHCNMLKCLPEGLQH 953
Qy 950 LIALNLSEVFCPTLAKRC 968
Db 954 LITLITSLKIRGCPOLIKRC 972

RESULT 10
US-10-360-522-57
; Sequence 57, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1040
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; NAME/KEY: SITE
; LOCATION: (1)..(1040)
US-10-360-522-57

Query Match 69.1%; Score 3542; DB 15; Length 1040;
Best Local Similarity 68.4%; Pred. No. 6.2e-267;
Matches 716; Conservative 105; Mismatches 160; Indels 66; Gaps 10;

```

```

Qy 307 YELSNLSOEDCWLLFNQRAFQHOEINLNLVAGKEIVKCGGVPLAAKTLGGILFRKE 366
Db 360 YHLSNLSPHDSLLFPQRAFGQCKEANPNLVAGKEIVKCGGVPLAAKTLGGILFRKE 419
Qy 367 EROWEHYRDEIWKLPQESSILPARLSYHNLPLRQCFYCAVPPDTEBKNLIS 426
Db 420 ESEWEHNRDEIWSLPQDESSILPARLSYHNLPLRQCFYCAVPPDTEBKNLIT 479
Qy 427 LMAHGFILSKNLEENYVNEVWNELYLSFQSEIVKSGQGYFFOMDLIHDLSLFS 486
Db 480 LMAHGFILSKNLEEDVNEVWNELYLSFQSEIVKSGQGYFFOMDLIHDLSLFS 539
Qy 487 ASTSSNIREIYENYIHMSIGFTKVSSYSLSHLOKQVSLRYNLSDIKOLQESSIG 546
Db 540 ASASCGNIREINVDYKHVVISGFAAVSSSPSLKKFVSLRYNLSDIKOLQESSIG 599
Qy 547 DLVHRLYLNLSGNTSIRSLPNOCLQNLQTLHDGHSICCLPKETSUKLSRLNLLDG 606
Db 600 DLVHRLYLNLSGNTSIRSLPNOCLQNLQTLHDGHSICCLPKETSUKLSRLNLLDG 658
Qy 607 CYGLTCMPRIIGSLTCLTSRFRVVGIOKSCQGLGELRNILYGSIEITHLEKVDMDA 666
Db 659 C-PLTSTPRPIGLTCLTKTIGFPIVG-SKKGYQGLKNNLNGSISITHLERKNDTDA 716
Qy 667 KEANLSAKENLHSLMKWDDERPRIYESKRYVLEALXPHSNLTCUTIRGFRGILPDW 726
Db 717 -EANLSAKENLHSLMKWDDERPRIYESKRYVLEALXPHSNLTCUTIRGFRGILPDW 774
Qy 727 MNHSLVKNVSIETISCKNCSCLPPFGLPCLSLBEMRGAEEVYD-----SGPPTRR 781
Db 775 INHSLVKNVSVKSKCKNCLCPPFGLPCLSLBEMRGAEEVYD-----SGPPTRR 834
Qy 782 RFPSLRKINIREFNLKGLKKEGEOCVLEIEIKCPMPVYIPYLSYKLVSGDGS 841
Db 835 SFPSLKRLIMFPRLKGLKKEGEOCVLEIEIKCPMPVYIPYLSYKLVSGDGS 893
Qy 842 DAIPSSISNLMALTSQIRYNKEDASLEPEMFKSIANKYINISFYFNLPTSLASL 901
Db 894 NTRGLSSISNLSLTSIRIGANYRATSLPEEMFSLNLFSPDRKMLKDLPTSLASL 953
Qy 902 NALHRLHSCYALBESLPEGVKGLISLQOLSTYCEMLQCLPEGLOHNTALNLSVEFC 961
Db 954 NALHRLHSCYALBESLPEGVKGLISLQOLSTYCEMLQCLPEGLOHNTALNLSVEFC 1013
Qy 962 PTLAKRCEKIGEDWYKIAHPRVFIY 988
Db 1014 PEVEKRCDEIGEDWYKIAHPRVFIY 1040

RESULT 11
US-10-437-182454
; Sequence 182454, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182454
; LENGTH: 1110
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

```


OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1.pep
US-10-437-963-182454

Query Match 29.6%; Score 1517; DB 16; Length 1110;

Best Local Similarity 34.9%; Pred. No. 7e-109; Indels 206; Gaps 35;
Matches 396; Conservative 189; Mismatches 345; Indels 206; Gaps 35;

```
4 AFLQVLLDNLTCFIGELGLIL---GPKDFEKLQSTFTTIOAVLEDAQKQKQKALEN 60
9 AFMQLTFOQLS---EATLDHFIWMGIGHGKLESISTLSQAFIDDAEKKLTALASRG 65
61 WLQKNAAYEADTILDECKTEAPIRQKKNYGCVHPNVITF-----RHKIGR 109
66 WLAKIKDIAVDLDDLDSDYSKAS-WRMKQRC-VIFPTVASFLSSPLSLNLYQHRIRHK 122
110 MKKIMEKIDVIAERIKPHLDBRTIERQVATR---QTGVNLEPQVQDKDKKDIYK-I 165
123 INILERLDKIAQEBDTTGLQMICEMRRYDTSERQSSLDVSAVFGEREDEEMVRLV 182
166 LINNVSNQTLFVLPILGWSGLGKTTTLAQMVFNDDRVIEHFPRKIWICVSEDFNEKRLIK 225
183 LSDNHNCGNLCVIVVGWGLGKTTLMQVYHDRVHFPRLIWIYVSEDFDKRLTQ 242
226 EIVSEIE-EKSLGMDLAPLQKKLBDLNGKYYLLVLDVNNEDQKNAKLQVLKVAS 284
243 ETLASDYDQSVASTNMNMLQETLSRVLRGKRYLLVLDVNNEDDKMHSYRAALISGAF 302
285 GASVLTTRLEKVGSIKGTLOPYELSNISQEDCMLLFQORAF-----GHQEIYMLNVA 338
303 GSKIVVTSRNENVGRIWGIEIPYKLOKLSDDSVSFSGHARDDCSAHPF-----LEA 357
339 IGKEIVKCKGCVPLAAKTLGGLRFRKEERQWEHREDEIMWLPOESSILPALRLSYNH 398
358 IGMELVAKLKLPLASKLGLSLPCKTDBEKKDILQNDIMELKADKNIIIPALRLSYNH 417
399 LPLDROCFYCAVFPKOTEMKGNLISLMAHGFILSKNLELVNENVEWNLVLRSF 458
418 LPHLKQCFACSVYPKDYFRREKLVKIMLGLIRQSRKKRMBDTGNAYNELLSRSF 477
459 FOEIEVKSQGYTFKMHDLIDLATSL----- 484
478 FQPYE---NNYVMDAMHDLAKSISMEDCDHLDYGRHDNAIKTRHLSPCKDAKCMH 532
485 FSASTSSNIREIYENYIHMMSIGFTKVSYSLSHLQKFSYLRVNLSDIKLQKLPSS 544
533 FNPLYGFKRLTLT---IH---GYKSRMSQLPHGLPMKLELYLRVLDHMGGLKELPES 585
545 IGDVHLRLYVNLSGTISRSLPNQCLQNTQTLDLHGCHSLCCLPKETSKLGLSLRL-- 602
586 IGNLKQALFLDLS-STELIETLPASLVKYNQILKSDCNFLREVPQGITRLINRHLBA 644
603 ---LIDGCTGLTCLMPRIIGSLTCLTSLRFVVGIOKKS-CQLGEIRNLN-LYGSIEITHL 657
645 STRLSLRHIG-----IGSLVLCQLEIEFPVY--QKRSGHNVTEILANNDELOGLSIRGL 695
658 ERYKNDMAKREANLSAKENHLSLMSKMPDD--ERRPRIESEKVEYLEALKPHSNVTCITI 715
696 NNVPNGDVAVCALKKKEHLKTLHLIMDECSNP---SEQOEVLBGLPDLIDKELYI 751
716 RGFRIQLRPLDMNHNVLKVVSIIEISCKNSCLPPFGLPCLKSLIELMRSGAEVEYDS 775
752 KGFPEVRFPMSLASFPLKLOTIHCNCRS--TRLPALQOLPFLAKLYI-AGVTBVTQJSS 809
776 ---GPTTRRRPPLSLKLNIREFGNKLGLKKEGEGOCVLEIEIKCCPMF--VITPLSS 830
810 EFTGQCPKGFPADELLELDMPNLSEWIFDVAQOLFQOLTELGLIKCPOLKPKPIPIST 869
831 VKKLVASGDKSDAIGFSSISNLM-----ALPSL 858
870 LRTWLISSES-----GLSELPLEONNSCPSSPTSLYINDCPNLISLRVGLLAIRPPLKSL 924
899 QIRYNKEDASLPEEMFKSLANLKYLNISFY-----FNLKE---LPTS----- 897
```

```
DB 925 TIHCEGLVLSPECFRPLSLRSLSLH--YECPLVPWTALEGLLPTSIEDIRLNSCTP 982
QY 898 -----IASIANLKLHEIHSYALBSLPEEGVGLSLTQLSITYCEMLQCLPEGLQH 949
DB 983 IASVINGLSTLPHLRHREIADCEPDINFPBGLPH--TLQPLFISCCDDIQCLPGLH 1040
QY 950 LTA-----LTNLSVEBCPTLAKCEKIGEDWYKIAHI 982
DB 1041 ISSLETLRISNCPGVESLPKEGLPMGLNELYIKGCPQIKQCCQCGG-GEYHAKIAHI 1095
```

RESULT 12

US-10-437-963-153490

/ Sequence 153490, Application US/10437963

/ Publication No. US20040123343A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David R.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ APPLICANT: Mu, Wei

/ APPLICANT: Boukharov, Andrey A.

/ APPLICANT: Barbazuk, Brad

/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

/ FILE REFERENCE: 38-21(53221)B

/ CURRENT APPLICATION NUMBER: US/10/437, 963

/ CURRENT FILING DATE: 2003-05-14

/ NUMBER OF SEQ ID NOS: 204966

/ SEQ ID NO 153490

/ LENGTH: 1222

/ TYPE: PRT

/ ORGANISM: Oryza sativa

/ FEATURE:

/ OTHER INFORMATION: clone ID: PAT_MRT4530_53440C.1.pep

US-10-437-963-153490

Query Match 29.6%; Score 1516; DB 16; Length 1222;

Best Local Similarity 32.9%; Pred. No. 9.7e-109; Indels 284; Gaps 35;
Matches 408; Conservative 194; Mismatches 355; Indels 284; Gaps 35;

```
QY 1 MAE---AFLQVLLDNLTCFIGELGLILGFKDFEKLQSTFTTIOAVLEDAQKQKQK 57
DB 1 MAELSLALPLRLKKAABESLSTERSFIGIERRSELYTLLANQVINDBDQASKKPA 60
QY 58 IENWLQKNAAYEADTILDECKTEAPIRQKKNYGCVHPNVITFRHKIG 107
DB 61 VKSWIATKLTLAACADALDELHAYELRCEALRGHKNIGVRAFPSSHVPLLFKYRIG 120
QY 108 KRMKIMEKIDVIAERIKF-----HDBRTIERQVATRGTFVANEPOVYGRDKEXD 160
DB 121 KRLQOIERIDQVLSQNRKGFNLCSMPVDER-----MOTSYVDEBEVIGRDKERD 172
QY 161 EIVKLINNVSNQTLFVLPILGWSGLGKTTTLAQMVFNDDRVIEHFPRKIWICVSEDFNE 220
DB 173 EIVMMLS--AETBELILPLVIGIGSLGKTTLAQVAVNDKVKVHFGKHMVVCSENFVS 230
QY 221 KRLIKEIVESI--EKSIGMDLAPLQKKLBDLNGKYYLLVLDVNNEDQKNAKLQV 278
DB 231 PVIYKGIIDTIAIGNDGCLKFEDNELLOQLREELGQKRYLLVLDVNNEDQKNAKLRTL 290
QY 279 LKVASGASVLTTRLEKVGSIKGTLOPYELSNISQEDCMLLFQORAFGHQOEINLNUVA 338
DB 291 LGSCGMSAAVVTTRNVKVASIMESISPLCLENINPDSWIVFSRRAFGTGVETPELVE 350
QY 339 IGKEIVKCKGCVPLAAKTLGGLRFRKEERQWEHREDEIMWLPOESSILPALRLSYNH 398
DB 351 VGRKIVKCGGLPLATISMGALMSTKQETDMLSTILESNTM---DESSQLPLASLGYKN 407
QY 399 LPLDROCFYCAVFPKOTEMKGNLISLMAHGFILSKNLELVNENVEWNLVLRSF 458
DB 408 LPSHMQCFACFAVFPQVDEIDKODLILHWVNSGFIPIKSKSDIEBGNHVFMLVRSF 467
```


Db 859 LHPSTLVELKIS-----EAGFSVLPVHAPRFLPSLRLQIHKCPNLTSLQOGLSQQLS 913
 Qy 870 -----PEEMFKSLANKYLNISFYFNKLPTS----- 897
 Db 914 ALQOLTTNCPELHPPEEGKRTLTALQSLHI---YDCPRLATVHEHRLPRMIEDLRIT 970
 Qy 898 -----LASLNAIKHLEIHS CYALESLEPPE-----GVKGLIS----- 928
 Db 971 SCSTNIINPLDELNELFPLKVLVADCVSLNTPPEKLPATLKLEIFNCSNLASLPACLO 1030
 Qy 929 ---LTLSTIYCEMLQCLP-EGLOHTALTNLVSFPCPTLAKRCEKIGEDWYKIAHI 982
 Db 1031 EASCLTWTITNVCYSIKCLPAHGLP--LSLEELYKECPFLAERCQENSGEDWPKXISHI 1087

RESULT 14
 US-10-437-963-199180
 ; Sequence 199180, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Mu, Mei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 199180
 ; LENGTH: 1401
 ; TYPE: PRP
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: clone ID: PAT_MRT4530_9476C.1.pep
 ; US-10-437-963-199180

Query Match 28.1%; Score 1442.5; DB 16; Length 1401;
 Best Local Similarity 31.6%; Pred. No. 6.5e-103;
 Matches 394; Conservative 189; Mismatches 375; Indels 287; Gaps 32;

Qy 1 MAE---AFLQVLLDNLTCFIOGELGLILGFYDEFEKLOSTFTTIOAVLEDAQKQKDKA 57
 Db 1 MAELLSALLPLALKKAGSLSTBPSFIGIEHRSBELVTLALINQVLYGABEQSKKPA 60
 Qy 58 IENMLQKINAAAYEADLDLDECKTEAPYRQKKKNG-----CYHENVITFRKI 106
 Db 61 VKSWITTKKLKLAACADADALDELHYEA-LRSEALRGHINSGVRAFPSSHNPLLFKYRI 119
 Qy 107 GKRMKIMEXKDVIAERIKFHL-----DERTIERQVATRGQFVNEPOVGRDEX 159
 Db 120 GKQIQOIVEQIDQVLSQNMQFPLNCPMBEDR-----MQYTSYDEQEGIRHKEK 171
 Qy 160 DEIVKILINNVSNQTLFVLPIILGWLGLKTTLAQMVNDQVLEHFPKIMICVSEDPN 219
 Db 172 DEFTHMILS--AKSDKLLILPIVIGIGLKTTLAQVLVNDVKVKAHFGKHMVVCSENF 229
 Qy 220 EKRLIKEIVESI--EKSLSGMDLAPLOKLRDLINGKKLYLLVDVNNEDQKRAKRO 277
 Db 230 VPDIVKGIIDALIGDCIKSDNLELQORLREELSQRYLLVLDVNNEDQKRAKRT 289
 Qy 278 VLKYGASGASVLTTRLEKVSIMGTLOPYELSNLSQDCMLFMQARFGQHEINILVY 337
 Db 290 LLCGKMGSAVAVTTTRNSVASVMCTVPPALBQLSQSDSWTLFERRAFRGVAKSCFV 349
 Qy 338 AIGKEIVKCGVPLAAKTLGGLIFKREBERQWEHVRDSEIWKLPQESSILPALRLSYH 397

Db 350 EIGTKIVQKSGVPLAINSNGGLISRRHSVRDWLAIQNTW----EENNLTLYLSISK 405
 Qy 398 HLPDLRCQFTYCAVFPDTEMENGNLISLMAHGFILSKGNLELVNENVELYRS 457
 Db 406 HLPSPMQCFARFCAVFPDYIDDKDLILMISNGFIPSKETSIDIEBGNVPELILMRS 465
 Qy 458 FFOEIEVKSQ-----TYFKXHDLIHDIATS-----LFSASTSSNIR 495
 Db 466 FFOAKQTRSKEEYIYGKDVTTCKIHDLHMDLAVSISGDECYTLQNLVINEIKPKVH 525
 Qy 496 EIIYENTHMSIGFTK-----VVSYSL--SHIQKPSL-----RYNLSDIKLOL 541
 Db 526 HLV--FPHPKIGFVQRCPIIRSLFSLHKNHNSMKDVFEMVSPCCALGLHICDNRF 582
 Qy 542 PSSIGDVLHLYNLNGTSIRSLPNQICKLONTQTLDLHGCHSLCCPKETSKLSIRN 601
 Db 583 SVBPAYMKHLYLDLS--SSDKITLPEAVSALYNIQILMLNCRGLTHLPDGMKFMISLRH 641
 Qy 602 LLDGCVGLTCMPBRIGSLTCLKTLSPRVVGIQKSCQGLBLRNILNYGSIETHLERVK 661
 Db 642 VYLDGCSLQMPRGLQSLSLFTLWYMG--NESDCRHLKDLGLGKQLIHNLLKVT 700
 Qy 662 NDMAKKANLSAKNLSLSMKWD-----DERPRIYSEKVEVLEAKPHSNTL 710
 Db 701 NPLQAKENLKNKXNLQOLALCWDSRNFTCSHGSADBYQLCRPE--EVEDALKPPNGL 758
 Qy 711 TCLTRGPRGIRLDDMMHNSV-LKNVVSIBIISCKNSCLPPFGBLPCLKLELRGSAE 769
 Db 759 KYLKLQRYMGSNPFMMHEDGYTLQNIYKLSRGSVMCYKLPWPQOLPFLBYLRKR--MER 817
 Qy 770 VEYVDSGPTRR-----PSSLRKINIREFGNIKGLKKEGE--QCPVLEIEIK 818
 Db 818 LKYLCTYRPTDEBYGNQLVFOKLTLSLWMSLEMHXYDQVTSVTPPKDAMEII 877
 Qy 819 CCP-MFYIPTLSSYKVLVSGDSKDALGSSISNLMAL-----TSIQIR-----YKXE 865
 Db 878 DCPKLTALPNVPIILKSLTGNKVLLGLVSGISNLSYLYGASQSSRRVFTLYIYNGE 937
 Qy 866 -----DASL----- 869
 Db 938 REGSTDYDEHILDLHLSMGSLLTKLHLOGPNYAPENVKISGHHMSVQDLVLSGCCFC 997
 Qy 870 -----PEEMFKSL----- 877
 Db 998 IQHGLQSPLEFWISFGLOQLQELIWCDSLTFWEEBFRSLTSLEKLFIVDCNFTGVP 1057
 Qy 878 -----ANLKINISFYFN----- 891
 Db 1058 DRLSARSTDGGPCNLELYLQIDRCPNLVVPPTFNICLRIIVTDSNVLEGLPGGFGCGT 1117
 Qy 892 -----KELPTSLASLNAIKHLEIHS CYALESLEPPEGVKGLISTQLSTIYCEM 939
 Db 1118 LTTVILIGCPSSSLPNSIRCLSNLKSDELTSNNSLSLP-EGMQLNLTLTHPIKCPG 1176
 Qy 940 LQCLPEGL-CHLTALTNLVSFPCPTLAKRCEKIGEDWYKIAHI 983
 Db 1177 ITALPEGLQGRHLGLQFTVDEDCPALARCRG--GDVEXEKYDLP 1220

RESULT 15
 US-10-425-55552
 ; Sequence 55552, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack B
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 01:06:28 / Search time 52 seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAAEFLQVLDNLTCFLQGE.....EKIGEDWYKIAHPRVFY 988

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1240	24.2	1240 2 T06404	resistance complex
2	1212	23.6	1220 2 T06403	resistance complex
3	1020.5	19.9	571 2 T02213	NBS-LRR type resist
4	904	17.6	1802 2 T00020	bacterial blight-r
5	763.5	14.9	852 2 T08416	disease resistance
6	716	14.0	847 2 T12977	hypothetical prote
7	694	13.5	908 2 T48899	disease resistance
8	676.5	13.2	1584 2 F96573	protein F12M16.25
9	671	13.1	906 2 T48898	disease resistance
10	655.5	12.9	835 2 T45590	hypothetical prote
11	655.5	12.8	389 2 T04330	NBS-LRR type resist
12	655	12.8	906 2 G96621	probable disease r
13	649	12.7	797 2 T06219	probable cyst nema
14	635.5	12.4	831 2 T51185	resistance protein
15	632.5	12.3	926 2 T12979	hypothetical prote
16	632	12.3	926 2 A57072	disease resistance
17	625	12.2	820 2 T51186	resistance protein
18	618	12.1	821 2 A86243	hypothetical prote
19	618	12.1	907 2 F96617	probable disease r
20	614.5	12.0	839 2 B96538	hypothetical prote
21	609.5	11.9	1255 2 T06267	nematodes resist
22	585	11.4	269 2 T04394	NBS-LRR type resist
23	573	11.2	900 2 G96617	probable disease r
24	572	11.2	899 2 H96617	probable disease r
25	571.5	11.1	1257 2 T06269	root-knot nematode
26	570.5	11.1	483 2 T02226	NBS-LRR type resist
27	547.5	10.7	695 2 T52429	PM1 homolog (limp
28	540	10.5	919 2 T05746	hypothetical prote
29	527	10.3	885 2 B86257	NBS/LRR disease re

30	524.5	10.2	898	2 B96659	hypothetical prote
31	516	10.1	967	2 G96637	hypothetical prote
32	514	10.0	889	2 F96637	hypothetical prote
33	512.5	10.0	255	2 T04389	NBS-LRR type resist
34	512.5	10.0	909	1 A54809	disease resistance
35	509.5	9.9	925	2 H96638	protein T1F9.20 [i
36	503	9.8	921	2 D86293	F7H2.22 protein -
37	498.5	9.7	227	2 T07755	disease resistance
38	497.5	9.7	985	2 T06049	hypothetical prote
39	490.5	9.6	892	2 T01899	disease resistance
40	486.5	9.5	613	2 T52465	hypothetical prote
41	480	9.4	263	2 T02227	NBS-LRR type resist
42	475	9.3	889	2 C86257	resistance to Paeu
43	473.5	9.2	1824	2 T07589	disease resistance
44	470.5	9.2	893	2 H96651	protein T3P18.19 [
45	468	9.1	560	2 T52438	PM1 homolog (limp

ALIGNMENTS

RESULT 1
T06404
Resistance complex protein I2C-2 - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06404
R:Ori, N.; Eshed, Y.; Paran, I.; Presting, G.; Aviv, D.; Tanksley, S.; Zamir, D.; Fluhr,
Plant Cell 9, 521-532, 1997
A:Title: The I2C family from the wilt disease resistance locus I2 belongs to the nucleot
A:Reference number: 215652; MUID:97290204; PMID:9144960
A:Accession: T06404
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1240 <ORI>
A:Cross-references: UNIPROT:O24016; EMBL:AF004879; NID:92258316; PIDN:AAB63275.1; PID:92;
C:Genetics:
A:Gene: I2C-2
A:Map position: 11
C:Function:
A:Description: confers resistance against Fusarium oxysporum
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 24.2% Score 1240; DB 2; Length 1240;
Best Local Similarity 28.6%; Pred. No. 4.8e-63;
Matches 359; Conservative 211; Mismatches 378; Indels 306; Gaps 39;

QY 6 LQVLLDNITCFIQGE-LGLILGFKDE--PEKLSSTFTTIOAVLEDAQKQLKDKALENW 61
DB 16 LNVLFDRLLA--PNDGLNMFRRKHDHYKLLKDKMTLRGIQIVLSDAENKQASPSVRDW 73
QY 62 LQKINAAAYEADTILDECKTBPATROKKKNGCCYHN-----VITRRHKIGK 108
DB 74 LNEILRDVDSAEINLEEVNYEA---LRLKVEGQHONFSETSNQOVSEDFLNTKDLIED 129
QY 109 RMKIMKELDYIAERIKFHLDEKRTIEROVATROGVLNPOVYGGDKDEIVLKILIN 168
DB 130 TTEFLKDLQDGLGSLKKEIFDSTKLTETRPST--LIDEPDLFGQSEIEDLIDRLLS 186
QY 169 NVSNAQTLPVLPITLGGGLGKTTLAQVFNFDORIEHFHPKIMWICVSEDFNEKRLKEIV 228
DB 187 EGSAGKRLTVPIVGMGLGKTTLAQVFNDESXKHFDFLKAWECAVEAVNAPFITGLL 246
QY 229 ESTIEKSLGMDLAPLQKLRDLNKKYLLVLDVNNEDQAKAKRQVYLKVGASGASV 288
DB 247 QEIGSIDLVDDNINLOQVKKERLKEKKFLIVLDVNNEDVNEDELRYNFVQGDIGSKI 306
QY 289 LITTRLEKVSINGTQPYELSNLSQEDCWLLFQRAE-----GHQEEINLNVALIGKE 342
DB 307 IVTRKDSVALMNGEN-ISMGNLSTASWSLQRRHAFENMDPWGSH-----LEEYGRQ 360
QY 343 IVKCGGVPLAATKLTGLIFKREERQWEHVRDSEIWKLPQEESSILPALRLSYHHLPLD 402

```

Db      361  IAAKCGPLPLAKTLAAGMLRSKSEVEEWKCLIRSEIWEI--RNDNIIPLALMLSYNDLPAH 418
Qy      403  LRQCFYCAVFPKDTMEKGNLISLMAHGFIISKNLLENVGNENETYLSPFOEI 462
Db      419  LKRCFSFCALFPKDYPRFKQVHILMIANGLVPEDEI-IDDLGQFPLELSSRSLEFRV 477
Qy      463  EVKSG---QYFKKHMDLHDLATSLFS-----ASTSSNIRELIVNYIMMSIGFTK 512
Db      478  PNSEGNIKELFLMHMDLVNLAQGLASSKLCIRLESQSQSHMLECRHLSYMGVGDGFEK 537
Qy      513  VVSSYSLSHLQKPY-----SLRVNLSDIKLKQLPSSIG 546
Db      538  LTPYIKLEQLATLPTGSSVNVFVNPFLTKRVLHNLPTLRSLRALSLSHYKMEELPNLF 597
Qy      547  -DLVHLRYNLNSGNTSIRSLPNQCLKNLQTLIDHGHSICCPKETSIGSLRNLLD 605
Db      598  IKLKLRLPLDIS-PTNIRKLPLDISICVLYNLETLILSSG-KLEELPLQMEKILNRHLDIS 655
Qy      606  GCGYGLTQMPRIISLTCLKTL--SRFVVGIOKSKSQGLBELNMLNLYSIEITHLERVND 663
Db      656  NTMHLK-MPLHLSRKSLQVLVGAKEFLVGWRME-DLGEAQ-NLYGSLSVKLENVDR 711
Qy      664  MDAKEANLSAKENLSLSMKWDDDERPRIYSEKVEVLEALKPHSNLTCLTIRGFRGL 723
Db      712  REAVKPKREKNHVEQLSLEWSESISADNSQTER-DIIDELRPHKNIQEVKILIGYGTNF 770
Qy      724  PDMNHSLVKNVSVLEIISCKNCSCLPRFGELPCIKSLIELWRGSAFEVYVDSGF---PT 779
Db      771  PNWVADPLFLKLVKLISLNCKDCYSLPALGQPLCKFLSV-KGMHGIRVYVEEFGRLSS 829
Qy      780  RRRPSLAK-----LNIRFEGNLKGL-----LKEGEE 807
Db      830  KKPENCKLEKPEDEMTWKQMHALIGFPLLEKLSIINCELSLEIPIQSSSLKRFVVF 889
Qy      808  QCPV-----LEETIEIKC-----PMFVPIPTSSVKLVVSG----- 838
Db      890  GCPVVFYDAQVLRSQLBGMQOIEEYIRDNSVTSFPSILPT-TLKTIDISGCPKLL 947
Qy      839  -----DSSDAIGPSSINL 852
Db      948  EAPVCENSMFLBESVSEBGCVPSEFLPTARELRIGCHNVRFLPTATELHTRNCENV 1007
Qy      853  ---MA-----LTSLOIRYKKEDASLPE----- 871
Db      1008  EKLMACGGAQULISLDSGCKKLKCLPELPSLKELOLTNCPREIEGLPNNLOKLYIRD 1067
Qy      872  -----EMF-----KSLAN 879
Db      1068  CKKLVNGRKEWHLQRLTKLYIYHDSDEDIHEWMLPCSIITRLEVENLITLSSQHLKSLTS 1127
Qy      880  LKYNLISYVFNKELP-----TSLASLMAKLELHSCVLESLEPBEVKGILSLTSLI 934
Db      1128  LQYLCID--GNLSPIQSQGISFSFHLTSLQTLQIWNHNLQSSLESALPS--SLSQLEI 1183
Qy      925  TYCEMLQCLP-EGLOHTALTNLVSFPCPTLAKRCEKIGEDWYKIAHPRVFI 987
Db      1184  FHCPLQSLPLANGM--SLSKTLISGCPRLPLLEPRKGEVWPQIAHPIITILI 1235

```

RESULT 2

```

T06403
Resistance complex protein I2C-1 - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06403
R:Ori, N.; Bshed, Y.; Paran, I.; Presting, G.; Aviv, D.; Tankalev, S.; Zamir, D.; Pluhar,
Plant Cell 9, 521-532, 1997
A:Title: The I2C family from the wilt disease resistance locus 12 belongs to the nucleot
A:Reference number: Z15652; MUID:97290204; PMID:9144960
A:Accession: T06403
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1220 <ORI>

```

```

A:Cross-references: UNIPROT:O24015; EMBL:AF004878; NID:g2258314; PIDN:AAB63274.1; PID:g22
C:Genetics:
A:Gene: I2C-1
A:Map position: 11
C:Function:
A:Description: confers resistance against Fusarium oxysporum
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat
Query Match      23.6%; Score 1212; DB 2; Length 1220;
Best local similarity 29.2%; Pred. No. 1, 98-61;
Matches 361; Conservative 207; Mismatches 378; Indels 290; Gaps 39;
Qy      6  LQVLLDNLITCFIOGE-LGLILGFKDE--FEKLGSTFTTIOAVLEDAQKQKDAIENW 61
Db      16  LNVFLDLA--PNDDILNMFRRKHTDVELEFKGLDILSLQIYVLSDAENKKAQNSQFSOW 73
Qy      62  LQKNAAAVEADLIDE-----CKTEAPRQKKNKYGCHPNVITFRKHIGRMMKIM 114
Db      74  LHKLQTVADAENLIEOVNVEALRLKVEISNQVSDNLCLSD--FFLNIRKKLEDTI 130
Qy      115  EKLQVIAERIKEHLDERTERQVATR-QTGFVINEPQVYGRDKEDKIYKILINYSNA 173
Db      131  KGLSEVLKQIGRLGKHEFISTKQETTPSTLVDSGIFGRKNIEINLVGRLLSMOTKR 190
Qy      174  QTLFVPLILGNGIGKTTLAQWVFNQDVLEHFRPKIMCVSEDENEKRLKEIVESIEE 233
Db      191  KNLAIVVIVGNGKGTTLTAKAAYNDERVOGHFLTAMFCVSEAYDAFRITKGLQREIGS 250
Qy      234  KSLGMD-----LAPLQKLRDLNKGKYLAVTDVNMEDQKAKLRQYL 279
Db      251  TDLKADNINLQVYKLKADNINLQVYKLKERNKGFVLVLDVMDNVPEDDLNLF 310
Qy      280  KYGASGASVLTITTELEKYSIMGTLOPELNSLSQEDCWLTFMORAGHOE-EINLNLVA 338
Db      311  LQDGISKIIYTRKESVALMDSGALY-MGILSSESMALFKRHSLEHOKRKHPEEE 369
Qy      339  IGKEIVKCGVPLAAKTLGILRFKREERQWEHVRDSEIWLQPOESSITPALRLSYH 398
Db      370  VGQIADCKKGLPLALKALAGMLRSKSEVDEWRNIRLSEIWEIPLSCNGIILPALMLSYND 429
Qy      399  LPLDLRQCFYCAVFPKDTMEKGNLISLMAHGFIISKNLLENVGNENETYLSPFOEI 458
Db      430  LPAHLKOCFACALPYDQYFRKEQVHILMIANGV-----HOFHSNQVFIELRSLSL 483
Qy      459  FOEIEVSSGQTY--FKKHMDLHDLATSLFSASTSSNIR-----EIVENYIHM-MSIG 509
Db      484  PEMASPESEPRVEEFLMHDLVNDLA---QIASNNHCIRLEDNKGSHMLECRHMSYSIG 539
Qy      510  ---FTRVSSYSLSHLQKPY-----SLRVNLSDIKLKQ 540
Db      540  QDGFEFKLSLFSQQLRTLLPIDIOFHYSKLSKRVLYNHLPTLRSLRALSLSHYQIEV 599
Qy      541  LPSSIG-DLVHLRYNLNSGNTSIRSLPNQCLKNLQTLIDHGHSICCPKETSIGSL 599
Db      600  LPLNLFILKILRLPLDIS-ETSIYTKLPDSIFVLNLETLILSSCYLBEPLQMEKILNL 658
Qy      600  RNLLIDGCGYGLTQMPRIISLTCLKTL--SRFVVGIOKSKSQGLBELNMLNLYSIEITHL 657
Db      659  RHLDISNTRLK-MPLHLSRKSLQVLVGAKEFLVGWRME-YLGEAH-NLYGSLSLIEL 714
Qy      658  ERYNDMAKEANLSAKENLSLSMKWDDDERPRIYSEKVEVLEALKPHSNLTCLTIRG 717
Db      715  ENNVDRREAVKAKRREKNHVEQLSLEWSESISADNSQTER-DIIDELRPHKNIAVEITG 773
Qy      718  FRGRLPDMNHSLVKNVSVLEIISCKNCSCLPRFGELPCIKSLIELWRGSAFEVYVDSGF 777
Db      774  YRGNPNWVADPLFVKLVHLYLNCKDCYSLPALGQPLCKFLSV-KGMHGIRVYVEEFG 832
Qy      778  PTR-----RRPSPRLKINIR-----EFGNTL 797
Db      833  YGRLSKKKPPNSLVKLRPEDMPEKQMHNTLIGFPLTEKLSINCELSLEIPIQFSSL 892
Qy      798  KGL-----LKEE--GE----- 806

```

Db 893 KRLLICDCKSVTSFPFSLPTTLKRIKISGCPKLTLEAPVGMFEVYLVIDCGCVDDIS 952
Qy 807 -EQCPVLEIEIKKC--PMFVLP----- 827
Db 953 PEPLPTARQSLIENCHNVTREPLTPATESLHINCEKLSMACGGAOLTSINWGCKK 1012
Qy 828 ----LSSVKKL-----VSGDKSDAIGFSSISIMALT 856
Db 1013 CLPELPLPKELRLTYCEIEGELPFPNQLIDIRCKLVNCRK-----WHLQRLT 1064
Qy 857 SLQIRYNKD-----ASLPEMEKSLANLKYL---NISFYNLK 892
Db 1065 ELWIKHDSDEHIEHWELPSSIORLPFNLTLSGQHLKSLTSLQFLRIVGNLSQFQSG 1124
Qy 893 ELPTSLALNKLHLEHSCALBESLPREGVKGLISLTQLSITTCMOCPL-BELQHLT 951
Db 1125 QL-SSFSHLTSLQTLQIWNFNLOSPLPSALPS--SLSHLILISNCPNLSPLKGM--S 1179
Qy 952 ALTNLSVEFCPTLAKRCEKIGEDWYKIAHPRVPI 987
Db 1180 SLSTLSICKPLPLLEPFDKGEWTETIAHIFTIOI 1215

RESULT 3

T02213
NBS-IRR type resistance protein - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02213
R/Leister, D.; Kutch, J.; Laurie, D.A.; Yano, M.; Sasaki, T.; Devos, K.; Graner, A.; Sch
Proc. Natl. Acad. Sci. U.S.A. 95, 370-375, 1998
A/Title: Rapid reorganization of resistance gene homologues in cereal genomes.
A/Reference number: Z14623; MUID:98081880; PMID:9419382
A/Accession: T02213
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-571 <LEI>
A/Cross-references: UNIPROT:O48981; EMBL:AF032688; NID:g2792219; PDB:AA96985.1; PID:g2
C/Genetics:
A:Gene: r1
C/Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 19.9%; Score 1020.5; DB 2; Length 571;
Best Local Similarity 41.1%; Pred. No. 6,1e-51; Indels 81; Gaps 18;
Matches 250; Conservative 98; Mismatches 179;
Qy 105 KIGKMKKIMEKLDVIAERIKFHLDERTIEROVATROGFEVLEPYGGRDKEDKDIYK 164
Db 2 RAGPDMSTMR-----EETK-----ERP-----KTSLLIDGSSVFGREEDKENVK 43
Qy 165 ILIN-NVSNAOPTLVPLTGMGIGKTTLAQWVENDQVIEHFAPKINICVSEDFNEKRL 223
Db 44 MLTPNNNSNHNANVSPLPIVGMGIGKTTLTQLVYNDPVRKEVFOLRVWPVCSNFDEKML 103
Qy 224 IKEIVESIE---EKSLGMDLAPLOKRLDLNGKKVLLVDDVWNEODDKAKIROYLK 280
Db 104 TKETTESVAGRSSVTTMMNL--LOEDLSKLEGGKFLVLDVWNEDEKMDRRCALV 161
Qy 281 VGASGASVLTTRLEKVSINGTLOPELSNLSQEDCMLLFMQARFGH-OEININLVAI 339
Db 162 SGSNSGRVLTTRNNQVKGKMGMPFYLKQLSENDCMNLFPSYAFADGSDSIHHEIIT 221
Qy 340 GKEIVKCGSVPLAAKTGLGILRFREERQWEHVDSIWKLPQESSILPALRISTYHL 399
Db 222 GKEIVKKGKGLPLAKAIGSLCTKOTEDDMKCNVRSRIWELPSKNNILPALRISTYHL 281
Qy 400 PLDIROCFTYCAVPEKOTEMEKGNLSLMAHGFLLSGNLELVNGVNNELVLRSEF 459
Db 282 PAILRGCAFCSVFKDVFVEKETLVQIWMALGFIQSFGKRTIEELGSSYFDELGRSFF 341
Qy 460 QEIEVKSQGTQFKMDLIDHLATSLF-----SASTSSS-----NIREII 498

Db 342 Q--HHKG--VYNHADMHDLAQSVMDECLRLDDPNNSSSTSSRHLSTSCNRSRTS 396
Qy 499 VENTYHMMSIGFTKVSSYSLSHLOKFS-----LRYNLSDIKLKQLPSSIG 546
Db 397 FEDF-----LQFKARTILLANGYKSRSPISDPLFMLRLHYLELNRRRITELPDIG 451
Qy 547 DLVHLRYNLISGNTSIRSLPNQCKLQNLQTLDLHGCHSLCCLPKETSILGSLRNL--- 603
Db 452 NLKMLRYNLISG-TGITVLPSSIGRLFNLTQLTKLNCHVLECP-----GSITLVNLR 504
Qy 604 -LDGCTGTCMPRPISGTLCTKTSRFPVGIQKSCQGLERN-LNLVGSIEITLERVK 661
Db 505 WLEARIDITIGIAGINLTCLQOLEEFVH-NDKGKXISELKTWMSIGRICIKNLEAVD 563
Qy 662 NDMAKKA 669
Db 564 SAERNGA 571

RESULT 4

T00020
bacterial blight-resistance protein Xal - rice
C/Species: Oryza sativa (rice)
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C/Accession: T00020
R/Yoshimura, S.; Yamanouchi, U.; Katayose, Y.; Toki, S.; Wang, Z.X.; Kono, I.; Kurata, N.
Proc. Natl. Acad. Sci. U.S.A. 95, 1663-1668, 1998
A/Title: Expression of Xal, a bacterial blight-resistance gene in rice, is induced by bac
A/Reference number: Z14057; MUID:98132648; PMID:9465073
A/Accession: T00020
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1802 <YOS>
A/Cross-references: UNIPROT:O48647; EMBL:AB002266; NID:g2943741; PDB:BA425068.1; PID:g2
A/Experimental source: strain IR-Bel; green leaves inoculated with *Xanthomonas oryza pv. c*
C/Genetics:
A:Gene: Xal
A/Map position: 4

Query Match 17.6%; Score 904; DB 2; Length 1802;
Best Local Similarity 29.2%; Pred. No. 1.5e-43;
Matches 280; Conservative 138; Mismatches 362; Indels 178; Gaps 27;
Qy 143 TGFVLEPYQVGRPEKKEIKILINNVSNAQTLPVPLTGMGIGKTTLAQWVENDQVR 202
Db 288 TSTVLPETIVYGRAHEMTTILQILMSNRNSGIT--VLPVNGGIGKTTLAQVYKDLVI 345
Qy 203 IEHFPKIMCVSBDPNEKRLIKEIVSIEKSLGGM-DLAPLOKRLDLNGKKVLLV 261
Db 346 KSGFNVKIMVYSDKFDVVKITRQILDHVNSQSHGISNLTLOQDEOKSKKFLIVL 405
Qy 262 DDVWNEODDKAKIROYLAKV-----ASGASVLTTRLEKVSINGTLOPELSNL 312
Db 406 DDVWEIRTRDMKKLAPLRPDQVNSQGEATGMIIITTIQISLAKSLGTVOSTKLEAL 465
Qy 313 SQEPCWMLFMQARFGH-OEININLVAIGKEIVKCGSVPLAAKTGLGILPFKEEROME 371
Db 466 KDDIIVSLFKHAAGNDKHSSPGLQVIGKQIASELKNPLAAKTVGSLLGTNLIDIMD 525
Qy 372 HVDSIEIKWLPOEBSIILPALRYSYHLPLDIROCFTYCAVPEKOTEMEKGNLSLMAH 431
Db 526 SIISSEKWSLQAYGIMQALKLSDYHLSNPLQCVSYCSLFPKGYSPSKQLDIQWIAQ 585
Qy 432 GFILSKNLELVNGVNNELVLRSPFOELE-VKSGQTYRKMDLIDHLATSLFS---A 487
Db 586 GFV-EESSEKLEQGWKYLAEVNSGFLQVESYRFSSEYFVMDLMDLQKVSQTEYA 644
Qy 488 STSSNIREI-----IYENYI---HMMSIGFTKVSSYSYL--- 519
Db 645 TIDSECTELAPSRHLSIVTDSAYRKEKYNISRNVEFEKRLKYNVRSRLRSIVLIGQ 704
Qy 520 --SHLOKFSVLRYNLSDIKLKQLP-----SISGDLVHLRYNLISGNTSIRSLPN 567

Db 705 YDSHFKEFKDAFKEAQHRLRLQITATYADSDSFSLVNSTHLRLYLKITEESGRTLP 764
 QY 568 QLCQNQLDLDHGCHSLCCLPKETSKLSLRNLIDGCGLTMP-PRIGSLTCTLT 626
 Db 765 SLRKYTHQVLDIGRFPGIPRIISNDINNLISLRHV--AYDEVCSSTIANIGKTSLOEL 821
 QY 627 SRPVVGIQKSKCOLGELNLNLVGSIEITHEERVNDMDAKEANLSAKENLSIMKV-- 684
 Db 822 GNFTVQNNLSGFBEVQLKSNMKIVQLSVSQLENVRTQGEAGCAKLDKQKHLEKHLMSKD 881
 QY 685 -----DDERRRIYSE----- 703
 Db 882 AMNGYDSDES---YDEYSGDMNITEGEELVSGDANGAQSILQHSNISSELASSEVLEEG 938
 QY 704 LKPSNLTCLTIRGPRGIRLPDMNHSVTKNVVSEIISCKNCSCLPPFGLPCIKSELEL 763
 Db 939 LEPHGLKYLIRISGYNSTSTWLPSS-LTCLQTHLEKCGKQWL-PLEKILGLVLYL 996
 QY 764 --WGSAAVEVYDGSFPTRRFPRLKLNIREFGNLKGLKKEGBOCPVLEIEIKCP 821
 Db 997 IKMNATELSTPSLEELVIALPSLNTGSCISIRNLNSLKVLIKNCPPV-----KVFP 1051
 QY 822 MFVPTLSSVKKLVYSGDKSAIGPSSISNLMALTSLQIRYKEDASLP----- 870
 Db 1052 LFEISQKFEIERT-----SSWLPRLSKLTYNCPISCVHSILPSPSAISGYEYG 1100
 QY 871 -----BEMFKSLANKYLNISFYFNKELPTSIASLNLKH-----LEHSCVLES 917
 Db 1101 RCTLPOSLEELYHESQETLOPCPSGNL---TLRKHLVAGSNLVSLDHSCTALE- 1155
 QY 918 LPERGVKGLISLTQLSITYCEMLQCLPEGLQHTALTNLVSEFCPTLAKRCEKIGED 975
 Db 1156 -----ELIIQSCESISL-DGLQLGLNLRLR-----AHRCLSGHGED 1192

RESULT 5

T08416

disease resistance protein homolog F18B3.230 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 26-May-2000

C/Accession: T08416; S71195

R/Querier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16409

A/Accession: T08416

A/Molecule type: DNA

A/Residues: 1-852 <QUB>

A/Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.230

A/Experimental source: cultivar Columbia; BAC clone F18B3

R/Route, D.T.; Heazlewood, J.L.

submitted to the EMBL Data Library, January 1995

A/Description: Incomplete sequence of an Arabidopsis gene with similarities to myosin he

A/Reference number: S71195

A/Accession: S71195

A/Molecule type: DNA

A/Residues: 'LKNMDFWMLRFRYSRWLIDFMVKQSSDDTHNRKLNCLVIVQLEIFLEVAGSEK', 1-36, 'K', 38-128, 131

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z17586

A/Accession: T12977

A/Molecule type: DNA

A/Residues: 1-847 <CHO>

A/Cross-references: UNIPROT:Q9STE7; EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240

A/Experimental source: cultivar Columbia; BAC clone T6H20

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T12977

R/Querier, N.; Robert, C.; Broctier, P.; Wincker, P.; Cattivico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, July 1999

A/Reference number: Z1

Query Match 14.0%; Score 716; DB 2; Length 847;
 Best Local Similarity 25.5%; Pred. No. 3e-33;
 Matches 260; Conservative 174; Mismatches 316; Indels 270; Gaps 40;

1 MAEAFVQLVLDNLTCFIOGELGILGFKDEPEKLOSTFTTIOAVLEDAOKKOLDKAIEN 60
 1 MVDVATGVLNKKIGGYILNEVLAALMGVDDBELTELTCHYGILKADVEAREDEBSKE 60
 61 WLQKLNAAVEADLDLDECKTEAPLRQKNKYGCYHPNVITFRHKIGRMKM-K-KIMEKLD 118
 61 WTKVLADIAVIDEDLDYTFKLEBSLR-----GLALVTNKGIGKRRANVIVE--- 110
 119 VIAARIKHLDERTIEROV---ATROTFV--LNEPO----- 151
 111 -----DITLKRRIIDITRKRETFGIGSEFNERGNTITVVRQLRRAAPVDQ 159
 152 --VYG-RDKEDEIVKILINNVSNAQTLPLPLTGMGGLGKTTLAQWFPNQRYIENHP 208
 160 ELVVGLEDVVKILVKKLSDBKDSY--IISIFMGGLGKTTALARKLYNSGDVRRPDC 217
 209 KIWTCSDEPEKRLIKEIVESIEKSLGMDL-----APLOKLDLNGKKYLLVL 261
 218 RAVTYVSGEYTRILIRIISLQIVSAEMBEKIKMEFEDELEVLYLGLGKNYVYV 277
 262 DVVNEODKRAKLRQVLKVGASGVLTTRLEKVG-SINGTLOPYELSNLSQEDCWL 320
 278 DDVA--DPDAWESIKRALPCDHRSKVIITTRIRALAEVGEYVAHKLRLTFREESWTL 335
 321 FMQAFQHOEININVAIGKEIYKCGSVPLAKTGLGILRFKREBOMHYVDSLETWK 380
 336 FERRAFNIEKVDDLTORTGEMWKCCGLPLATVLSGLSRK-TWEMIEVACS-LMR 393
 381 LPORES-SILPALRSYHHLPLDRQCFYCAVFPKOTEMEGNLSLMAHGFILSKGN 439
 394 RIKONSIHISTVPLSPKEMHKLCLFLYSVPEDEIYVEKLIHLVAGSTIQEDBE 453
 440 LELENVGENWNLVLSRFQEIYKSGQTY-FKQHDILDLA-----TSLFSA 489
 454 MMEDVARCVIDELVDRSLVKAERIERGKVMSCRIHDLRLAKAKELNFVNVNEKQ 513
 490 SSSNI-REITVEYIHMMS-----IGTKVVSYSLSHLOKPVSLR 529
 514 HSSPICREVV---HHLMNDYVLCRRVNRKMSFLFIEGRRFGVYNTNL-KLKILR 568
 530 VLNDSIKL-----KOLPSIGDLVHLRYNLNSGNTSIRSLPNOLCKLQNLQTLDLHG 583
 569 VLNNEGILFYSKINSITLPLVIGELIHLRYLGLA-DTVVSLPSSISNLRFLQTLDSG- 626
 584 HSLCCLPKETSGLSLNLLDGCYGLTCEMPRIGSLTCLTSLRFVVGIOKSCQOLGE- 642
 627 NDPRQYTTDLSKLSLAH-----VIGKRVGECILGEG 658
 643 -----LRLNLVYSIEITHLERVKNDMAKANI-SAKENHLSMKWDDDER-PRYIES- 695
 659 VNLQTLSSISSYSKLNH-ELLRLDLLEIYD-----HS--KWDQORVVLNPFV 707
 696 EKVEVLAKRHSNLJLCTLRGFRGIRLPMNMHSVLKNVYSIRIIGCKNSCLPPGEL 755
 708 SKPNLNVLK-----LEMENFK-----LSEBSRTTIGLVV-----NF 740
 756 PCLSKLEIMRGSAREVEYDGFPTRRRPSLRKINIREFNLKGLKKKEGECQVLEEI 815
 741 PSLSESLTLVGTLE-----ENGMPLAQK-----PRLEDL 770
 816 EIKCCPEFVIPTLSSVKVLVSGKSDAIGSSISNIMALTSLQIR-YNKEDASLPBEMF 874
 771 VLKDC-----NYSGVYIMSSIS--AAGRGRLKMLE--MSMERGRGGLDELRIEEM 817
 875 KSLANLKYNISFFPNKLEPTSLASNALKHLIEHSCVYALIESLPBEGVGLITLQDST 934
 818 PSLIKLT-----VKGRLSLTYKMTI 836

RESULT 7

T48899

disease resistance protein rp8 [similarity] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000

C/Accession: T48899

R/McDowell, J.M.; Dhandaaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dengl,

Plant Cell 10, 1861-1874, 1998

A/Title: Intragenic recombination and diversifying selection contribute to the evolution

A/Reference number: 224999; MUID:99030193; PMID:9811794

A/Accession: T48899

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-908 <MCD>

A/Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AACT8631.1; PID:g3901294

A/Experimental source: Columbia

A/Genetics:

A/Gene: rp8

A/Introns: 293/1; 342/1

C/Function:

A/Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 13.5%; Score 694; DB 2; Length 908;

Best Local Similarity 25.1%; Pred. No. 6.1e-32;

Matches 268; Conservative 175; Mismatches 377; Indels 246; Gaps 37;

1 MAEAFVQLVLDNLTCFIOGELGILGFKDEPEKLOSTFTTIOAVLEDAOKKOLDKAIEN 60
 1 MAEAFVFGLEKLDLRSERLQSIDGLKRLQRLSGLSKADAKKHSKDRVN 60
 61 WLQKLNAAVEADLDLDECKTE-----APLRQKNKYGCYHPNVITFRHKIGRMKMIM 114
 61 FLEVDKOLVDADIDIESVYLNKLSGKGVKQVHRVLAFC---LDRHKVADIDIGIT 116
 115 EKLDVIAERIKYHL-----DEKTERQVATROTFVNLPEPVYGGDKEDK 161
 117 KRISVEIGEMQSFQIQQIIDGRLSLQERORVOREI--RQYVDSSESDLVGEQSVKE 174
 162 IVKILINNVSNAQTLPLPLTGMGGLGKTTLAQWFPNDQRYIHFHFKIMVCSDEPNEK 221
 175 LVGHVLEN---DVHQVVSIAWGIGIKTTLARQVFNHDLVRRHFDGFPAWCVSQFTQK 230
 222 RLKIEIVESIE--EKSIGMDLAPLOKRLDLNGKKYLLVLDVWNEODKRAKLRQVL 279
 231 HWMRITLQELQPHDGLDQMDVYALQKRLFQLEAGYVLVDVWKKED--MDVIAVF 288
 280 KVGASGASVLTTRLEKVG-SINGTLOPYELSNLSQEDCWLFMQAFQHOEININL-- 336
 289 P-RKRGWKMLLTSRNBEVGIHADPTCLTFPRASTLNPEBSWKLCEIRIVFPRDTEVRIDE 347
 337 --VAIGKEIYKCGSVPLAKTGLGILRFKREBOMHYVDSLETWKLPQRESS 387
 348 EMEAMGEMVTHCGGLAVKALGGLANRGTVPENRVRVDNIGSQVGSWLDNSLNS 407
 388 ILPALRSYHHLPLDRQCFYCAVFPKOTEMEGNLSLMAHGFILSKNLELVN 447
 408 VYKILSISTYEDLPYHLKHCYLANAHPEDEISIGYSLFYMAAGIY---DGSITDESGE 464
 448 EVNNEVLSRF-FOEIVKSGQTY-FKQHDILDLATSLFSASTSSNIREIIVE---N 501
 465 YLLEELVRNMLVIADDDYLSWQSKYCOMHDMREVCIS---KAKENPFIQIIDIIPCTS 520
 502 YIHMSIGTFKVVSSV-----LSHQK-----FVSLRV 530
 521 TINAQSPSRRLRSHSGAFHILGHKNTKRVSLVPREEDYWRASAVFHNLTLLRV 580
 531 INTSDIKL--QPPSISGDLVHLRYNLNSGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCC 588
 581 LDSLWKFEGGKLPCLSIGLIHLRYLSLV-BAVYSHLPSTMRNLKLLVYLNLR----- 632
 589 LPKETSLGSLNLLDGCYGLTCEMPRIGSLTCLTSLRFVVGIOKSCQOLGELRLN- 647
 633 --VDTEEPRIHVPNVLKE-----MQLRYLSLPLKMDDKTKLELDLVNLEY 676

QY 648 LYG-----SIEITHLERYKNDMAKEANLSAKENLSLSMKWDDEPRRIYSEKEVYLEA 703
Db 677 LYGSTHSHSVTLDIRM-TKRLAYALSLSEKCNFETLS-----SS 715
QY 704 LKPSNLTCLTIRGFRGIRLDPMMNHSVTKNVSIEIISCNCSCLPPFGLPCLKSLEL 763
Db 716 LRELRNLTETLNFSLSELYWVDYNGEPFLDHFH-----LKQGL 755
QY 764 WRGSAEVEYVDSGPTRRRRPSLRKLNIRFBNGLKGLLKEGEECCPLIEIEIKCCMF 823
Db 756 AVMSKI-----PDHQFP-----PRLVHLFLYICGM- 782
QY 824 VIPLSSVKKLIVSGKSDAIGFSSISNLMLTSLQIRYNKEDASLPEEMFKSLANIKYL 883
Db 783 -----EED--PMPLEKLIHLKSV 799
QY 884 NIS-FYFNLIKELPTSLASLNALKHLHSCYALBS-LPBGVKGLISLTOLSTYCEMLQ 941
Db 800 RLAKKAFISRMVCSKGGFPQLCVLIEISKESLEEWIYEBG--SMPCLRTLITDDCKLK 857
QY 942 CLPBGLOHLTALTNLSVEFCPTLAKRCEKGI--GEDMYKIAHPRV 985
Db 858 ELPGDLKYITSLKELKIEGMKREWK--EKLVPGEEDYKVOHIDPV 901

RESULT 8

Protein F12M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96573
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Comai, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Saldeberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1584 <STO>
A:Cross-references: UNIPROT:Q9MAG6; GB:AE005173; NID:g7769860; PIDN:AAF9538.1; GSPDB:GN
C:Genetics:
A:Gene: F12M16.25
A:Map position: 1

Query Match 13.2%; Score 676.5; DB 2; Length 1584;
Best Local Similarity 25.0%; Pred. No. 1.4e-30;
Matches 266; Conservative 183; Mismatches 347; Indels 269; Gaps 44;

QY 10 LDNLTCTPQIGELGILGFDEPEKLOSTFTTQAVLDEDAQKOLDKALBNMLOKLNA 69
Db 323 VEKMWELLSRESARLNGIDQVDGKRGLOSLKDKADAKETERKYNFLLEVXIV 382
QY 70 YEADDI-----LDECK-TEAPTRQKNKYGCVHPNVITFRNK-----IGRMKIMEK 116
Db 383 YDADDIISPLNLRKGEKGIKKQVRLTAC-----LVDRKRFASDISGITRKISSEVIVG 438
QY 117 LDVIAAERI-----KFLHDEFTTERQVATROTGTGLVNEPQVYGGDKEDKELIVKLLINV 170
Db 439 MOSLGIQHADCGGSLSLQER--QREI--RQTFERNSSSDLVGIDQSVIEELVDHLVFN- 493
QY 171 SNAQGLPVLPLITGMGGLGCTTTLAOMVENDQRYIEHFRKIVCVSEDFNKKLIEIYES 230
Db 494 ---DSVQVAVSGMGWIGIKTTLARQVFNHDIVRRHFDGFSWVCQOQFRKQVWRILQD 550
QY 231 IE--EKSLGMDLAPLQKTLRDLNGKTYLVLVDVWNEDDQKAKLRQVLKVGASGASV 288

Db 551 LRPYDEGIQWDEYTLQGLFELLESGRYLLVDVWKEED--WDRKAVFP-HKRMKM 607
QY 289 LTTTRLEKVG-SIMGTLQPYELNLSQEDCMLFMORAFHOEINLNL-VAIGKEIVK 346
Db 608 LITSRNGLGIDHADPTCFARPRILITPQSKLPERIVSSRDKTERKVEAMKENVY 667
QY 347 CGGVPLAAKTLGGLIRKREERQWEHVRDSEIKL-----POESSILPALRSTYHL 399
Db 668 CGGLPLAVKVLGGILAKKHVLEWKRVHSNIVTHIVGSGLSDDNSSVYRVLSTYEDL 727
QY 400 PLDIRQCTTCAYFPKQOTEMEKGNLSLMAHGFILS-KNLELEANTGNVMELYRSF 458
Db 728 PMQLKHCFYLAHPBEDYKIDVXLLFMYWVAEGITTFHDGSTIQDTGESYLEBVRNM 787
QY 459 --FOEIEVKSQGYTFKMDLIHDLATS-----LFSASTSSNI-----REI 498
Db 788 VVVEESTYLSRIEYQCHMDMREVCLSKAEENFIRVVKVPTTSTTNNOSPCRSRIV 847
QY 499 VE--NYIHMSIGFTKVSSYSLSHL-QKFS-----LRYNLSDIKLK--QLPSS 544
Db 848 LHSGNALHMLGHKDKKARAVLIFGVEKFKWKGFGCLPLRLVLDLSYVQFEGKLPSS 907
QY 545 IGDIVHLRYNLNSGNTSIRSLPNOLCKLQNLQTLDLHGHSLOC-LPKETSKLSLNL 603
Db 908 IGDILHRLFLSLY-EGVSHLPSLSGLKLLCLNLGVADRLLVHVNVNLKEMQELYYLR 966
QY 604 LDGCVGLTQWPPR-----IGSLTCLKTLRFPV--GIQKSCQGLERLNLVGSIEITHL 657
Db 967 LP-----RSMFAKTKLEGLDVNLSELTNSTGISTYDILLRWKLSLVAVIFSGECT-- 1019
QY 658 ERVKNDAKEANLSAKENLSLSMKWDDEPRRIYSEKEVYLEALKPSNLTCLTIRG 717
Db 1020 -----FET-----LILSLRELRNLTETLSFHD 1040
QY 718 FRGIRLDPMMNHSVTKNVSIEIISCNCSCLPPFGLPCLKSLELRGSAEVEYVDSGF 777
Db 1041 FOKVSV--ANHG--GELVLDFTLHLDLTL-----SMHLPR-----P 1073
QY 778 PTRRRPSLRKLNIRFBNGLKGLLKEGEECCPLIEIEIKC-----PMEVIPTLSSVK 832
Db 1074 PDQRRP-----PHAIHWLIGCMEDDPMTLEKLIHLK 1108
QY 833 KLIVSGDKSDAI-----GFSSISNLMLTSLQIRYNKEDASLPEEMFKSLANIKY 882
Db 1109 SVYLS--SGAFLGRMVCSKGGFPQ-----LIALKMSYKCE----- 1142
QY 883 LNTSFYRNKELPTSLASLNALKHLHSCYALBSLPEBGVKGLISLTOLSTYCEMLQ 942
Db 1143 -----LVEWRVYEBG--SMPCLRTLITDCKKLQ 1169
QY 943 LPEGLOHLTALTNLSVEFCPTLAKR--CEKGI--GEDMYK-IAHI 982
Db 1170 LPDGLKYITCLKELKIE--RMKREWTERIVIGEDYKGLKHI 1210

RESULT 9

T48898

disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48898
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl,
Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evolution
A:Reference number: Z24999; MUID:99301093; PMID:9811794
A:Accession: T48898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-906 <MCD>
A:Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AA03165.1; PID:g3928862
A:Experimental source: Landberg erecta

A:Gene: RPP8
A:Introns: 293/1; 342/1
C:Function:
A:Description: promotes resistance to *Petronospora parasitica*

Query Match 13.1%; Score 671; DB 2; Length 906;
Best Local Similarity 24.9%; Pred. No. 1.3e-30;
Matches 267; Conservative 173; Mismatches 372; Indels 260; Gaps 38;

QY 1 MAAEFLQVLNLTFCIGELGLIGFDEPEKOSTTTTQAVLEDAQKQKQKAIEN 60
DB 1 MAEAVSGLEKMDLRSERLQGVQDGLRQRLSLQSLKDKADAKHGSDRYRN 60
QY 61 WLQKLNAAAYEADILDECKTEAPFROKK--NKYGCYHPNVYTFPHKIGKMKIMEKLD 118
DB 61 FLEVDKDLVPFADIEDIESYLVNKLKRGEGYKHYRRLARFLTDHKAASDIEGTTKIS 120
QY 119 VIAERIKFHL-----DETERIQVATRGTFVLEPQVYGRDEKDEIYKI 165
DB 121 DVIGMQSGFIQQLIDGVRSLSLGRQVQREI--RQTYPPDSSEDLVGVEQSVKELVGH 178
QY 166 LINNVSNAGTLPVPLIGMGGLGKTTLAQWPNDRVLEHHPKWTICVSEDFNEKRLIK 225
DB 179 LVEN---DVHQVSIAGMGGIGKTTLARQVFNHDLVRRHFGFAMVCVSOQFTQKHWMQ 234
QY 226 EIVESIE--EKSIGGMDLAPLOKRLDLNGKKYLLVDVWNEDQDKAKLROYLKVGA 283
DB 235 RILQGLQHDHDDILQMDERYALQKRLFQLEBAGKYLVLDDWKKED--WDVIKAVFP-RK 291
QY 284 SGASVLTTRLEKVG-SINGTLQPYELSNLSQEDCMLFMORAFGHEINMLT---VA 338
DB 292 RGMKMLTIRNMGVGIHADPTCLTFRASILNPEBSMKLCERLVFRRDETEVLDEEMEA 351
QY 339 IGKEIVKCGGVPLAATLGLILKPKREKREMEHVRDEIKTL-----POEBSIIPA 391
DB 352 MGKEVWTHCGGIPYAVKVLGGLANKHTVPEWKRVSNDIGQIVGSGCLDINSINSVRI 411
QY 392 LRLSYHHLPLDROCFYCAVFPKOTEMEGNLSLMAAHGF-----ILSKNLELENVG 446
DB 412 LSLSTEDLPHLKRFLFLAHPPEYSKISAYDLFMYAVVEGIYDSTIQDSEGYLEELV 471
QY 447 NE---VNNELYSRFPFOEIEVKSQGYFQMDLIDHLATS-----LFSASTSSNI 494
DB 472 RRLVIADNRKYLSSKNCO-----MEDWMEVCLSKAKKEBNPQIHKDPTSTSTI 522
QY 495 -----REIIVENYIMMSIGF--TKV-----VSSYLSHLQKFTSLRYLN 532
DB 523 NAQSPRSRRRLSIHSGKAFHLGHNKNTKVSLLIYWDEDFGIRASAVFH--NLTLRLVLD 580
QY 533 LSDIKLK--OLPSSTIGDLVHLRYLNLSGNTSIRSLPNQLOKQ-----NLQTLDHGHS 585
DB 581 LYMWKFBGCKLPSSIGSLIHLRYSLF--LAGVSHLPSTMRNKLKLLYLNLSVNNKEPH- 638
QY 586 LCCLPKETSKLSLRLNLLDGCYGLTCMPRIIGSLTCLKTLRSFVVGIOKKSQOLGELRN 645
DB 639 ---VPNVLAKEMIQLRYL-----SLPLKDD-----DKTKLEIGDLVN 671
QY 646 LN-LYG-----SIEITHLERVKNDMAKEANLSAKENLSLSKMDDDRPRRIYSEK 697
DB 672 LEFLFGFSTQSSVYDLDHMTKLR---YLAVSLSERCNFETLS----- 711
QY 698 VEVLALKHSHNLTCLTIRGRGIRLPRDMNHSVLKXNVSIISICNKGSCLPFGELPC 757
DB 712 ---SSLELRKLETLVYLFSPBEIFMVDYMGEFVLDHIT----- 747
QY 758 LKSLLEMGASAVEVYDGSFPTRRRFPRLKLNITREFGNLKLKKEBQCPVLEIEI 817
DB 748 LKEIGLAARMSKI-----PDQHQLP-----PHLAQIYI 775
QY 818 KCCPMEFVYPTLSSVKLVVSGDKDAIGFSSISNLMALTSIQIRNKDASIPPEMFSL 877
DB 776 CNGRM-----EBD-----PMEILKEL 791

QY 878 ANLKYLNISF-YPNIKELPISLASINMLKULEHISCALIES-LPEGVKGLISTQLSIT 935
DB 792 LHLKSVKTLFKAFARMRVCSKGGFTQCALEISQSELEEWIEEG--SNPCLRTLTTH 849
QY 936 YCEMLQCLPEGLQHLTALTNLSVERCPFLAKRCKGI--GEDWKIATIPRV 985
DB 850 DCEKLELPDLKLYTSLIKEIKIGMKREWK--EKLVGSGEDYKQVHPDV 899

RESULT 10

745590
hypothetical protein F12A12.50 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Mar-2000
R:Choi, N.; Robert, C.; Brottier, P.; Winkler, P.; Catcolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223008
A:Accession: T45590
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-835 <CHO>
A:Cross-References: EMBL:AL133314
A:Experimental source: cultivar Columbia; BAC clone F12A12
C:Genetics:
A:Map position: 3
A:Note: F12A12.50

Query Match 12.9%; Score 660; DB 2; Length 835;
Best Local Similarity 26.2%; Pred. No. 4.8e-30;
Matches 230; Conservative 175; Mismatches 302; Indels 170; Gaps 35;
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

QY 9 LLDNLTCIGELG-----LILGPRDEPEKOSTTTTQAVLEDAQKQKQKAIEN 60
DB 1 MVDATIEFVVGKIGNYLLIEASMEVAVEDLEELTELCTHGYLKQVAREDEDESKS 60
QY 61 WLQKLNAAAYEADILDECKTEAPFROKKYGCYHPNVYTFPHKIGKMKIMEKLDV- 119
DB 61 WSKVLDEPAYVEVDLDTYHKLKEERSGR-----GLRLTYLKIGKQMDAYSIVDIR 113
QY 120 IAAERIKFHLDETERIQVATRGTFVLEPQVY-----RDXKDEIV-- 163
DB 114 ILKRI---LD---ITRRETYGIG-GLKEPQGGNTSLRQLRRARSVDQEVVGL 166
QY 164 ---KILINVSNAQTLP--VPLILMGGLGKTTLAQWPNDRVLEHHPKWTICVSE 217
DB 167 EDDAKILLEKLDYEBKRRPFIISIFMGGLKTLARQLYNSRDVKEFEYRAWTYSQ 226
QY 218 FNEKRLIKETIESIEKSLGMDLAPLOK-----KLARDLNGKKYLLVDVWNEDQ 269
DB 227 YKTGDILKRIIRSLGNTS--GEELKIRKPAEELVYLYGLSGKYLVAVDIIV--ER 282
QY 270 DKMAKRLQVLNVGASGAVLTTRLEKVG-SINGTLQPYELSNLSQEDCMLFMORAGH 328
DB 283 EAWDSLKRALPCNHGSKVITITRIKAVABGVDRFPAHKRLRFLPEBSWELFQGRARN 342
QY 329 QEEINLNLVAGKIVKCGVPLAATLGLILKPKREKREMEHVRDEIKTLPOEBS-S 387
DB 343 IQRDDEDLKTKGEMVQKCRPLPCIVVLAGLS--RKTPSMDNVQNS-LWRRLKDSIH 400
QY 388 ILP-ALRLSYHHLPLDROCFYCAVFPKOTEMEGNLSLMAAHGFILSKNLELENVG 446
DB 401 VAPVDFDSFELNHEKSLCPYLSIFPEDEIIDEKLIHLVABGFIQGBEEMMEBVA 460
QY 447 NEVNNELYSRFPFOEIEVKSQGY-FQMDLIDHLA-----TSLFS--ASTSSN 493
DB 461 RYIEELIDRLDLAVRREKGVMSCRHDLRLVALIKSKELNFVYVYNDHVAQHSST 520
QY 494 IREIIVENYIMMSIGTKVSSYLSHLQKFTSLRYLNLSDTLQK-----LRSI 545
DB 521 CRREVVHQFQKRVYSSEKRRKRRMSFLYFGEFHLVGLDEFTLKLRLVLDGSLMLPFI 580


```

QY 589 LPKETSKLGSRLNLLDGCYGLTCMPRIGSLTCLKTLSPFVVGIOKKSQCLGELRLN-N 647
D 629 -----RINS-----GQLINPN 640
QY 648 LYGSIEITHLERVKNMDAKKANLSAKR-NLHSLSMKDDDERPRIYSEKVEVLELTK 705
D 641 VF-----KEMLEIRYLSLFW----- 656
QY 706 PHSNLTCLTIRGFRGIRLPLDMNHSVLKNVYSIEI-----SCNKSCLPFGELPCLKSLR 762
D 657 -RSLTLKLE-----LGNLKLKELTLNPFSTK----- 680
QY 763 LMRGSAEVEYVDGSGPTRRRPPSLKLNIREFGNLKGLLKKGEQCVLEIEIKCCPM 822
D 681 -----DSSVTLDRHTKRLTQLILSG--EGLHMETLSALSMLGHLR---DL 723
QY 823 FVITPLLSVK---KLVSIGKSDAIGRSSISNMLATSLQIRYKKEASLPEEFKSLA 878
D 724 TVTSENSVQPKHPLIYRPMIPVQHPPS-----HLTTLISLVY---CFLSEDEMPYLE 774
QY 879 NLKTLN-LSFYENL---KEPLTSLASLNAHLKHLTHSCYALRS-LPEEGVKGSLSTQLS 933
D 775 KLLQKLVSLWYNVAVGRMYCTGGGFPPLRLHRLWGLDLEBWIVEGSMPL-LHTLH 832
QY 934 ITCCEMLQCLPEGLQHLTALTNLSVEFC-PTLAKRCEKIGEDWYKIAHPRV 985
D 833 IVDCKKLKEIPDGLRFLISSLKEMLARTMEKVFQKKVSKG-GEDEYKMGHVPLI 884

```

RESULT 13

```

106219
Probable cytochrome resistance gene - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: 106219
R:Lagudah, B.S.; Mouillet, O.; Appels, R.; Chandramohan, S.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z15543
A:Accession: 106219
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-797 <LNG>
A:Cross-references: UNIPROT:O65113; EMBL:AF052641; NID:G2967836; PIDN:AA05834.1; PID:92
A:Experimental source: cv. AUS 18913
C:Genetics:
A:Gene: Cre3
A:Map position: 2DL

```

```

Query Match 12.7%; Score 649; DB 2; Length 797;
Best Local Similarity 25.2%; Pred. No. 1.9e-29;
Matches 245; Conservative 146; Mismatches 309; Indels 272; Gaps 37;

```

```

QY 105 KIGKRMK-----IMKLDVIAERIKFHLDERTIRQVATROTGVLANEPOVYG 154
D 5 KLVSLKKEININEAHQILEKLNIS-----ISDNIRHTWVNPPTTAVSPQKVF 57
QY 155 RDKKDEIVKTLIN-----NVSNAOTLPVLPILMGSLKKTLLAQVVF-----NDQR-- 201
D 58 RDNORDKTIANLHKEKGLDPSSTGKLCFSVYIGHVSGSGSTLAQCVVAHEKNDKDN 117
QY 202 VIEHFPKIMIVCSDEPNKRLIKEIVSIEKSL---GMDLAPLQCKLDLNGKYL 258
D 118 KEDHFDLVMMVHVQDPSVWGIPEKELYEASDPKPCQGFNNINLLEBELRKDKGRFL 177
QY 259 LVLDVW-NED--ODKMLROVLKVGASGASVLTTLTL-----EKVSGINGTLQPYELS 310
D 178 LVLDVWGNADVGNQELPKLSPLEKKGKSKILVTTSKYALPDLCPGVYTMP--IT 235
QY 311 NLSGEDCGLLTMQARF--GHOEINLNLVAIGKEIVKCGVAPLAAKTLIGLRKREER 368
D 236 EVDDTAFPEELFMHVALEDGQDSMPQN--IGVEIAKLLKSPLAARTVGNLRQGDVD 292
QY 369 QMEHVRSDE---IWKLQDESSILPALRLSYHHLPLDLRQCFYCAVPKDTMEKGLI 425

```

```

D 293 HMRVQDULPKVWTGP-----LWMSYQGEQARCFACVCSIFRRHRLYRDELV 343
QY 426 SLMAHGFILSKG-NLELVENGVNMLYLRSPFO---EIEVSGQTYFKMHLIDLA 481
D 344 RLMABEGRITBDGADVEDVGLIPNELLSISFLQPGQGMVNHGKEYIVLHDLVYLA 403
QY 482 -----TSLFS-----ASTSSNIREIIVENY-----IHMM--S 507
D 404 GAVAGTCOFRLDNNMIOKBSMAKDVPRVHRLVFQSDALITGLVLENLHTLVYS 463
QY 508 IGFTRVSVSLSLQFV-SLRVLNLS-----DYLKQLPSSIGLVHLRYNL 556
D 464 VGGDTVVEEIVIKNILSLPLRVLATLALCLEKQGFICRPNILSVESIQLKRLRYLAF 523
QY 557 SGNISIR-SLPNOCIKONLTLDLHGCHSLCCLPKETSKLGSRLNLLDGCYGLTCMP 615
D 524 RTDIECRYLPSLSNOLYOMOLDPFGVCANL-----VFSCGDLIN-LRHVCSGFGLOPS 576
QY 616 RIGSLTCLKTLSPFVVGIOKKSQCLGELRLN-LYGSIEITHLERVKNMDAKKANLSAK 674
D 577 NIGRLVSLQITPAKVS-HEQGHEAKQRLYNRLSGELSIYGLQSVESREBALAFDLAAK 635
QY 675 ENHLSMKWDDBRPRIYSEKVEVLEALKPHSNLTCLTTRGFRGIRLPLDMNHSVLKN 734
D 636 KRLAELTSLFSGS-----SEVAEVLGCLPVGVLVTLDRDYDGLVYPRKM----- 682
QY 735 VVSIEIISCKNCSCLPFGELPCLKSLLEMRGSAEVEYVDGSGPTRRRPSLRKLNIREF 794
D 683 -----V 683
QY 795 GNLKGLKKEGEEOCPVLEIEIKCCPMFVITPLSVKLVVSGDKSDAIGSSISNLMA 854
D 684 GRQNGAPEK-----LQQLSGWSQSG----- 705
QY 855 LTSIQIRYNKDALPEEMFGLANLKYLNISFYFNKLEPLTSLASLNAHLKHLTHSCYA 914
D 706 -----PAPALKAFFNLICLNL-MICSMNALPCNNHLSLETLVYIIKCLN 749
QY 915 LESLPEBVGKLSLTQLSIYCEMLQCLPEGLQHLTALTNLSVEFCPTLAKRCEKIGE 974
D 750 IRLSP-----TLPO-SLTYFWLKC-DUGF-----WESCOTVGH-----P 782
QY 975 DWYKIAHPRVF 986
D 783 NMKTIQHCRKC 794

```

RESULT 14

```

751185
Resistance protein Rpp13 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C:Accession: 751185
R:Altner-Boddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L.
Plant J. 21, 177-188, 2000
A:Title: Rpp13 is a simple locus in Arabidopsis thaliana for alleles that specify downy mildew resistance
A:Reference number: Z25333
A:Accession: 751185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-831 <BIT>
A:Cross-references: EMBL:AF209731; PIDN:AAF42831.1
A:Experimental source: cultivar Rid
C:Genetics:
A:Gene: RPP13
A:Map position: 3
C:Superfamily: disease resistance protein Rps2; leucine-rich alpha-2-glycoprotein repeat

```

```

Query Match 12.4%; Score 635.5; DB 2; Length 831;
Best Local Similarity 26.6%; Pred. No. 1.2e-28;
Matches 239; Conservative 173; Mismatches 335; Indels 153; Gaps 38;

```


Db 832 DGATKMI 839

Search completed: April 16, 2005, 01:23:21
Job time : 62 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 01:11:09 ; Search time 188 Seconds

(without alignments)
2691.140 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFQLVLDNLTCFIQGE.....EKIGEDMYKIHPRVFIY 988

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprotc:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3766.5	73.5	970	1	RGAA2 SOLBU
2	3753	73.2	1025	1	RGAL SOLBU
3	3745	73.0	948	2	OGTAFF
4	3687.5	71.9	947	2	OGTAFF
5	3669	71.6	948	2	OGTAFF
6	3587	70.0	988	1	RGAA3 SOLBU
7	3483.5	67.9	947	1	RGAA3 SOLBU
8	1517	29.6	1110	2	OG4J89
9	1516	29.6	1222	2	OG4J89
10	1479.5	28.9	1035	2	OG4XG0
11	1479	28.8	1024	2	OG4XG0
12	1477.5	28.8	1108	2	OG4XG0
13	1464.5	28.6	1259	2	OG4XG0
14	1463.5	28.5	1259	2	OG4XG0
15	1436	28.0	1048	2	OG4XG0
16	1414	27.6	1081	2	OG4XG0
17	1395	27.2	1124	2	OG4XG0
18	1385	27.0	1124	2	OG4XG0
19	1381	26.9	1129	2	OG4XG0
20	1367.5	26.7	1189	2	OG4XG0
21	1366	26.6	1217	2	OG4XG0
22	1362	26.6	1217	2	OG4XG0
23	1359.5	26.5	1133	2	OG4XG0
24	1355.5	26.4	1210	2	OG4XG0
25	1350.5	26.3	1124	2	OG4XG0
26	1346.5	26.3	1292	2	OG4XG0
27	1331.5	26.0	1066	2	OG4XG0
28	1312.5	25.6	1274	2	OG4XG0
29	1311.5	25.6	1261	2	OG4XG0
30	1307	25.5	1322	2	OG4XG0
31	1299	25.3	1105	2	OG4XG0

32	1288.5	25.1	1054	1	R131_ARATH
33	1287	25.1	1118	2	OG3V16
34	1284.5	25.1	1211	2	OG8ZF0
35	1277.5	24.9	1315	2	OG8ZD0
36	1251	24.4	1406	2	OG13G4
37	1244	24.3	1266	2	OGXET3
38	1243	24.2	1312	2	OG8ZD5
39	1240	24.2	1240	2	OG4016
40	1234	24.1	1279	2	OG6A87
41	1221.5	23.8	1073	2	OG6A36
42	1212	23.6	1220	2	OG4015
43	1211.5	23.6	1297	2	OG4556
44	1211	23.6	1286	2	OG9A83
45	1197	23.3	1284	2	OG13K6

ALIGNMENTS

RESULT 1
RGAA2 SOLBU STANDARD: PRT: 970 AA.
ID RGAA2 SOLBU
AC Q7XBQ9; Q7XA18; Q7XA41;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disease resistance protein RGA2 (RGA2-b1b) (Blight resistance protein RPI)
GN Name=RGAA2; Synonyms=177013.40, CB3A14.5, RB, RPI-BLB1;
OS Solanum bulbocastanum (Wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Solanum.
CC NCB1_TaxID=147425;
CC [1]
CC SEQUENCE FROM N.A. AND VARIANTS.
CC RP PubMed=12872003; DOI=10.1073/pnas.1533501100;
CC RX Song J., Bradeen J.M., Naess S.K., Raesch J.A., Wielgus S.M.,
CC RA Haberlach G.T., Liu J., Kuang H., Auecht-Phillips S., Buell C.R.,
CC RA Helgeson J.P., Jiang J.;
CC RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
CC resistance to potato late blight."
CC Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).
CC [2]
CC SEQUENCE FROM N.A.
CC RP PubMed=14675451;
CC RA Van Der Vossen E., Sikkema A., Heekert B.C., Groen J., Stevens P.,
CC RA Muijken M., Wouters D., Pereira A., Stiekema W., Alfaro S.;
CC RT "An ancient R gene from the wild potato species Solanum bulbocastanum
CC confers broad-spectrum resistance to Phytophthora infestans in
CC cultivated potato and tomato."
CC Plant J. 36:867-882 (2003).
CC RL
CC -1- FUNCTION: Disease resistance protein. Resistance proteins guard
CC the plant against pathogens that contain an appropriate avirulence
CC protein via a direct or indirect interaction with this avirulence
CC protein. That triggers a defense system which restricts the
CC pathogen growth. Confers a broad resistance to all known races of
CC P. infestans.
CC P. infestans.
CC -1- INDUCTION: Constitutively expressed.
CC -1- BIOTECHNOLOGY: Can be introduced into cultivated potato
CC (S. tuberosum) or tomato (L. esculentum) to transfer a broad-
CC spectrum late blight resistance to cultivated Solanaceae from
CC sexually incompatible host species.
CC -1- MISCELLANEOUS: Belongs to a four-gene family located at the same
CC locus. Although the four genes are expressed in the resistant
CC haplotype, only RGA2 confers the resistance to P. infestans. In the
CC susceptible haplotype, RGA1 and RGA4 are likely to be pseudogenes
CC created by deletions and mutations, while RGA2 contains also
CC several modifications.
CC -1- SIMILARITY: Belongs to the disease resistance NB-LRR family.
CC -1- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 NB-ARC domain.
CC -1- CAUTION: Ref.1 (AAP45164) sequence differs from that shown due to

```

CC      an internal deletion of the corresponding genomic clone.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY336128; AAP86601.1; -
DR      EMBL; AY303170; AAP45164.1; -
DR      EMBL; AY303171; AAP45188.1; -
DR      EMBL; AY426259; AAR29069.1; -
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR002182; NB-ARC.
DR      Pfam; PF00560; LRR; 10.
DR      Pfam; PF00931; NB-ARC; 1.
KW      ATP-binding; leucine-rich repeat; Plant defense; Repeat.
FT      NP_BIND 182 189      ATP (Potential).
FT      DOMAIN 135 438      NB-ARC.
FT      REPEAT 525 548      LRR 1.
FT      REPEAT 550 571      LRR 2.
FT      REPEAT 573 594      LRR 3.
FT      REPEAT 595 619      LRR 4.
FT      REPEAT 638 662      LRR 5.
FT      REPEAT 672 697      LRR 6.
FT      REPEAT 752 777      LRR 7.
FT      REPEAT 787 811      LRR 8.
FT      REPEAT 813 832      LRR 9.
FT      REPEAT 833 857      LRR 10.
FT      REPEAT 859 882      LRR 11.
FT      REPEAT 884 906      LRR 12.
FT      REPEAT 907 931      LRR 13.
FT      REPEAT 946 970      LRR 14.
FT      VARIANT 22 22      V -> A (in susceptible haplotype).
FT      VARIANT 449 540      Missing (in susceptible haplotype).
FT      VARIANT 889 894      Missing (in susceptible haplotype).
SQ      SEQUENCE 970 AA; 110346 MW; 3727029C3CAD9C47 CRC64;

Query Match 73.5%; Score 3766.5; DB 1; Length 970;
Best Local Similarity 75.6%; Pred. No. 2,1e-205;
Matches 753; Conservative 76; Mismatches 130; Indels 35; Gaps 8;

```

```

DB      420 EKEKTLISMAHAGLTLKSKNNMELSDVGDEWVKELIYLSFQELBVKQDKTYFKMHLIHD 479
QY      480 LATSIPGASTSSNIREIIVENTYIMHMSIGFTKVSSYSLSHLOKFSVLRNLSDIKK 539
DB      480 LATSIPGASTSSNIREIIVENTYIMHMSIGFTKVSSYSLSHLOKFSVLRNLSDIKK 539
DB      480 LATSIPGASTSSNIREIIVENTYIMHMSIGFTKVSSYSLSHLOKFSVLRNLSDIKK 539
QY      540 QLPSSIGDVLHRLNLSGNTSIRSLPNQCLQNLQTLDLHGCHSLCCPKETSKGSL 599
DB      540 KLPSSIGDVLHRLNLSGNTSIRSLPNQCLQNLQTLDLHGCHSLCCPKETSKGSL 598
QY      600 RNLLDGCYGTGMPPIGSLTCLKTLSPRVFVGIQKSCQGLGELRNILVGSIEITLER 659
DB      599 RNLLDGSQSLTCTMPPIGSLTCLKTLGQVVG-RRKGQYQGLGELRNILVGSISHLER 657
QY      660 VKNDMDAKKANLSAKENHLSLNMKDDDERPRIYESKEVLEALKPHSNLTCTITGRF 719
DB      658 VKNDMDAKKANLSAKENHLSLNSMSW--NNFGPHIYESKEVLEALKPHSNLTSLKIYGFR 716
QY      720 GIRLPDMNHSVYLNKIVSTELISCRNCSCLPPRGELPCLKSLBLMRSAAVEEYVD 774
DB      717 GIIHLPDMNHSVYLNKIVSTELISCRNCSCLPPRGELPCLKSLBLMRSAAVEEYVDID 776
QY      775 --SGFPTRRRPPSLRKINIREFGNLKGLKKGEBOCPVLEIEIKCCPMFVITLSSVK 832
DB      777 VHSGFPTRRRPPSLRKINIREFGNLKGLKKGEBOCPVLEIEIKCCPMFVITLSSVK 830
QY      833 KLVVSGDKSDAIGFSSISNLMALTSQIRYNKEDASIPREMFKSLANLYKINISFYFNK 892
DB      831 -----SNLRALTSLRICYNKVAATSPPEMFKNLANLYKLTISRNNLK 873
QY      893 ELPTSLASLNALKHLIEHSCYALESLPEBGVKGLISTOISTYCEWLOCLPGLQHLTA 952
DB      874 ELPTSLASLNALSKLQICLCALESIPBEGLSITELFVBCNNMLKCLPGLQHLTT 933
QY      953 LTNLSVECPPTLAKRCEKSGIGEDMYKIAHPIRYFIY 988
DB      934 LTNLSKIRGCPQLIKRCEKSGIGEDMYKISHIPNNIY 969

RESULT 2
RGAL SOLBU STANDARD; PRT; 1025 AA.
ID RGAL SOLBU
AC 07XA42; 07XA21.
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative disease resistance protein RGAL (RGA3-b1b).
GN Name=RGA3; Synonyms=17013.37, CB3A14.4;
OS Solanum bulbocastanum (Wild potato).
OC Caryophyta; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=147425;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANTS.
RX PubMed=12872003; DOI=10.1073/pnas.1533501100;
RA Song J., Bradeen J.M., Naess S.K., Raesch J.A., Wielgus S.M.,
RA Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
RA Helgeson J.P., Jiang J.;
RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
RT resistance to potato late blight."
RL Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Hekkert B.T., Groe J., Stevens P.,
RA Mekens M., Wouters D., Pereira A., Stiekema W., Allefs S.;
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato."
RL Plant J. 36:867-882 (2003).
CC -I- FUNCTION: Disease resistance protein. Resistance proteins guard

```



```

Db      890 ALTSIDISDNVATSPSEEMFKSIANLKYLIKISFENLKEPLTSLASINLAKSIFECED 949
QY      914 ALESIPBEVGVKLISITOUSITYCEMLQCLPBGLOHTLTMLTSVEFCCTLAKRGKIG 973
Db      950 ALESIPBEVGVKLISITELSVSNCMWLKCLPBGLOHTLTMLTTLTQCPVKEKCEGIG 1009
QY      974 EDMYKIAHIPRVFIY 988
Db      1010 EDMYKIAHIPVLTLY 1024

RESULT 3
Q6TAF7 PRELIMINARY; PRT; 948 AA.
AC Q6TAF7;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Blight resistance protein T118 (Fragment).
OS Solanum tajiense.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=257458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Hekkert B.T., Gros J., Stevens P.,
RA Muskens M., Mouters D., Pereira A., Stiekema W., Allefs S.,
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato."
RT Plant J. 36:867-882(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA van der Vossen E., Allefs S.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426266; AAR29076.1;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR03058; wing_hlx_DNA_bnd.
DR Pfam; PF00560; LRR_1; 9.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT NON_TER 948
FT SEQUENCE 948 AA; 108444 MW; 09E14450231751D5 CRC64;

Query Match 73.0%; Score 3745; DB 2; Length 948;
Best Local Similarity 76.0%; Pred. No. 3.4e-204;
Matches 744; Conservative 84; Mismatches 116; Indels 34; Gaps 6;
QY 1 MAEAFLOVLLDNLTCTFOGELIGLFGKDEFEKLQSTFTTIOAVLEDAOKKOLKDKAIEN 60
Db 1 MAEAFIOVLLDNLTCTFOGELIGLFGKDEFEKLQSTFTTIOAVLEDAOKKOLKDKAIEN 60
QY 61 WLQGLNAAAYEADLDLDECTEAPIRKKNKYGCYHENVITFRHKGKMKIMKELDVT 120
Db 61 WLQGLNAAAYEADLDLDECTEAPIRKKNKYGCYHENVITFRHKGKMKIMKELDVT 120
QY 61 WLQGLNAAAYKVDLDLDECKA---ARLEQSLGRHHPKAIIVFRHKGKIKEMMEKLDAL 117
Db 61 WLQGLNAAAYKVDLDLDECKA---ARLEQSLGRHHPKAIIVFRHKGKIKEMMEKLDAL 117
QY 121 AAEIRKPHLERTEROVATKRGFVINEPOYVGRDKEKDEIKYLLINNSNMQTLPLP 180
Db 121 AAEIRKPHLERTEROVATKRGFVINEPOYVGRDKEKDEIKYLLINNSNMQTLPLP 180
QY 118 AKERTDFHLEKTIEROVAREPTEPVLTPEOVYGRDKEDEIKYLLINNSNMQTLPLP 177
Db 118 AKERTDFHLEKTIEROVAREPTEPVLTPEOVYGRDKEDEIKYLLINNSNMQTLPLP 177
QY 181 ILGNGGIGKTTLLAQMVENDQVLEHFPKWTIMCVSEDFNEKRLIKETIVESIEKSGMD 240
Db 178 ILGNGGIGKTTLLAQMVENDQVLEHFPKWTIMCVSEDFNEKRLIKETIVESIEKSGMD 240

```

```

QY 241 LAPLOKRLDILNKKYLLVLDVWNEDODKALROVLKYVGASGVLTTRILEKYSI 300
Db 238 LASFOKRLQOLNKGRIYLLVDVWNEDQCKMDLIRVLKYVGASGVLTTRILEKYSI 297
QY 301 MGLTQPYELNLSQEDCMLLFMQRAFQHEBINLNLVAIGKEIYKCGGVPLAKTGGI 360
Db 298 MGLTQPYQSLNSQDDCMLLFQRAFRQHEBINLNLVAIGKEIYKCGGVPLAKTGGI 357
QY 361 LRFGRERQWEHVVDSEIWKLPQESSILPALRLSYHLLPDLNQCTTYCAVFPKOTEME 420
Db 358 LRFGRERQWEHVVDSEIWKLPQDEMSILPVLRLSYHLLPDLNQCPAYCAVFPKOTEME 417
QY 421 KGNLISLMAHGFLLSKGNLELVNGEVMWVETLYRSFPOEIEYKSGQTFKMHDLIHD 480
Db 418 KKVYISLMAHGFLLSRNLELEVDGNEVMWVETLYRSFPOEIEYKNTYFKMHDLIHD 477
QY 481 ATSLPSASTSSNIREIIVENYIH-MMSIGFTKVSSYSLSHLQKPVSLRVNLSDIKLK 539
Db 478 ATSLPSASTSSNIREIIVENSYTHMMWSIGPSEVSSYSLSHLQKPVSLRVNLSDIKLK 537
QY 540 QLPESIGDLYHRLNLSGNTSIRSLPNOICLQNLQTLDLHGCHSLCCLPKETSKLSL 599
Db 538 ELPSIGDLYHRLNLSGNTSIRSLPNOICLQNLQTLQYCTRLCCLPKQTSKLSL 597
QY 600 RNLLDGCYGTGMPPIGSLTCLKTLRSFVVGIOKKSQCLGELRNMLNLYGSIETHLER 659
Db 598 RNLLHGHCHLTLTPRIGSLTCLKTLGQFYVK-RKKGYOLGELGSLNLYGSIKISHLER 656
QY 660 VKNDMAKEANLAKENLHSLSMKMDDERPRIYESKVEVLBALRPHSNLTCLITRGFR 719
Db 657 VKNDKEAKEANLAKENLHSLSMKMDDERPHRYESEVVLBALRPHSNLTCLITISGR 716
QY 720 GIRLPDMNHSVLYKNVSTETIISCKNCSCLPPEGELPCLKSLLEMGSAE-----VEYV 773
Db 717 GIRLPDMNHSVLYKNVLTILHISCKNCSCLPPEGDLPCLESILQLYGSAEYVEVDIVAE 776
QY 774 DSGFPTRRPRLRKINIREFNGIKGLKKEGEGQCPVLEIEIRKCPMFIPTLSVVK 833
Db 777 DSGFPTRRIRPSLRKICICIKFDMLKGLVKGEGEQPVLEEMIRYCP---IPTLS---- 829
QY 834 LVVSGDKSDAIGPSSISNLMALTSIQIRYNKEDASLPSEMFKSILNLYKINSFYNNLKE 893
Db 830 -----SNLKALTSILNISDNKEATSPSEEMFKSIANLKYLINISHFNNLKE 873
QY 894 LPTSLASINLAKLHLSHCYALSELPEBGYKGLISITOUSITYCEMLQCLPBGLOHTLT 953
Db 874 LPTSLASINLAKSLKIQWCCALSESIPBEGVGLTSLTELIVKCKMLKCLPBGLOHTLT 933
QY 954 TNLSEFCPTLAKRC 968
Db 934 TRVKGCCPQLIKRC 948

RESULT 4
Q6TAF8 PRELIMINARY; PRT; 947 AA.
AC Q6TAF8;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Blight resistance protein SH20 (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Hekkert B.T., Gros J., Stevens P.,
RA Muskens M., Mouters D., Pereira A., Stiekema W., Allefs S.,
RT "An ancient R gene from the wild potato species Solanum bulbocastanum

```

```

RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato.
RL Plant J. 36:867-882(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA van der Vossen E., Allefs S.,
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426265; AAR29075.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 9.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT NON TER 947 947
SQ SEQUENCE 947 AA; 108156 MW; ED8B31B5044339EE CRC64;

Query Match 71.9%; Score 3687.5; DB 2; Length 947;
Best Local Similarity 75.4%; Pred. No. 6.3e-201;
Matches 734; Conservative 83; Mismatches 124; Indels 33; Gaps 7;

QY 1 MAEAFLOVLDNLTCTFIOGELGLIGFDEBEKQSTFTTIOAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFIOVLENTITSFIOGELGLIGFENDPENISSRSTIOAVLEDAQKQKLDKAIEN 60
QY 61 WLQQLNAAVYVADDDILDECKTEAPIRQKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 120
DB 61 WLQQLNAAVYVADDDILDECKTEAPIRQKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 117
QY 121 AAERIKTHLDEBTEROVATQTFQVFNLEPOVYGSDKDEIKVILLNNVNAQTLPLVP 180
DB 118 AKERTDTHLHEKIIERQVAREPETGFVLTEPOVYGSDKDEIKVILLNNVNAQTLPLVP 177
QY 181 ILGNGGIGKTLAOMVFNDOVVIHFHFKIWCSESDNEKRLLKEIYESIEEKSLGMD 240
DB 178 ILGNGGIGKTLAOMVFNDOVVIHFHFKIWCSESDNEKRLLKEIYESIEEKSLGMD 237
QY 241 LAPQKRLDLDLNGSKYLLVLDVWNEBQDKMAKLQVLYKVGASGASVLTTRLEKYSI 300
DB 238 LASFOKQLQQLNGKRYLLVLDVWNEBQDKMAKLQVLYKVGASGASVLTTRLEKYSI 297
QY 301 MGLQPYELNSLQSEDCWLLFMQRAFGHQBSEINLVAIGKIVKCGVPLAAKTGSI 360
DB 298 MGLQPYQVLSLQSEDCWLLFMQRAFGHQBSEINLVAIGKIVKCGVPLAAKTGSI 357
QY 361 LRFKREBROWHVDSEIWKLPQESSILPLRLSYHNLPLDLQCFYCAVPKDTOME 420
DB 358 LRFKREBROWHVDSEIWKLPQESSILPLRLSYHNLPLDLQCFYCAVPKDTOME 417
QY 421 KGNLISLMAHGFILSKNLELVNNGVNMELVRSFQIEVYSQTYFKMDLIHDL 480
DB 418 KKKYISLMAHGFILSKNLELVNNGVNMELVRSFQIEVYSQTYFKMDLIHDL 477
QY 481 ATSLFSASTSSNRIEIVENYIH-MMSIGFTKVVSYSLSLQKFSVLYALNLDIKL 539
DB 478 AXSLFSASTSSNRIEIVENYIH-MMSIGFTKVVSYSLSLQKFSVLYALNLDIKL 537
QY 540 QLPBSIGDVLVRLNLSGNTSISLPLQCLQNLQTLDLHGHSGLCCLPKESKLSL 599
DB 538 ELPSISIGDVLVRLNLSGNTSISLPLQCLQNLQTLDLHGHSGLCCLPKESKLSL 597
QY 600 RNLLDGCYGLTCLMPRIIGSLTCLTSLRFPVGIQKSCQGLGELRNLLNLSYSEITHLER 659
DB 598 RNLLDGCYGLTCLMPRIIGSLTCLTSLRFPVGIQKSCQGLGELRNLLNLSYSEITHLER 656
QY 660 VKNDMAKEANLSAKENISLSMKWDDERPRIYSESEVYVLEALKPHSNLTCLTIRGER 719
DB 657 VKNDMAKEANLSAKENISLSMKWDDERPRIYSESEVYVLEALKPHSNLTCLTIRGER 716

```

```

QY 720 GIRLPDMNNSVLRKNVSIIEISCKNSCLPPFGELPCLKSLIMKRSAAE-VEX-----VD 774
DB 717 GIRLPDMNNSVLRKNVSIIEISCKNSCLPPFGELPCLKSLIMKRSAAEVEEVDIDVD 776
QY 775 SGFPTRRRPSRLKLTNIREGNLKGILLKSGEBCPVLIEIEICCPMFVPTLSSVKL 834
DB 777 SGFPTRRRPSRLKLTNIREGNLKGILLKSGEBCPVLIEIEICCPMFVPTLSSVKL 828
QY 835 VVSGDKSDAIGFSSISNLMALTSQIRYNKEDASLPREMFKSLANLYLNISFYNLKEL 894
DB 829 -----PVLKALTSANISDNKEATSFPBEMFKSLANLYLNISFYNLKEL 873
QY 895 PTLASINALKHLEIHSQYALLESIPBEGVKGSLSTQLSITYCEMLQCPBGLQHLTALT 954
DB 874 PTLASINALKHLEIHSQYALLESIPBEGVKGSLSTQLSITYCEMLQCPBGLQHLTALT 933
QY 955 NLSVEPCTLAKRC 968
DB 934 RLKIMGCPQLIKRC 947

RESULT 5
Q6TAF9 PRELIMINARY; PRT; 948 AA.
ID Q6TAF9
AC Q6TAF9;
DT 05-JUL-2004 (TREMBLERL. 27, Created)
DT 05-JUL-2004 (TREMBLERL. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLERL. 27, Last annotation update)
DB Bilgult resistance protein SH10 (fragment).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
CX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Hekkert Bt B.L., Gros J., Stevens P.,
RA Muijken M., Moutere D., Pereira A., Stiekema W., Allefs S.;
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato."
RL Plant J. 36:867-882(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA van der Vossen E., Sikkema S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426264; AAR29074.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 8.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT NON TER 948 948
SQ SEQUENCE 948 AA; 108223 MW; 593E29C0EBCBFC06 CRC64;

Query Match 71.6%; Score 3669; DB 2; Length 948;
Best Local Similarity 75.7%; Pred. No. 7.1e-200;
Matches 734; Conservative 70; Mismatches 142; Indels 24; Gaps 5;

QY 1 MAEAFLOVLDNLTCTFIOGELGLIGFDEBEKQSTFTTIOAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFIOVLENTITSFIOGELGLIGFENDPENISSRSTIOAVLEDAQKQKLDKAIEN 60
QY 61 WLQQLNAAVYVADDDILDECKTEAPIRQKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 120
DB 61 WLQQLNAAVYVADDDILDECKTEAPIRQKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 117

```

```

Db      61  WLQKLNATYEVDDILDDEYKTKA-TRFSQSAVGRHYHFKVIFPRHVKGRMDQVKKLNAI 119
QY      121  AAEIKTHLDEBRTIEROVATKOTGFVNLNEPQVGRDKEDEIKVILINNVSNAOQLTPVLP 180
Db      120  AAEKKNFHLHEKTIIRQAVRRETSVLTEPOVYGDKEDEIKVILINNVSNAOQLTPVLP 179
QY      181  ILGNGGIGKTTIAQVNFQDQVHIFHFKIWCYSEDPENKRLIKEIVESIEEKS-LOGM 239
Db      180  ILGNGGIGKTTIAQVNFQDQVHIFHFKIWCYSEDPENKRLIKEIVESIEEKS-LOGM 239
QY      240  DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVSGASVLTTLTLEKSGS 299
Db      240  DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVSGASVLTTLTLEKSGS 299
QY      300  IMGTLOPYELSNLSOEBCWMLFMORAFGHOEINLVAISKEIYKKGCVPLAKTIGG 359
Db      300  IMGTLOPYELSNLSOEBCWMLFIQCAFQHOEINLVAISKEIYKKGCVPLAKTIGG 359
QY      360  ILRPFKEBROWEHVRSSEIWLPOESSILPALRLSYHHLPLDROCFYCAVFPKDTM 419
Db      360  ILRPFKEBROWEHVRSSEIWLPOESSILPALRLSYHHLPLDROCFYCAVFPKDTM 419
QY      420  EKMGLISIMAHAGTILSKNLELVNGVWNNELYSFQFQIEYKSGQTYFKMHLHD 479
Db      420  EKMGLISIMAHAGTILSKNLELVNGVWNNELYSFQFQIEYKSGQTYFKMHLHD 479
QY      480  LATSLSFASTSSNIREIIVENYIH-NMSIGFTKVSSYSLSLQKQFSLVNLSDIKL 538
Db      480  LATSLSFASTSSNIREIIVENYIH-NMSIGFTKVSSYSLSLQKQFSLVNLSDIKL 538
QY      539  KQLPSSIGDLVHLVYLNISGNTSIRSLPNQCLQNIQTLDLHGCHSLCCLPKETSKGS 598
Db      540  EELSSSIGDLVHLVYLNISGNTSIRSLPNQCLQNIQTLDLHGCHSLCCLPKETSKGS 599
QY      599  LRNLILGCGYGLTQMPRIISGLTCLKTSRPVNGIQKSCQGLRMLNLYGSIETITLE 658
Db      600  LRNLIFHCGBELNSMPRIISGLTCLKTSRPVNGIQKSCQGLRMLNLYGSIETITLE 659
QY      659  RVKNDMDAKEANLSAKENLHLSMKMDDEPRRIYSESEKVEVLALPKHSLVLTCLTIRGF 718
Db      660  RVKNDMDAKEANLSAKENLHLSMKMDDEPRRIYSESEKVEVLALPKHSLVLTCLTIRGF 718
QY      719  RGIRLPMMHNSVLKAVSIRIISCKNCSCLPPFGEIPLCLSKLSLELWGSAAVEVYDGGFP 778
Db      719  RGIRLPMMHNSVLKAVSIRIISCKNCSCLPPFGEIPLCLSKLSLELWGSAAVEVYDGGFP 778
QY      779  TRRRFSLRLKLTIEFGNKLKLGEGEQQPVLEIEIKCCPMFVPLTSSVKKLVVSG 838
Db      779  TRRRFSLRLKLTIEFGNKLKLGEGEQQPVLEIEIKCCPMFVPLTSSVKKLVVSG 838
QY      839  DKSDAIGFSSISNIMALTSLQIRYKEDASLPPEMFKSLANLKYINISFYNLKELPTSL 898
Db      830  -----SNRALTSLHSHNNKATSLPEEIFSPALUKTLKLSLFPNLKELPSL 878
QY      899  ASLNALKHLTHSCYALLESIPREGVKGILSTQISTYCEMLQCLPGLQHLNLTNLV 958
Db      879  ACNALATLHSCYALLESIPREGVKGILSTLTFVYDCEMLKELPGLQHLNLTNLV 938
QY      959  EFCPTLAKRC 968
Db      939  RRCPOLIKRC 948

```

```

OC      119  WLQKLNATYEVDDILDDEYKTKA-TRFSQSAVGRHYHFKVIFPRHVKGRMDQVKKLNAI 119
OC      180  AAEIKTHLDEBRTIEROVATKOTGFVNLNEPQVGRDKEDEIKVILINNVSNAOQLTPVLP 180
OC      179  AAEKKNFHLHEKTIIRQAVRRETSVLTEPOVYGDKEDEIKVILINNVSNAOQLTPVLP 179
OC      239  ILGNGGIGKTTIAQVNFQDQVHIFHFKIWCYSEDPENKRLIKEIVESIEEKS-LOGM 239
OC      239  ILGNGGIGKTTIAQVNFQDQVHIFHFKIWCYSEDPENKRLIKEIVESIEEKS-LOGM 239
OC      299  DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVSGASVLTTLTLEKSGS 299
OC      299  DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVSGASVLTTLTLEKSGS 299
OC      359  IMGTLOPYELSNLSOEBCWMLFMORAFGHOEINLVAISKEIYKKGCVPLAKTIGG 359
OC      359  IMGTLOPYELSNLSOEBCWMLFIQCAFQHOEINLVAISKEIYKKGCVPLAKTIGG 359
OC      419  ILRPFKEBROWEHVRSSEIWLPOESSILPALRLSYHHLPLDROCFYCAVFPKDTM 419
OC      419  ILRPFKEBROWEHVRSSEIWLPOESSILPALRLSYHHLPLDROCFYCAVFPKDTM 419
OC      479  EKMGLISIMAHAGTILSKNLELVNGVWNNELYSFQFQIEYKSGQTYFKMHLHD 479
OC      479  EKMGLISIMAHAGTILSKNLELVNGVWNNELYSFQFQIEYKSGQTYFKMHLHD 479
OC      538  LATSLSFASTSSNIREIIVENYIH-NMSIGFTKVSSYSLSLQKQFSLVNLSDIKL 538
OC      538  LATSLSFASTSSNIREIIVENYIH-NMSIGFTKVSSYSLSLQKQFSLVNLSDIKL 538
OC      598  KQLPSSIGDLVHLVYLNISGNTSIRSLPNQCLQNIQTLDLHGCHSLCCLPKETSKGS 598
OC      599  EELSSSIGDLVHLVYLNISGNTSIRSLPNQCLQNIQTLDLHGCHSLCCLPKETSKGS 599
OC      658  LRNLILGCGYGLTQMPRIISGLTCLKTSRPVNGIQKSCQGLRMLNLYGSIETITLE 658
OC      659  LRNLIFHCGBELNSMPRIISGLTCLKTSRPVNGIQKSCQGLRMLNLYGSIETITLE 659
OC      718  RVKNDMDAKEANLSAKENLHLSMKMDDEPRRIYSESEKVEVLALPKHSLVLTCLTIRGF 718
OC      718  RVKNDMDAKEANLSAKENLHLSMKMDDEPRRIYSESEKVEVLALPKHSLVLTCLTIRGF 718
OC      778  RGIRLPMMHNSVLKAVSIRIISCKNCSCLPPFGEIPLCLSKLSLELWGSAAVEVYDGGFP 778
OC      778  RGIRLPMMHNSVLKAVSIRIISCKNCSCLPPFGEIPLCLSKLSLELWGSAAVEVYDGGFP 778
OC      838  TRRRFSLRLKLTIEFGNKLKLGEGEQQPVLEIEIKCCPMFVPLTSSVKKLVVSG 838
OC      838  TRRRFSLRLKLTIEFGNKLKLGEGEQQPVLEIEIKCCPMFVPLTSSVKKLVVSG 838
OC      898  DKSDAIGFSSISNIMALTSLQIRYKEDASLPPEMFKSLANLKYINISFYNLKELPTSL 898
OC      878  -----SNRALTSLHSHNNKATSLPEEIFSPALUKTLKLSLFPNLKELPSL 878
OC      958  ASLNALKHLTHSCYALLESIPREGVKGILSTQISTYCEMLQCLPGLQHLNLTNLV 958
OC      938  ACNALATLHSCYALLESIPREGVKGILSTLTFVYDCEMLKELPGLQHLNLTNLV 938
OC      968  EFCPTLAKRC 968
OC      948  RRCPOLIKRC 948

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Solanum.
OX NCBT_TaxID=147425;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX PubMed=12872003; DOI=10.1073/pnas.1533501100;
RA Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
RA Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
RA Heigeson J.P., Jiang J.;
RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
RT resistance to potato late blight.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Heekert Bt B.L., Gros J., Stevens P.,
RA Muskens M., Wouters D., Pereira A., Sikkema M., Alfefs S.;
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato.";
RL Plant J. 36:867-882 (2003).
CC -I- FUNCTION: Disease resistance protein. Resistance proteins guard
CC the plant against pathogens that contain an appropriate avirulence
CC protein via a direct or indirect interaction with this avirulence
CC protein. That triggers a defense system which restricts the
CC pathogen growth.
CC -I- INDUCTION: Constitutively expressed.
CC -I- MISCELLANEOUS: Belongs to a four-gene family located at the same
CC locus. Although the four genes are expressed in the resistant
CC haplotype, only RGA2 confers the resistance to P.infestans. In the
CC susceptible haplotype, RGA1 and RGA3 are likely to be pseudogenes
CC created by deletions and mutations, while RGA2 contains also
CC several modifications.
CC -I- SIMILARITY: Belongs to the disease resistance NB-LRR family.
CC -I- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.
CC -I- SIMILARITY: Contains 1 NB-ARC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY303170; AAP45166.1; -.
DR EMBL; AY303171; AAP45174.1; -.
DR EMBL; AY426262; AAR29072.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF00931; NB-ARC; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR ATP-binding; Leucine-rich repeat; Plant defense; Repeat.
KW DOMAIN
FT NP BIND 184 191
FT REPEAT 526 548
FT REPEAT 549 572
FT REPEAT 574 595
FT REPEAT 596 620
FT REPEAT 638 662
FT REPEAT 674 696
FT REPEAT 751 776
FT REPEAT 784 808
FT REPEAT 829 851
FT REPEAT 852 876
FT REPEAT 878 900
FT REPEAT 901 925
FT REPEAT 927 950
FT REPEAT 966 988
FT VARIANT 45 45
L -> V (in susceptible haplotype).

```

FT VARIANT 120 120 S -> A (in susceptible haplotype).
 FT VARIANT 305 305 L -> S (in susceptible haplotype).
 FT VARIANT 512 512 A -> S (in susceptible haplotype).
 FT VARIANT 692 692 K -> E (in susceptible haplotype).
 FT CONFLICT 145 145 K -> V (in susceptible haplotype).
 FT YEFKYLCTPKVGARCC (in Ref. 2).
 SQ SEQUENCE 988 AA; 11395 MM; D04DFP348BCPDAD3 CRC64;
 Query Match 70.0%; Score 3587; DB 1; Length 988;
 Best Local Similarity 72.1%; Pred. No. 3,4e-195;
 Matches 717; Conservative 105; Mismatches 159; Indels 14; Gaps 9;
 1 MAEAFQVLLNLTCFQIGELGLIGFQDEFEKQSTFTTQVLEDAQKQKQKALEN 60
 1 MAEAFQVLENTLTFIDGLKLVLFQFEKECKSSVSTIQAVLQDAQKQKQKALEN 60
 61 WLQKLNAAAYEADDLDECKTEAPRQKKKGGCHPVVITFRKATGGMKIMKLDVI 120
 61 WLQKLNAAAYEADDLDECKTEAPRQKKKGGCHPVVITFRKATGGMKIMKLDVI 119
 121 AAEIKFLDERTIERO--VATROTGFVLEPOVYGRQKDEIKVILINNVSNQTLPV 178
 120 SEERKFFLEKITERQAAATRETFVLEPKVGRQKDEIKVILINNVNAEELPV 179
 179 LPIQMGIGLKTTLQAVVFNQVLEHFPKIMVCSDFNEKRLIKESIVESIEKSLGG 238
 180 PPIQMGIGLKTTLQAVVFNQVLEHFPKIMVCSDFNEKRLIKESIVESIEKSLGG 239
 239 MDLAPLQKKADLNGKTYLLVLDVWVEDQKAKLQVTKVSGASVLTTRLEVYG 298
 240 EDLASFOKKQELNKGKTYLLVLDVWVEDQKAKLQVTKVSGASVLTTRLEVYG 299
 299 SIMGTLOVLESLNQDECMILFMQARFGHOETILNVAIGKEIVKCGGAPLAAKTLG 358
 300 SIMGTLOVLESLNQDECMILFMQARFGHOETILNVAIGKEIVKCGGAPLAAKTLG 359
 359 GILNFKEREROMEHVRDEIWKLPQESSILPALRLSYHHLPLDRQCFYCAVFPKOTE 418
 360 GILNFKEREROMEHVRDEIWKLPQESSILPALRLSYHHLPLDRQCFYCAVFPKOTE 419
 419 MEKGNLSLMAHGFILSKNLELVNENVEWNLVLRSPFOELRVKSGQTYPKMHDLIH 478
 420 MIKELTILMAHGFILSKNLELVNENVEWNLVLRSPFOELRVKSGQTYPKMHDLIH 479
 479 DLATSLFASSTSSIRIIEYENYIHMSIGFTKVVSSYSLSHLOKFTSLVNLSDIKL 538
 480 DLATSLFASSTSSIRIIEYENYIHMSIGFTKVVSSYSLSHLOKFTSLVNLSDIKL 539
 539 KQLPSSIGDLVHLRYLNTSGNTSIRSLPNOLCKLQNLQTLDLHGSHLCLCPKETSXLS 598
 540 KQLPSSIGDLVHLRYLNTSGNTSIRSLPNOLCKLQNLQTLDLHGSHLCLCPKETSXLS 598
 599 LRLNLLDGCYGLTCMPRIGSLTCLKTLSPVVGIOKKSQQLGELRLNLTGSIETIHL 658
 599 LRLNLLDGCYGLTCMPRIGSLTCLKTLSPVVGIOKKSQQLGELRLNLTGSIETIHL 656
 659 RYKNDMDAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENL 718
 657 RYKNDMDAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENLAKENL 714
 719 RGIRLPDMNHSVLEKVVSIIEISCKNCSCLPPFGEELCLSLIELMRSAEVEYD--- 774
 715 GGFRRPSINHSVLEKVVSIIEISCKNCSCLPPFGEELCLSLIELMRSAEVEYD--- 774
 775 -SGFTRRRPSSLKLNIREFENLKGILLKKGEGOCVLEELIKCCPMFYIPLISSYK 833
 775 HSRFSTRSPSLKLNIREFENLKGILLKKGEGOCVLEELIKCCPMFYIPLISSYK 834
 834 LVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPREPKSLANLYINISFYNK 893
 835 LEVHNN--TNTGLSSISNLTSTLSIRIGANRYATSLPEEMFSLTNLLEFPDPKLNKD 893
 894 LPTSLSANLAKHLEIHSQVLALESIPREGVKGLISTQLSITYCBMLQCLSEGLQHTAL 953

DB 894 LPTSLSANLAKHLEIHSQVLALESIPREGVKGLISTQLSITYCBMLQCLSEGLQHTAL 953
 QY 954 TNLSVECPCLAKRCCKGIGEDWYKIAHIFRVFY 988
 DB 954 TNLSVECPCLAKRCCKGIGEDWYKIAHIFRVFY 988
 RESULT 7
 RG33 SOLBU STANDARD; PRT: 947 AA.
 ID RG33 SOLBU STANDARD; PRT: 947 AA.
 AC Q7XA40; Q7XA25; 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative disease resistance protein RG33 (RG33-b1b) (Blight resistance protein B149).
 GN Name=RG33; Synonym=177013.36, CB3A14.6;
 OS Solanum bulbocastanum (Wild potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 CX NCBI_TaxID=147425;
 RN [1]
 RP PUMED=12872003; DOI=10.1073/pnas.153501100;
 RA Song J., Bredsen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
 RA Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
 RA Helgeson J.P., Jiang U.;
 RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
 RT resistance to potato late blight."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133(2003).
 RN [2]
 RP PUMED=14675451;
 RA Van Der Vossen E., Sikkema A., Heekert B. B.L., Gros J., Stevens P.,
 RA Muijken M., Wouters D., Pereira A., Sikkema W., Alfefs S.;
 RT "An ancient R gene from the wild potato species Solanum bulbocastanum
 RT confers broad-spectrum resistance to Phytophthora infestans in
 RT cultivated potato and tomato."
 RL Plant J. 36:867-882(2003).
 CC -1- FUNCTION: Disease resistance protein. Resistance proteins guard
 CC the plant against pathogens that contain an appropriate avirulence
 CC protein via a direct or indirect interaction with this avirulence
 CC protein. That triggers a defense system which restricts the
 CC pathogen growth.
 CC -1- INDUCTION: Constitutively expressed.
 CC -1- MISCELLANEOUS: Belongs to a four-gene family located at the same
 CC locus. Although the four genes are expressed in the resistant
 CC haplotype, only RG33 confers the resistance to P. infestans. In the
 CC susceptible haplotype, RG31 and RG32 are likely to be pseudogenes
 CC created by deletions and mutations, while RG32 contains also
 CC several modifications.
 CC -1- SIMILARITY: Belongs to the disease resistance NB-LRR family.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 NB-ARC domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC
 CC EMBL: AY303170; AAP45165.1;
 CC EMBL: AY303171; AAP45181.1;
 CC EMBL: AY426260; AAR29070.1;
 CC EMBL: AY426263; AAR29073.1;
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR003591; LRR typ.
 CC InterPro: IPR002182; NB-ARC.
 CC Pfam: PF00560; LRR; 7.

DR	Pfam: PF00560; LRR 1; 8.	DR	Pfam: PF00931; NB-ARC 1.	DR	PRINTS: PR00364; DISEASERISIT.	DR	SEQUENCE 1110 AA; 126126 MW; C43D1BDB40C33A3F CRC64;
Query Match	29.6%; Score 1517; DB 2; Length 1110;						
Best Local Similarity	34.9%; Pred. No. 1,5e-77;						
Matches 396;	Conservative 189; Mismatches 345; Indels 206; Gaps 35						
QY	4 AFLOVLDNLTCFIOGELGIL--GPKDEBFKLOSTFTTQAVLEDAOKQKDAIEN 60						
DB	9 AFMOTLFQKLS---EATLDHFISWKGINGIKLESISTTSLOLAFIDDAEKKOLTASVARG 65						
QY	61 WLQKMAAYADIDIDECTEAPRROKKNYGCHPNVITF-----HKIKGR 109						
DB	66 WLAKQIDIAVLDLDDLSYSAKS-RRMKQRO-QVIFPKVSLSSPFLSRMLYDHRIYHK 122						
QY	110 MKKIMEKLDVAARERIKFHLDERTERQVAT--QTGFVINEPOVYGRDXEKDEIVK-I 165						
DB	123 INILERRDKIAQERDITGLQMICEMRYDPTSERQSSIVYDSAVFRERDRREMAVRL 182						
QY	166 LNNVSNAGTLPLVPLIGMGELGTTLAQMYFNQDVIYEHHPKTIWCVSDEPNKKLIK 225						
DB	183 LSDGNHNSCNLCVPIVVGMGIGKTTLMQMYADHVRVHEHFLRIWIVYSESFDERKLTQ 242						
QY	226 EIVSISIE-EKSLGGMDLAPLOKKLDLNGKYLIVLDVWNEDODKAKLQVYLKVAGS 284						
DB	243 ETLASLDSDQSVASTNMMDLDETLISRVLRGKRYLLVLDVWNMEDLDKMSYRALISGAF 302						
QY	285 GASVLTTLTRLEKVSIMGTLQPYELSNLSQEDCWLPMQRAF-----GHOEINLVVA 338						
DB	303 GSKIVTISRNVGRINGIEPIYKLOKSLDDDSVGFSAHFRQDGSAPHE-----LEA 357						
QY	339 IGKRIYKCCGAVPLAAKTLGGILRFKREERQWEHVRSEIMKLPOEBSIILPALRLSTH 398						
DB	358 IGMEIVKLLKCLPLASKALGSLPFCKTDEEBEKDILQNDIMELPADKNNIILPALRLSTH 417						
QY	399 LPLRLROCFYCAVFPKQTEMEKGLISLMAAHGFIILSKGNLELNVGNVWNNELYLSRF 458						
DB	418 LPLHLKQCFACSYPKDYMFRREKLVKIMLGLFIROSKRKMEDTGNAYFNELLSRF 477						
QY	459 FOEIEVNSGQTYFKMGDILHDLATSL----- 484						
DB	478 FQPYE-----NNYVMDAMHDLAKSISMEDCDHLYGRHNDALKTRHLSFPCQAKCMH 532						
QY	485 PSASTSSNIREIIVENTYIMMSIGFTVVSYSLSHLQKVLRLVNLSDIKLKOLPSS 544						
DB	533 FNPILYGRFKLTTLTYI---IH---GYSRMSQLPHGLPMKIEYLRLVDMHGQGLKEPES 585						
QY	545 IGDVLVHLRYNLISGNTSIRSLPNOLCKLQNTLDLHGCHSLCCLPKETSKLGSRLN- 602						
DB	586 IGNLKQRLRFDLIS-STELIETPLASLVKLYNQLILKSCNPLREVRQGITRLINIRHLEA 644						
QY	603 ---LDDGCGYLTCPMPRIAGSLTCLTKLTSRFVVGIIQKKS-CQLGELRLNL-LYGSIEITHL 657						
DB	645 STLLLSRIHG-----IGSLVLCQELDEEFPV--QKSGHNVTEILNMDELQCGLSIRGL 695						
QY	658 ERYVDMDAKANISAKENLHSLSKMKDD--ERRRIYSESEVLTLEALKPSHNTLCITI 715						
DB	696 NNVNNGODAVCAKRNKKEHLRTLIHLIMWDESNP---SBOQVLEBGLQPHLDLKEVLI 751						
QY	716 RGFRGIRLPMWNHNSVLKNVVISIEISCKNSCLPPFPELPCLSLELMRSGAEVEYDS 775						
DB	752 KGFGGVRRPSPVLASSFLPKQTIHICNCRS-TRLPALQQLPELKLVI-AGVTETVQTGSS 809						
QY	776 ---GPPIRRRFPSLKTNIREBGNIKGLIKKEBGEQCVLEIEIKCCPMF--VIPTLSS 830						
DB	810 EFTFGGQKGFPAEDLLLEMPNLSEMI PDVADQLFQOLTGLIKPOLKCLPPIRST 869						
QY	831 VKKLVASGSDKDALGFGSSISNM-----ALSL 858						
DB	870 LRTLMISS-----GLSELPTELQNNSCSSPSPSYLINDCPNLTSRLVGLALVAPRLAKSL 924						

Oy		859 QIRNKEDALPERMFSKLANIKYINISFY-----FNKE---LPTS-----	897
Dd		925 TIACHCEGVALPEECFPPILSLNSH--YBCPLVWMTALBGLLTSTIEDIYNCTP	982
Oy		898 -----IASLNALKRLRHSCVALESPEBGVKGIIISTOLSIYVCMLQCPREGIOH	949
Dd		983 IASVLINGLSYLPHLRPFELADCPDINNPAEGPH- TLQFLIESCCDDIQCLPPGIHN	1040
Oy		950 LTA-----	
Dd		1041 ISSLETLRISNCGVESLPREGIPMGINEIYIKGPCKOOCOGG-GEYHAKIAHI	1095
RESULT 9			
06LAD9			
AC	06LAD9	PRELIMINARY;	PRT; 1222 AA.
Dt	05-JUL-2004	(TREMBlrel, 27, Created)	
Dt	05-JUL-2004	(TREMBlrel, 27, Last sequence update)	
Dt	25-OCT-2004	(TREMBlrel, 28, Last annotation update)	
DE	Putative NBS-LRR resistance protein (Putative NBS-LRR protein).		
GN	Name=OSUNBA008HM05.1; Synonyms=OI1126_B11.12;		
OS	Oryza sativa [Japanica cultivar-group].		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatopsida; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Bharatioidae; Oryzaceae; Oryza.		
OX	NCHI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-W.,		
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,		
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsieh S.-H.,		
RA	Hsiung J.-N., Hou C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,		
RA	Lai Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,		
RA	Wu H.-P., Shaw J.-F.;		
RL	Submitted (May-2004) to the EMBL/GenBank/DDBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-W.,		
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,		
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsieh S.-H.,		
RA	Hsiung J.-N., Hou C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,		
RA	Lai Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,		
RA	Wu H.-P., Shaw J.-F.;		
RL	"Oryza sativa BAC OJ1126 B11 genomic sequence.";		
RT	Submitted (SEP-2004) to The EMBL/GenBank/DDBJ databases.		
RU	EMBL; AC136222; AAT38049.1; -		
DR	EMBL; AC136222; AAT38049.1; -		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0042829; P:defense response to pathogen; IEA.		
DR	InterPro; IPRO00767; Disease_resist.		
DR	InterPro; IPRO01611; LRR.		
DR	InterPro; IPRO03591; LRR_typ.		
DR	InterPro; IPRO02182; NB-ARC.		
DR	Pfam; PF00560; LRR_1; 7.		
DR	Pfam; PF00931; NB-ARC; 1.		
DR	PRINTS; PR00364; DISEASERESIST.		
SR	SMART; SM00369; LRR_TYP; 4.		
DQ	SEQUENCE 1222 AA; 138744 MW; 74AE8E99BA12BB5B CRC64;		
Query Match	29.6%; Score 1516; DB 2; Length 1222;		
Best Local Similarity	32.9%; Pred. No. 2e-77;		
Matches	408; Conservative 194; Mismatches 355; Indels 284; Gaps 35;		
Oy	1 MAE---AFLOVLDNLTCFIGELIGLIFGRKDEFKKQSFTTTQAIVLEDAOKQLDKX	57	
Dd	1 MAETLSALTALTKRGESLGTERSFSGIGERRSELYTLILLANVOINDADEASKPA	60	
Oy	58 IENWLQGANAAVEADDIID-----ECKTEAPIRKKNKYG-----CYHPVINFRKHG	107	
Dd	61 VKSMIAGKAIACDADDADELRIYEELRCALRRGHKIINTGVAAFPSSHNPPLFKRIG	120	

108 KRMKIMKLVIAERIKF-----HDERTIEROVAITROTGFVNLNPOVYGRDKRD 160
121 KRLQOIVIRIDQVYQMMRFGLNCSMPYDER-----MOTYSYVEQEVIGDKRD 172
161 EIVKILNNVNAQTLPVLPILMGGLGKTTLAQVFNVDORVIEHPKIMVISEDNE 220
173 EIVHMLTS--AETDELLILPIVIGLIGKTTLAQVFNVDVKAHFGQHMVAVSENSV 230
221 KRLKEIYESI--EKSJGMDLAPLOKKARDLNGKTYLVDVNMEDODKAKLQV 278
231 PVIYVGIIDTVAIGNCCGKLPNDLELQRLREELGQKRYLLVLDVNMEDQKMGALMTL 290
279 LKVGASGASVLTTLTLEKVGSMGTLOVEYLSNLSEQDCWMLFMORAGHOEITNLVA 338
291 LGSCMGSAVVVTRNVAVASIMESISPLCENLNPELMSIVFSRAAGTGVETPELVE 350
339 IGKEIVKCGVPLAAKTLGGLRFREROMEHVDESIKLPQESSILPALRLSYH 398
351 VGRIVEKCCGIPLAIKMGALMSTQETRDMLSTLESNTW---DEESQILPALSLGYKN 407
399 LPDLROCFETCAVPPKDTMEKGNLISLMAHSGTILSKNLELVNENVMNLVLRSE 458
408 LPSHMOCFACAVPKDYEDKDLHLNWSNGTIPSKMSDLEENGNHVPWELWMSF 467
459 FOEIEV-----KSGQTYFKMHDILHDLATSLF--SASTSSNIREI--IVENY 502
468 FQVKGQISIFQKRYRYGSDVTFPKIHDLMHDLAVHISDECEALLENLAKIKIPNV 527
503 IHM-----MSIGF---TKVVS--YSLV---HLOKYS---LRVNLSDIKKOLPS 543
528 HHMAFEGQOKGIFLMQHCVRIRSFALDKNDMHIADIKFENSPILRVGLHIFGIEKFPV 587
544 SIGDLVHLRYNLNGTSIRSLPQOLCKQNLQTLTDLHGCHSLCCLPETSCKLSNLIL 603
588 EPAMKHLRYDLDSG--SYINTLPRASALYMLQVILNRCRLTHLPDGMKFMSLHAY 646
604 LDGCGYGLTMCPPRIGSLTCLTSLRFPVVGIOKSCQJGELNMLYGSIEITHLERYND 663
647 LDDCARLTSPWAGQGLINLTTLTKFPVG--NESGRINELNDLKGGLQIFNLIKVTNP 705
664 MDAAENLISAKENHLSMKRDD-----ERRPIYSEVAVYLEAKLPHSNITCTLR 716
706 IEAEANLECKTNLQOLALCWGTSKSAELQAEIDLHLYRHE--EVLDMKPPNGJLVTKLR 763
717 GFRGIRLPDMNHSV--LKNVYSIEIISCKNSCLPPGELPCLSKLEIMGSAVEVYDS 775
764 QYMGTTPIIMENGTIRNIVKAVTDSINCMKLPVWKLRFLEVLKL--KOMKJLKYCN 822
776 GFPTRR-----PSLRKLNIREFNLKGLKKEGEE---OCPLYELEIKCCP--MF 823
823 GFCSDKCDHQLVAFPKLKLSTLERMESLEWQYDVEQVTPANFPVLDAMEIIDCPKLT 882
824 VIPTLSSVKLVSGSDSALGF--SSTSINL----- 853
883 AMPAPAVLKSLSVGNKI--LIGLSSVSNSLYIYLGASQGSLEKRTLYHYKENLEGTT 941
854 -----ALTSLO-----PEMFKSLANIKYIN----- 884
942 DSKOHLVLAHHFSSWGSITLKLHLGFSALAPEDIONISGHVMSYQNLIDISCDCIQTDL 1001
866 DASI-----PEMFKSLANIKYIN----- 884
1002 QSPLMFWKSPACLOHLTLEYCNSLTLPWGEFOSITLAKRLDIRYCNFTGMPAPQVSVK 1061
885 -----ISFYNLKELPTSLASINAKHLEHSCVABLESP----- 920
1062 SFEDEGMNLERIEIEFCYMLVAFPTLS-----YLRICSANVLELDPGLGCLGLARS 1115
921 -----EGVGLISLTQSLSTIYCEMLQCL 943
1116 LSLDYNRLKSLPSPISQRLSNLTRLVYIGTNDLSLTLPEGMHNTALANDLAINWCPSLKAL 1175
944 PBGL-QHLTALTNLSVEFCPTLAKRCEKIGEDWYKIAHP 983

DB 1176 PBGLQRLHSLKLPFRCQPLVLRCKRG--GDWYSKYDLP 1215
RESULT 10
084XGO PRELIMINARY; PRT; 1035 AA.
AC 084XGO.
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE NBS-LRR resistance protein RGL1.
OS Manihot esculenta (Cassava) (Manihot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids I; Malpighiales; Euphorbiaceae; Crotonoideae; Manihoteae;
OC Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2835941; PubMed=12827500; DOI=10.1007/s00438-003-0868-5;
RA Lopez C.E., Zuluaga A.P., Cooke R., Delseny M., Tohme J., Verdier V.,
RT "Isolation of Resistance Gene Candidates (RGCs) and Characterization
of an RGC cluster in cassava."
RL Mol. Genet. Genomics 269:658-671 (2003).
DR EMBL: AY188523; AAC37645.1; -.
DR GO: GO:0005524; F-ATP binding; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0042829; P:defense response to pathogen; IEA.
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR 1; 5.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERIST.
SQ SEQUENCE 1035 AA; 118190 MW; 60A081C6F6DD176 CRC64;
Query Match 28.9%; Score 1479.5; DB 2; Length 1035;
Best Local Similarity 35.8%; Pred. No. 1.9e-75;
Matches 363; Conservative 196; Mismatches 354; Indels 101; Gaps 25;
20 ELGILIGFQDEFEKOSTFTTIOAVLEDAQKQDKAKALENMLQKLNAAAYEADTIDEC 79
24 EIGLMGVCKELKTLBATVSSIRNVLLDAEQDKLRQYGVLEERLEEVYDADDLVDPF 83
80 KTEAPIRQ-----KKNKYGCTHPNVITFRKIKGRMKKIMKLDVIAERIKHYDE 131
84 ATEALRRVWVTGNMTKEVSLFFSSSNKLVYGFRRMGRKVKALIRELADIADLR--KFNLEV 142
132 RTIERQVATG--OTGFVLANPQVYGRDKEDYKILINNVSNAQTLPVLPILMGGLGKGT 190
143 RTQGERIWRWDQYTTSSLPF--VVGREGDKKAITQVLSS--NGECCSVSLSYIGLIGT 200
191 TLAQVFNVDORVIEHHPKIMVCSDEPNKRLIKEIVIESIEKSIQMDLAPLOKKRD 250
201 TLAQIILNDEMINKSPEPRITWCVSEHPVVKMTVVGKILLESATCNKSESDGLEALKSLRK 260
251 LKNGKRYLLVDVNMEDODKAKLQVYLKVGASGASVLTTRTLEKVGSMGTLOVEYS 310
261 IISGKRYLLVDVNMENKREKEMNLRLLVGSSSGSKILITTRSKRVADISGTTAHHVLE 320
311 NLSQDCWMLFMORAGHOEINLNLVAIGKEIVKCGVPLAAKTLGGLRFRERORW 370
321 GTSIDSGWSLFLVHNLGEGEPKNAVRENKGEIKKCHVPLAKITIASLVAKNPETEM 380
371 EHVROSEIKLPOESSILPALRLSYHNLPLDROCFETCAVPPKDTMEKGNLISLMA 430
381 LPLTELKELRISQDGDNIMPTLKYSDHLPKHLKHFAYCAVYKDYVIDVTLTLLMLTA 440
431 HGFILSKNLE--LENVGNVMEILYRSFQRE-----VSGQTYFGMHLHDLATS 483
441 QGFISPTSDCLDIEGLYFNLKMWRSFQEVERDRGCVNES---CRMHDLMDHLATT 496

QY 484 LFSASTSSNIREIIVENYIHMSIGF-----TKVSSYSLSHL----QKFV--- 526
DB 497 VGGKRIQLVNSDTPNIDKTHVNLNVAVPQEIINKAKRVASILLSEHVNDQLFIYKN 556
QY 527 --SLRVNLSDIKKOLPSTIGDLVHLRYNLNSGTSIRSLPNOCKQNIQTLDHGH 584
DB 557 LKFLVFTWYSYRI--MONSIKMLRYLRDLVSDNEKALKALSNTITDLNQLVDVSYCV 614
QY 585 SLCCLPKETSRLGSLRNLLDGCYGLTCMPPRIGSLTCLTSLRPVVG---IQKSC-QI 640
DB 615 QKLEIPKIKLVNRLHYCEGCSNLTTHMPRGQLTSLQTLISLFPVAKGHISDQVKI 674
QY 641 GELRNL-NLYGSEITLHRYKNMDAKANLSAKENLSLSMKWDDERPRIVSEKYE 699
DB 675 NEINLNLNLRGLERINLGCY--DDEIVNVNLKEKPLQLSLRWEESS-----WEDSNVD 727
QY 700 ----VLKLRHSNLTCLTIGFRGIRLPDMNHSVLKNVSIETISCKNSCLPFGEL 755
DB 728 RDEMAFQNLQPHPNLKELLVFGYGGRRPSPWF--SSLNVLVYLCTMCKRYOHLPPMDQI 785
QY 756 PCLKSLRLMRGSAEVEYVD-SGPTRRRPPSLRKINIREFNLKGLLKEGEGCPVLEE 814
DB 786 PSLQYLEI-LGLDDEIYMEIGOPT-SFPPLSKSLGLYNCPLKGMQKK--EDDSTALEL 842
QY 815 IEIKCCPMFV--IPTLSSVKKLVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPE 871
DB 843 LQFPLSYFVCEGDCNLSIPIQF-----PSLDD 870
QY 872 EMFKSLANLKLNTISFYNNLKEPLTSLASLNLKLEIHSCLALSPREGVKGLISLTQ 931
DB 871 SLHLHASPQVLVHQFTFPTSISSSSIIIPPLSKLNLWIRDIKELESPPDGLRNLTCLQR 930
QY 932 LSITFCENLQCLPBGLOHLTALTNLSVEFCPTLAKCEKGIQEDWYKIAHAPRV 985
DB 931 LTIEICPAIKCLPQEMRSLTSLRELDIDDCPOLKERCNRRKGADWAFISHIPNI 984

RESULT 11

Q84XFP9 PRELIMINARY; PRT; 1024 AA.
AC Q84XFP9; 01-JUN-2003 (TREMBLREL. 24, Created)
DT 01-JUN-2003 (TREMBLREL. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLREL. 26, Last annotation update)
DB NBS-LRR resistance protein RGH2.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Manihoteae;
OC Manihot.
CX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22835941; PubMed=12827500; DOI=10.1007/s00438-003-0868-5;
RA Lopez C.E., Zuluga A.P., Cooke R., Delseny M., Tohme J., Verdier V.;
RT "Isolation of Resistance Gene Candidates (RGCs) and characterization
of an RGC cluster in cassava".
RL Mol. Genet. Genomics 269:658-671(2003).
DR EMBL; AY188524; AAC37646.1; .
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease-resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 4.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1024 AA; 116977 MW; 99EAE9E39364A9C2 CRC64;

Query Match 28.8%; Score 1479; DB 2; Length 1024;
Best Local Similarity 35.0%; Pred. No. 2e-75;
Matches 355; Conservative 208; Mismatches 350; Indels 100; Gaps 24;

QY 20 ELGILGKQEFKLGSTFTTITQAVLEDAQKQOLKXAIBNMLQKLNAAAAYEADTIDEC 79
DB 24 EIGLWGVKSLKLELATVSSIRNVLLDAEQQQLNQGKMLRLREIIVDADVDVDF 83
QY 80 KTEAPIRO-----KKNKCYCHPNVITFRHKIGKRMKIMKELDVIAERIKFHLDE 131
DB 84 ATEALRRVMTGNMTKEVSLFPSSNQLVYFGKGRKVKAIRRLIDEADR-NFNLEV 142
QY 132 RTIERQVATR-QTGFVNEPQVGRDKEBIVKILINNVSNAQTLPVLPILMGGLGKT 190
DB 143 RTDSEIWMRQDTSSLPE-VVIGREGKAITLVLS-NGEECVSLSTVGIGLAKT 200
QY 191 TLAQVFNDRQVIRHFPKIMICVSEDENERKILKEIIVESIEEKSIGMDLAPLOKLRD 250
DB 201 TLAQIIFNDELKNSFEPRIWCVSEFPDVMTYTKLLESATGNRSDDIGLEALKSLRLEK 260
QY 251 LUNGKTYLLVDVWNEQDQKMAKQVLYKVASGASVLTTRLEKYSIMGTLOPYELS 310
DB 261 IISGKTYLLVDVWNEENREKEMIKRLVGSSSGSKILLTTRSKYADISSTWAPVYLE 320
QY 311 NLGQEDCMILPMQAPGHOEINLVAIGKEIVKCGVPLAKTGLIRPREEERQW 370
DB 321 GLSPDESMSLFLVHLRGQEPKANVREMEKELIKCRGVPLAKTITASLYAKNPETEW 380
QY 371 EHVADSEIWMKLPQESSILPALRLSYNHLPLDRQCFYCAVPPKOTEMEKNLISLMA 430
DB 381 PPLITKLSRIQDQGNIMPTLKSTYDHLPSNLKHCATYCAIKYDVIDVKRIHLHMA 440
QY 431 HGFILSKGNLE-LENNVEWNNELYLSFPOEIE-----VKSQOTYFKMHLIDHATS 483
DB 441 QGFIESPSTDCLEDIDIGLEYFMKLMRRSPFOEVRDRYGVNES-----CKMHDLMDIATY 496
QY 484 LFSASTSSNIREIIVENYIHMSIGFTYVSSLSHLQKFVSRVL----- 531
DB 497 VGGKRIQLVNSDALNIKEIHHVALNL-DVASKELINNARKVRSLLEFKYCDQLFIYK 555
QY 532 NLSDIKL-----KOLPSSIGDLVHLRYNLNSGTSIRSLPNOCKLQNIQTLDHGH 585
DB 556 NLKFLRVFKHASTRYTMMNSIKILKTYIRLDVSDNKGKALKASHSTIDLLNQLVDVSYCV 615
QY 586 LCCLPKETSRLGSLRNLLDGCYGLTCMPPRIGSLTCLTSLRPVVG---IQKSCQ-LG 641
DB 616 LKELPDKIKLVNRLHCCGCVSLHMPGQLTSLQTLISLFPVAKGHISDQVKIN 675
QY 642 ELRNL-NLYGSEITLHRYKNMDAKANLSAKENLSLSMKWDDERPRIVSEKYE- 699
DB 676 ELNKLNNLGRLEIINLGCVDNEI--VNVNLKEKPLQLSLRWEESS-----WEDSNVD 728
QY 700 ----VLKLRHSNLTCLTIGFRGIRLPDMNHSVLKNVSIETISCKNSCLPFGELP 756
DB 729 DENAFQNLQPHPNLKELSVIGYGGRRPSPWF--SSLNVLVYLCTMCKRYOHLPPMDQI 786
QY 757 CLKSLRLMRGSAEVEYVD-SGPTRRRPPSLRKINIREFNLKGLLKEGEGCPVLEE 815
DB 787 SLOYLQIWM-GVDDLEIYMEIGOPT-SFPPLKTLTLDHGCPLKGMQKK--RDDSTALEL 842
QY 816 IEIKCCPMFV--IPTLSSVKKLVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPE 872
DB 843 QFPLSYFLEBECFNLSIPIQF-----PSLDDS 870
QY 873 MFKSLANLKLNTISFYNNLKEPLTSLASLNLKLEIHSCLALSPREGVKGLISLTOL 932
DB 871 LHLHASPQVLVHQFTFPTSISSSSIIIPPLSKLNLWIRDIKELESPPDGLRNLTCLQR 930
QY 933 SITFCENLQCLPBGLOHLTALTNLSVEFCPTLAKCEKGIQEDWYKIAHAPRV 985
DB 931 TIQICPAIKCLPQEMRSLTSLREININDCPOLKERCNRRKGADWAFISHIPNI 983

RESULT 12

Q8L182 PRELIMINARY; PRT; 1108 AA.
Q8L182

AC Q8L82; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NBS-LRR-like protein.
GN Name=YR48;
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OK NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Huang X.Q., Yang P.W., Zeng L., Wang Q., Cheng Z.Q., Yang B., Li J.R.,
Yang Q.Z., Yang P.W., Zeng L., Wang Q., Cheng Z.Q., Yang B., Li J.R.,
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF456247; AAN03742.1; -.
DR Gramene; Q8L82; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
SQ SEQUENCE 1108 AA; 125209 MW; DA015AAACBA4B471 CRC64;

Query Match 28.8%; Score 1477.5; DB 2; Length 1108;
Best Local Similarity 34.4%; Pred. No. 2.7e-75;
Matches 392; Conservative 181; Mismatches 345; Indels 221; Gaps 37;

QY 4 AFLQVLDNLTCFQGEGLILGFGEFEKIQSTFTTTQAVLEDAQKKOLKKAIEWMLQ 63
DB 10 AFWQALPEKAAVAASSELKFPONIAVELQNLSSISTILAHVEDAEERQLDQARSLTS 69
QY 64 KLNAAAYEADILDECKTEARIFROKKNKYGCGYCHNVI-----TRHHIGKRMK 111
DB 70 RLKQVAIEMDLDLDBHAAEV-LRSKLAGPSNYHILKVAICCCIMLKNGLRNDLVQIM 128
QY 112 KIMERLDVIAER-----IKFHLDERTIERQVATR-QTGVLNBPQVYGGDEKKEDEIVK 164
DB 129 RIEBKIDRLIKDRHIVDPIMKFNRE-----IRERPTSSLLIDSSVYGGDEKKEIVN 182
QY 165 ILI-NNVSNAGTLVPLILMGGLGKTTLAQMVFNDDQVLEHFRPKIWCYSEDPNKRL 223
DB 183 MLITNNNSNHVNLISILPIVGGVGKTTLLQLVNDDVAVKKGHQLRWMLCVSENFDEAKL 242
QY 224 IKELIVESIE---EKSLGMDLAPLOKKLRDLNKGKYLVLVDVWNEDQDQWALRQVLK 280
DB 243 TKETIESVASGLSATTNMNI--LQEDLSNKLKGRFLVLVDVWNEDPDMDYRCALV 300
QY 281 VGASGASVLTTRLEKVGSIWGLQPYELSNLSQEDCMLFMQAFGH-OEILNLTVAI 339
DB 301 AGAGSKIMVLTTRNENVGKLVGLTPYLLQSLVNDQMLFRSVAFAFDGSSAHNPLEMI 360
QY 340 GKELVKKCGGVPLAKLTGLLRKREBROWEHVDEIWKLPQESSIILPALRLSYHLL 399
DB 361 GKELVHKLKGLPLAARALGSLCKMDNEDWKNLISEIHELPSDKNNIILPALRLSYHLL 420
QY 400 PLDRQCFYCAVPPKQTEMEKGNLISLMAHGFILSKNMLELVNENWNLVYASFF 459
DB 421 PPLIKRFACSVNHQYFEKDLVQIMAVGIIQGRRRMEIGNNTFDELLSRSPF 480
QY 460 QELIEVKSQGYFKMHLIHDIATS-----LFSASTSSSNIREI-----I 498
DB 481 Q--KHKG---YVWHDAMHDLAQSVIDECRLDNLNNSTYTERNAHLSFSCKNSQGT 535
QY 499 VENVYHMSIGFTKVVVSYSLSHOK-----PVSILVNLSDI---KLQLPBSIG 546

DB 536 FEAF-----RGFNARSLILLNGYKSTSSIPSDLFLNRLVHLDNRQETELPESVG 590
QY 547 DLVHLRYLNSGNTSISLSPNOCLKQLQTLDIHGC-HSICCLPKETSKLGSIRNLID 605
DB 591 KLNKRLRYLNLSSG-TVVHKLPSISICKLYQLTKLRNCSHNLVNL-----LSLE 637
QY 606 GCGYGLTCMPPIGSLTCLTKTLSPVVGIOKSCCOLGELRYNLN-LYGSIEITHLERVKMD 664
DB 638 ARTLITIGIARIGTLTQCKLEEVVH-KDKGYVSELKMNKKGHICLNLSVSSAE 696
QY 665 DAKENLSAKENLHSLMKWDDDERPRIYSEK-----VEVLEALKPHSNLTCLTIRPFG 720
DB 697 EADBALSEKHAHISILLIWSS---RDFTESEANQDIETLTSLEPHDELKELTVKAFAG 753
QY 721 IRLPDMNHVTLKNVSIIEIISCNQSCCLPPFGSLPCLKSLIELMRGSAEVEYDSSGPT 779
DB 754 FEFPW---LHSLQTHLSDCTNCSILPALGQLPLKYI-----IIGFPPTI 798
QY 780 -----RRPFLKRLNIREFGNKLKLLKKEGECQPVLEIEIKCCPMFV-IP 826
DB 799 IKIGDERSSSEYKGFPSLKEIVVEDTPNLERMTSTODGEFLPPLRELQVLDCKYTEL 858
QY 827 TL-SSVKLVSGDKSDAIGPSSISN-----LMAITSQIRYNKEDASL----- 869
DB 859 LIPSTLVELKIS-----EAGFSYLPVEVHAPRFLPSLTRLIHKCPNLTSIQGLLSQOLS 913
QY 870 -----PEEMFKSIANKYXINISFYFNKLPTPS----- 897
DB 914 ALQQLTTNCPPELLHPTEGLRTLTALQSLHI---VDCPLATVAEHRGLLPRMIEDLRIT 970
QY 898 -----LASLNALKHLIHSQYALSLSPER-----GVKGLIS----- 928
DB 971 SCGNIINPLDELNEFLPALKNVIAVDCVSLNTPPEKLPATLKLLEIFNCSNLASLPACLO 1030
QY 929 ----LTDLSITTCBMLQCLP-BGLQHLTALTNLSVEFCPTLAKRCEKIGEDMYKTAHI 982
DB 1031 EASCLKMTIYNLCVSIKCLPAHGAP--LSLEELYIKRCPLARCOENSGEDWPKISHI 1087

RESULT 13
Q6L4D7 PRELIMINARY; PRT; 1259 AA.
AC Q6L4D7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative NBS-LRR resistance protein.
GN Name=OSUNBA0088X05.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OK NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chen Y.-L., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
Li H.-F., Lin S.-U., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC136222; AAT38051.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.

PRINTS; PRO0019; LEURICRPT.
DR SMART; SMO0369; LRR_TYP; 3.
SEQUENCE 1259 AA; 142887 MW; 7893B44D90685941 CRC64;

Query Match 28.6%; Score 1464.5; DB 2; Length 1259;
Best Local Similarity 31.8%; Pred. No. 1.7e-74;
Matches 398; Conservative 190; Mismatches 365; Indels 297; Gaps 32;

```

QY 1 MAE---AFLOVLNDLTCFIOGELGLIFGKDEBEKLOSTFTTIOAVLEDAOKQKLDKA 57
DB 1 MAELISALLPALPKKAGSISTEPAFIGIERKSELSTLAINOVITYGAEBOASKKPA 60
QY 58 IENMLQKLNAAVEADIIIDCKTEAPIRKKNKYG-----CYHPNVITFRHXI 106
DB 61 VKSMIAKLNAAACEDDALDELHYEA-LRSEALRGKHINSVAPAFSSHNPILFKRI 119
QY 107 GKRMKTKMEKLDVIAERIKF-----HLDERTERQVATROGFVINEPOVYGRDKEK 159
DB 120 GKRLQOIYEKIDKVLQWNRFGFLNCPMPVDER-----MQTVSYVDEQEVIGRQKER 171
QY 160 DEYKILINNNSAQTLVPLPIIGMGLGKTTIAQWVFNDQVIEHHPKIMICVSEDFN 219
DB 172 DEIITHMLLS--AKSDKLLIPIVIGIGIGKTTIAQVLENDVKVAHFQKHMMVCVSENF 229
QY 220 EKRLIKEIVESI--EEKSLGMDLAPLOKRLDLNGKRYLLVLDVWNEEDQDKAKLRQ 277
DB 230 VPDVKGITIDPAIGNDGLKSDNDELQORLREBSQGRYLLVLDVWNEEDQDKAKLR 289
QY 278 VLKVGASGASVLTTRLEKVSINGTLOPYELSNLSQEDCMLFMQAFGHOEBINLNLV 337
DB 290 LLLCCCKMSAVVVTTRNSNVASVNGTVPPLLEQLSQDSWTLFCERAFRTGVAKSCFEV 349
QY 338 AIGSEIYKKGCGVPLAATLGILRFKREERQWHEVRSEIWKLPQSESSILPLRLSYH 397
DB 350 EIGTKIVKCGVPLAINSMGGLSRKRSVRDMLAIIONNTM---EENNLITVLSISKY 405
QY 398 HLPLDLRQCTFYCAVFPKOTEMEKNLISLMMAHGFIISKNLELENVGNVNNELYRS 457
DB 406 HLPBFMOCFAFCVAFPKDYELDKODLHLMIINSFISKETSDEEFGNKVFLLELMRS 465
QY 458 PFOGIEVKSQ-----TYFKMDLIHDLATS-----LFSASTSSSNIR 495
DB 466 PFOAKQKRSRKEEYIGKDVCTCKIHDLMDLAVSISGECYTLQVLVEINMKPKVH 525
QY 496 EIIYENITHMSIGT---KVSSYSLSHQKPSLVNLSDIKLKQULPSSI----- 545
DB 526 HLTV---PFPHPKIGFVMQRCPIIRSLFSLHAKRMDSMK---DVRFVNSCVRVGLAIC 577
QY 546 -----GDLVHLRYLNLSGNTSIRSLPNOLCKLOVLTLDLHGCHSLCCLPKETSKL 596
DB 578 GNEIFSVEPAYMKHRLYIDLSSDIKTLFRAVSAVLYNLQILMLANRCGGLTHLPDGMKFM 636
QY 597 GSLRNLILDGCGYGLTCEMPRIIGSLTCLTKLTSFVVGIOKKSQOLGELRNMLVYSIEITH 656
DB 637 ISLRHVYLDGCSLQRMPPGGLGQLSLARTLTMYVWG-NESDRRLHELKDLGGLQIHN 695
QY 657 LERKQMDAKBANLSAKENHLSLMKDD-----DERPRIVESKRYVLEALK 705
DB 696 LLLKTNPLQAAKBALENKKNLQOALCWDSDRNFTCSHSHSADDEVYQLCCPR--EYLDALK 753
QY 706 PHSNLTCTTIGFGRIGRLPDMWNHNSV-LKNVSIIEIISKCNKSCLPFGGELPCLKSIELW 764
DB 754 PPNGLKYLAKQYMGSDFFPMHMEGDTLQNTVKLSLRSSVNCVKLPFWQJLPFLBVLRLK 813
QY 765 RGSAAVEVVDGFPFRRR-----PFLARKLNIREFGNLKGLLKKEGE-----QCPYLE 813
DB 814 R-MERLAKYLGRVYPTDEYGNQLVVFQKLKLSLEMMESLENNHMYDTQQTSTVTFPRLD 872
QY 814 EIEIKCCP-MVITPLTSSVKLVSGKSDAIGPSISNLMAL-----TSLQIR----- 861
DB 873 AMEIIIDCKLTAALPNVPILKSLSLTGNKVLGLVSGISNLVLYLGAQSSRRVRITLYY 932
QY 862 -YNKE-----DASL- 869

```

```

DB 933 IYNGEREGSTDTKDEHILPDHLLSMGS/LTKLHQFNTPAPENYKSGHMMSVQDVLVS 992
QY 870 -----PEEMFKSL----- 877
DB 993 SCDFIOHEGLQSPLMFWISFGLOQLEIYWCDSLTWPBEERFSLTSEKLFYVDCKNF 1052
QY 878 -----ANLKYNISFYENL----- 891
DB 1053 TGVPEDLSARPSITDGGPCNLEFYQIDRCRPLVVPFPIFCLRTLVITHSNVLEGLPGCF 1112
QY 892 -----KEPFSLASLALNKLHLSHCYALSESIPERGKGLISLTOLSI 934
DB 1113 GCQDTLTTLVLIGCPSPSSLPASIRCLSNLKSLELASNNLSLSP-BGMQULTAALKLHF 1171
QY 935 TYCEMLQCPREGL-QHLTALNLSVECPPLAKRCCKGIGEDWKIAHIP 983
DB 1172 IKCPGITALPBGLOQRLHGLQTFVEDCPALARRCRG-GDYWEKXVDIP 1220

```

RESULT 14

```

ID 065XG9 PRELIMINARY; PRT; 1259 AA.
AC 065XG9;
DT 25-OCT-2004 (TREMBlrel, 28, Created)
DT 25-OCT-2004 (TREMBlrel, 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel, 28, Last annotation update)
DE Putative NBS-LRR resistance protein.
GN Name=OJ1126_B11.11;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OJ1126 B11 genomic sequence."
RL Submitted (SRP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC105767; AAU3948.1; -
SQ SEQUENCE 1259 AA; 142923 MW; 635FD2CC81B24AE7 CRC64;

```

Query Match 28.5%; Score 1463.5; DB 2; Length 1259;
Best Local Similarity 31.9%; Pred. No. 2e-74;
Matches 397; Conservative 190; Mismatches 371; Indels 287; Gaps 32;

```

QY 1 MAE---AFLOVLNDLTCFIOGELGLIFGKDEBEKLOSTFTTIOAVLEDAOKQKLDKA 57
DB 1 MAELISALLPALPKKAGSISTEPFSGIEHRSELYTLILAINOVITYGAEBOASKKPA 60
QY 58 IENMLQKLNAAVEADIIIDCKTEAPIRKKNKYG-----CYHPNVITFRHXI 106
DB 61 VKSMIAKLNAAACADALDELHYEA-LRSEALRGKHINSVAPAFSSHNPILFKRI 119
QY 107 GKRMKTKMEKLDVIAERIKFHL-----DERTIERQVATROGFVINEPOVYGRDKEK 159
DB 120 GKRLQOIYEQIDQVSGMQNGFPLNCPMPDER-----MQTVSYVDEQEVIGRQKER 171
QY 160 DEYKILINNNSAQTLVPLPIIGMGLGKTTIAQWVFNDQVIEHHPKIMICVSEDFN 219
DB 172 DEIITHMLLS--AKSDKLLIPIVIGIGIGKTTIAQVLENDVKVAHFQKHMMVCVSENF 229
QY 220 EKRLIKEIVESI--EEKSLGMDLAPLOKRLDLNGKRYLLVLDVWNEEDQDKAKLRQ 277
DB 230 VPDVKGITIDPAIGNDGLKSDNDELQORLREBSQGRYLLVLDVWNEEDQDKAKLR 289
QY 278 VLKVGASGASVLTTRLEKVSINGTLOPYELSNLSQEDCMLFMQAFGHOEBINLNLV 337

```

Db 290 LKSCSKMSAAVVVTRNSNVASVMGTVPDLALBQLSQSDSWTLFCERAFRTGVAKSCFV 349
QY AIGKEIVKKGCGVPLAATKLGILAFKREERQMEHVROSEIWKLPQESSILIPALRLSYH 397
Db 338 EIGKIVKKGCGVPLAATKLGILAFKREERQMEHVROSEIWKLPQESSILIPALRLSYH 397
Db 350 EIGKIVKKGCGVPLAATKLGILAFKREERQMEHVROSEIWKLPQESSILIPALRLSYH 405
QY 398 HLPDLROCFYCAVFPKOTEMEKGNLSLWMAHGFILSKGNLELENGENEVNNELYLR 457
Db 406 HLPSPMKQCFACVAFPPDYEDKODLIHIMINSFISKEISDLEEGNKVFLLELWRS 465
QY 458 FPOEIEVKSQ-----TYRKMDLIHDLATS-----LFASSTSSNIR 495
Db 466 FPOAKQCRSKREXYIKYKDVTTCKIKHLMHDLAVISGDECYTLQMLVINKPKVNH 525
QY 496 EIIYENVYIHMMSIGFTK-----VVSYSLSL-----SHLOKFPVSL-----RVLMISDIKJOL 541
Db 526 HLV---FPHPKIGVVMORCPILRSFLHKNHMSMDVFPWMSPCALGHIHCNDRF 582
QY 542 PSSIGDVLHRLYLNLSGNTSIRSLPNOCLQNTQTLDLHGCHSLCCLPKETSKLGSIRN 601
Db 583 SVEPAYMGLHRLYDLSSDIKTLPEAVSALYNIQLMLNRCRGLTHLPDGMKFMISLRH 641
QY 602 LLLDGCYGLTGMPPRIGSLTCLKTLSPFVVGIOKKSQGLRLNLNLYGSIEITHLERVK 661
Db 642 VYLDGSSSLQRMPPGLQGLSSLRITLYMVG-NESDCRLHKLKDLGKQLQIHNLKVT 700
QY 662 NDMDAKEANLSAKENLHLSMKMD-----DERPRIYSEKVEVLEALKPHSNL 710
Db 701 NPLQAKENLKNLQOLALCWSRNPTCSHCSADRYLOCRPE-EVDAIKAPENG 758
QY 711 TCLTIRGFRGIRLPPMNHV-LKNVSIIEIISCKNSCLPPFGLPCLKSLLEMRGSAE 769
Db 759 KVLKLRQYMGSNFPMWEDVTLQNIYKLSRGSVMCYKLPVWQPLFVLELRKR-MER 817
QY 770 VEYVDSGPPRR-----PESLRKINIRFGLKGLKKEGEE-----QCPVLEIRIK 818
Db 818 LKYLCTRPIDEEYGNOLVFOKTLKLSLEWMSLENNHEYDQVTSVTFPKLDAMEII 877
QY 819 CCP-MFYIPLTSSVYKLVSGDKSDAIGFSSISNLMAL-----TSLOIR-----YNKE 865
Db 878 DCPRLTALPNVPIKLSLSTGNKVLGLVSGISNLSYIYLGASGSSRRVTLTYINGE 937
QY 866 -----DASI----- 869
Db 938 REGSTDTEHILPDHLSWGLSTKLHLOGFNTPAPENVKISIGHMSVQDLVLSCDF 997
QY 870 -----PEEMFKSL----- 877
Db 998 IQHGLQSPLMFWISFGCLQOLLEIWCDSLTFWPEEERSLTSLKFLFYDCKNFTGVP 1057
QY 878 -----ANLKYLNISFYENL----- 891
Db 1058 DRLSARSTGGPCNLEIQLDRCPNLVFPPTNFCIRLIIVITDSNVLEGLPGFGCGT 1117
QY 892 -----KELPTSLASIALKLELHSCYALESLPEEGYKGLISLTQUSTYCEM 939
Db 1118 LTTLVILGCPSSFLPASIRCLSNLKSLELSTNNLSLTP-EGQONTALTKLTHFIKCP 1176
QY 940 LQCLPEGL-OHLTALTNLSVEFCPTLAKRCEKJGENDMYKIANHP 983
Db 1177 ITALPBGLOQRHGLQFTTVEEDCPALAKRCRG-GDYWEKVDIP 1220

RESULT 15
06ZJF7 PRELIMINARY; PRT; 1048 AA.
AC 06ZJF7;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, last sequence update)
DE Putative NBS-LRR resistance protein RGH1.
GN Name=OJ1521 G02.25;
OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoidae; Oryzae; Oryza.
OK NCBI_taxid=35947;
RN
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF003914, BAD08985.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; IRR.
DR Pfam; PF00560; LRR.1; 8.
DR PRINTS; PR00364; DISEASERIST.
SQ SEQUENCE 1048 AA; 119519 MW; 503FCD4D055000 CRC64;
Query Match 28.0%; Score 1436; DB 2; Length 1048;
Best Local Similarity 34.4%; Pred. No. 5,7e-73;
Matches 372; Conservative 199; Mismatches 377; Indels 134; Gaps 32;
QY 1 MAEAFLOVLIDNLTCTPIQSEL---GLIGFKDFEKLQSTFTTQVLEDAEQKQIKDK 56
Db 1 MABSLILPVVRGVGKAAGALVQSVTMCQVDGDRHKLRLQLALVQCKLSDAEAKSETSP 60
QY 57 ALENWLOKNAAYEADLLIDBECKTEAPTRQKK-----NKYGCYHP-VNIFRHKIGK 108
Db 61 AVKRMKMDLAVAYEADVDLDDHYEALRRDAQIGDSTDKVLGYFTPHSPLLFRVAMSK 120
QY 109 RMKIMEKLDVIAERIKFHLDERTTERQVATRQGVFLNEPO-----VYGRDKE 158
Db 121 KMSVLAKINELVEMNKKFLVER-----ADQATVHVH-PTHSGLSLMEIVGRDD 173
QY 159 KDEIVKILINNVNAQTLPLPLTGMGGLKTTLAQVFNDOYVIEHFAPKIVTCYSEDF 218
Db 174 KEMVNVILLEORSK-RWEVLESLIVGWSGLKTTLAKVNVNDTVQORFELPMWLCVSDPF 232
QY 219 NEKRLKEIYESIEEKSIGMD-LAPLOKKRLDLNGKTYLALDVVNNEODKMKLRQ 277
Db 233 NVSVLRSTIELATRGNTLPDRIELRSLHNVGGRKYLVLDDVWNEEKKMEBLR 292
QY 278 VL-KVAGSASVLTTRLEKVSIMGTLOPYELSNLSOEDCWLIFMORAFGHOEINLNL 336
Db 293 LHSAGAPGSVVLVTRSGRVASIMGTVPAHTLSYLNHDSWELFKKAFSKEEQPER 352
QY 337 VAIGKEIVKKGCGVPLAATKLGILAFKREERQMEHVROSEIWKLPQESSILIPALRLSY 396
Db 353 AETGNRIYKCKGKPLALKTGMGMSKRIQEWELIAGSKSWEDVGTNEIILSTIKLSY 412
QY 397 HLPDLROCFYCAVFPKOTEMEKGNLSLWMAHGFILSKGNLELENGENEVNNELYLR 456
Db 413 RHLPLEMKQCFACVAFPPDYEDKODLIHIMINSFISKEISDLEEGNKVFLLELWRS 472
QY 457 SFPQIEVKS-----QGYFK-----NHDLIHDLATSLFASSTSS--NIREIIVENYIHM 505
Db 473 SFPQDVKVESFHVIGIKQTYKSLTCYMHDLHDLAKSVTEECVDAQOLNOQKASKMDOVRL 532
QY 506 MSIG-----FTKVSSYSL-----SHLOKVSIRVNLNSI-----KLQPLS 543
Db 533 MSSAKIQENSELFFKHGPLHTLLSPYWSKSSPLR--NIKRNLVTSRLALHNDKLVNSPK 590
QY 544 SIGDVLHRLYLNLSGNTSIRSLPNOCLQNTQTLDLHGCHSLCCLPKETSKLGSIRNL 603
Db 591 ALASITHLRLYLDLSSHSKLEHLPDSICMLYSIOLALRNGCLQHLPEGRKRMSTKLRLHY 650
QY 604 LLDGCYGLTGMPPRIGSLTCLKTLSPFVVGIOKKSQGLRLNLNLYGSIEITHLERVK 662
Db 651 LIGCHSLAKMPPRIGLQKULRTLTTFVVD-TKQGGLEBKDLHHLGRLLELFINLKAIGS 709
QY 663 DMDAKEANLSAKENLHLSMKWDDDERPRIYE-----SEKVTLEALKPHSNLT 711
Db 710 GSNAREANLHIDENVTLELHWHCHD---IFEYSDHDPDLVDVNDKELVEFSLPSPSRLE 765

This Page Blank (uspto)

KLK-2007